SUPPORTING INFORMATION

Proteomic evaluation of the acute radiation syndrome of the gastrointestinal tract in a murine total-body irradiation model.

Weiliang Huang*, Jianshi Yu*, Jace W. Jones*, Claire L. Carter*, Keely Pierzchalski*, Gregory Tudor†, Catherine Booth†, Thomas J. MacVittie‡, Maureen A. Kane* §.

*University of Maryland, School of Pharmacy, Department of Pharmaceutical Sciences, Baltimore, MD; †Epistem Ltd, Manchester, UK; ‡ University of Maryland, School of Medicine, Department of Radiation Oncology, Baltimore, MD

§Correspondence:

Maureen A. Kane University of Maryland, School of Pharmacy Department of Pharmaceutical Sciences 20 N. Pine Street, Room 723 Baltimore, MD 21201 Phone: (410) 706-5097 Fax: (410) 706-0886 Email: <u>mkane@rx.umaryland.edu</u>

Retinoid analysis.

Retinoid levels were determined by liquid chromatography-multistage tandem mass spectrometry (LC-MRM³) which is an LC-MS/MS method utilizing two distinct fragmentation events for enhanced selectivity (Jones et al. 2015). Preparation of mouse intestinal tissue included flushing out contents with PBS. The jejunum and ileum were isolated from the small intestine and snap frozen with liquid nitrogen and stored at -80 °C until extraction. Tissues were homogenized in saline and extraction of retinoids was performed under yellow lights using a two-step liquid-liquid extraction that has been described in detail previously using 4,4-dimethyl-RA as an internal standard (Kane et al. 2005; Kane et al. 2008b; Kane and Napoli 2010; Jones et al. 2015). Levels of RA were measured using a Shimadzu Prominence UFLC XR liquid chromatography system (Shimadzu, Columbia, MD) coupled to an AB Sciex 5500 QTRAP hybrid triple quadrupole mass spectrometer (AB Sciex, Framingham, MA) using atmospheric pressure chemical ionization (APCI) operated in positive ion mode as previously described (Jones et al. 2015). Retinol and RE were quantified via HPLC-UV according to previously published methodology (Kane et al. 2008a; Kane and Napoli 2010). Retinoid levels were measured using n=5 per condition except for control (0) which is an average of n=15 unirradiated control mice euthanized at day -6 (n=5), day 0 (n=5), or day 6 (n=5). The statistical analysis relied on the unpaired Student's *t*-test between groups and the data was represented as means \pm standard deviation. Retinoid data are shown in **Supplemental Fig. 11** and Supplemental Fig. 12.

References.

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- Kane MA, Folias AE, Wang C, Napoli JL. Quantitative profiling of endogenous retinoic acid in vivo and in vitro by tandem mass spectrometry. Anal Chem 80: 1702-8; 2008b.
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Supplemental Figures

Supplementary Figure 1. Expression of proteins most changed after radiation. Minimum FC > 10 of expression for at least one condition and FDR adjusted ANOVA p < 0.01. Data shown as a function of dose on a given day after dose. Data shown as a function of time after dose at a given radiation dose is shown in **Fig. 1**.

Supplementary Figure 2. Canonical pathways altered by radiation. (2a) Canonical pathways altered after radiation where criteria for pathway changes was activation z-score > 2 for at least one condition and Fisher's exact test p < 0.01. (2b) Protein changes associated with the top three pathways altered by radiation. Minimum FC > 2 for at least one condition with a FDR corrected ANOVA p < 0.05. Data shown as a function of dose on a given day after dose. Data shown as a function of time after dose at a given radiation dose is shown in Fig. 2.

Supplementary Figure 3. Upstream regulators altered by radiation. Criteria for transcription regulators was absolute activation z-score > 2 for at least one condition and a Fisher's exact test p < 0.01. Data shown as a function of dose on a given day after dose. Data shown as a function of time after dose at a given radiation dose is shown in Fig. 3.

Supplemental Figure 4. Venn diagram of differential protein expression showing the effect of day after 8 Gy irradiation.

Supplemental Figure 5. Venn diagram of differential protein expression showing the effect of day after 10 Gy irradiation.

Supplemental Figure 6. Venn diagram of differential protein expression showing the effect of day after 12 Gy irradiation.

Supplemental Figure 7. Venn diagram of differential protein expression showing the effect of day after 14 Gy irradiation.

Supplemental Figure 8. Venn diagram of differential protein expression showing the effect of dose on day 1 after irradiation.

Supplemental Figure 9. Venn diagram of differential protein expression showing the effect of dose on day 3 after irradiation.

Supplemental Figure 10. Venn diagram of differential protein expression showing the effect of dose on day 6 after irradiation.

Supplemental Figure 11. Retinoid quantification in small intestine (jejunum) after TBI radiation. Radiation doses and times after radiation dose are notated. (a.) RA, (b.) ROL, (c.) RE. Retinoid levels were measured using n=5 per condition except for control (0) which is an average of n=15 un-irradiated control mice euthanized at day -6 (n=5), day 0 (n=5), or day 6 (n=5). The statistical analysis relied on the unpaired Student's *t*-test between groups and the Data is mean \pm standard deviation, * *p*<0.05 using student's *t*-test between groups as compared to control (0). Data shown as a function of time after dose at a given radiation dose. Data shown as a function of dose on a given day after dose is shown in **Supplementary Fig. 12**. RA=retinoic acid, ROL = retinol, RE=total retinyl esters

Supplemental Figure 12. Retinoid quantification in small intestine (jejunum) after TBI radiation. Radiation doses and times after radiation dose are notated. (a.) RA, (b.) ROL, (c.) RE. Retinoid levels were measured using n=5 per condition except for control (0) which is an average of n=15 un-irradiated control mice euthanized at day -6 (n=5), day 0 (n=5), or day 6 (n=5). The statistical analysis relied on the unpaired Student's *t*-test between groups and the Data is mean \pm standard deviation, **p*<0.05 using student's *t*-test between groups as compared to control (0). Data shown as a function of dose on a given day after dose. Data shown as a function of time after dose at a given radiation dose is shown in **Supplemental Fig. 11.** RA=retinoic acid, ROL = retinol, RE=total retinyl esters



ratio vs control

>10 5 2 1 0.5 0.2

<0.1

Pathways Protein Kinase A Signaling Acute Phase Response Signaling LXR/RXR Activation Insulin Receptor Signaling Integrin Signaling Actin Cytoskeleton Signaling ILK Signaling Role of NFAT in Regulation of the Immune Response Intrinsic Prothrombin Activation Pathway Leukocyte Extravasation Signaling VEGF Signaling 14-3-3-mediated Signaling Paxillin Signaling ErbB2-ErbB3 Signaling

1 day

Ηр

		3 d	ays		6 days								
8 Gy	10 Gy	12 Gy	14 Gy	8 Gy	10 Gy	12 Gy	14 Gy	8 Gy	10 Gy	12 Gy	14 Gy		

Z-score>2, p<0.01

Genes	g	L0 Gy	L2 Gy	l4 Gy	ğ	L0 Gy	l2 Gy	l4 Gy	g	L0 Gy	l2 Gy	l4 Gv
H3f3a	<i>w</i>				~				~			
Hist1h1c												
Hist1h1d												
Hist1h1e												
Ppp1r1b												
Gsk3a												
Map2k1												
Pde4c												
Ppp1r7												
Add3												
Mapk1												
Sfn												
Gna13												
Ptprc												
Ahsg												
C3												
Ср												
Fga												
Fgb									_			
Fgg												
Fn1												
Hmox2												

3 days

5/6 days



b

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Upstream regulators	С С	10 (12 (14 (С С	10 (12 (4	С С	10 (12 (14 (
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NOS2													
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IL22													
APP													
NR1I2													
IL10RA													
NFE2L2													
PRDM1													
MYC													
STAT3													
SMARCA4													
TGFB1													
ERBB2													
IL1A													
HNF1A													
EIF4E													
NR1H4													
PPARA													
HNF4A													
laG													
TP53													
CEBPA													
PPARGC1A													
Insulin													
Akt													
miR-1-3p													
EGF													
NR3C2													
PPARG													





8 Gy 6 Days









14 Gy 5 Days





SF10 12 Gy 6 Days



10 Gy 6 Days



