Screen of DNA Repair Genes in Colorectal Cancer

Andrew Taylor

Helen Louise Lee Undergraduate Research Award Supervising Professor: Dr. Erdem Bangi

Colorectal Cancer

•2nd Leading cause of cancer related death in the western world

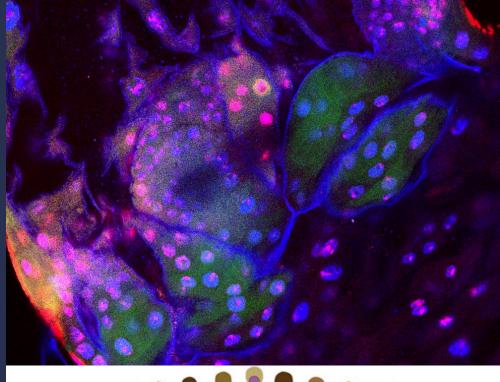
•1 in 20 people in the United States expected to have it over course of lifetime

Drug trials have low FDA approval rates (<5%)

Genetically complex and diverse disease

•Age of bioinformatics

 "Omics" data sets constantly expanding: transcriptomics, genomics, proteomics, epigenomics





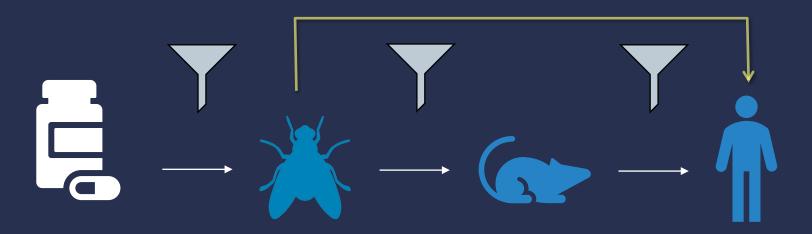
Drosophila Based Approach

•Over 90% of genes mutated in cancer have fly orthologs

 Practical Advantages as Model Organism: History, Life Cycle, Maintenance, Genetic Tools

•Drug Discovery Pipeline

•Fruit Fly Avatars of Human Patients



RPPA Cancer Model in Drosophila

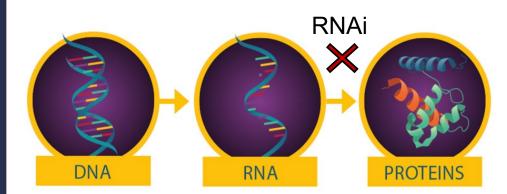
•Models 4 of the most frequently mutated genes in human colorectal cancer

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WNT pathy	vay	Represented by: UAS-apc ^{Ri}
APC	76%	
TCF7L2	14%	
AMER1	11% • ••••	
AXIN2	6% · • · • • • • • • • • • • • • • • • •	
CTNNB1	5% • • • • • • • • • • • • • • • • • • •	
FZD10	0%	
RAS/MAPH		Represented by: UAS-ras ^{G12V}
KRAS	41%	
BRAF	10% •	
NRAS	9% ••••	
ERBB2	6% • •	
ERBB3	6% •• •• ••	
PI3K pathw	vay	Represented by: UAS-pten ^{Ri}
PIK3CA	14%	
PTEN	6% ••••	
PIK3R1	4% • • • • • • • • • • • • • • • • • • •	
IGF2	2%	
IRS2	1%	
TGF-β path	way	Represented by: UAS-dSmad4 ^{Ri} (Med)
SMAD4	13%	
ACVR2A		
TGFBR2		
SMAD2	7% ••• • • •• • •••	
ACVR1B	7%	Variation of the second
SMAD3		
TGFBR1	3%	
TP53 path		Represented by: UAS-p53 ^{Ri}
TP53	52%	
ATM	12%	
	Genetic alteration: Amplification Deep deletion Missense mutation Truncating muta	ation

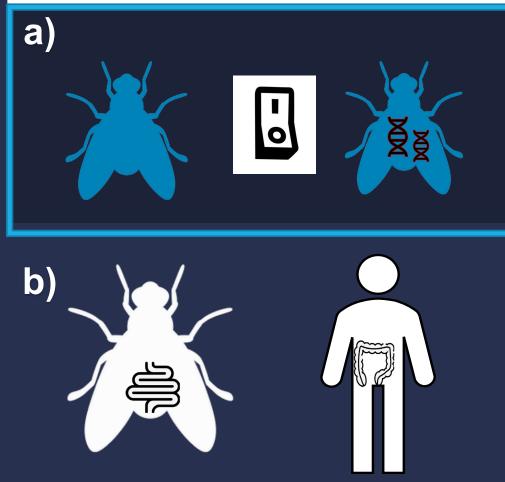
Bangi, E., Murgia, C., Teague, A. et al. Functional exploration of colorectal cancer genomes using Drosophila. Nat Commun 7, 13615 (2016)

RPPA Cancer Model

- Uses gene overactivation and knockdown to simulate cancer driving mutations in flies
- Cancer expression is
- a) Inducible
- b) Tissue Specific



Credit: National Cancer Institute



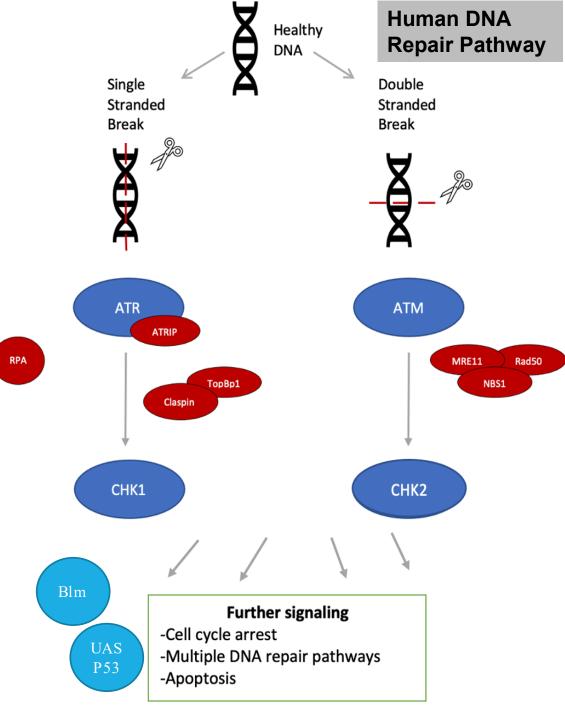
IDEA Grant Project

•Primary Question: How does reduced DNA repair gene expression affect tumor cells?

•DNA Damage Response essential for life

•DNA repair gene loss of function studied in RPPA Background





Functional Changes

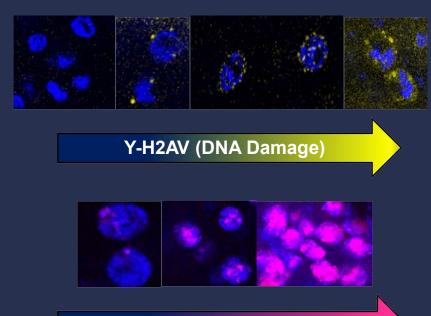
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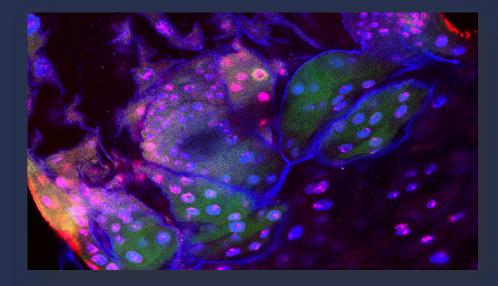


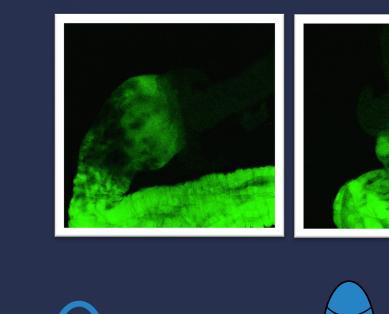
1. Analysis of cancer relevant proteins



H3K9me3 (Senescence)

- 2. Tumor size quantification
- 3. Organismal lethality



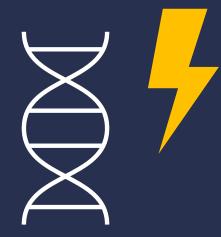


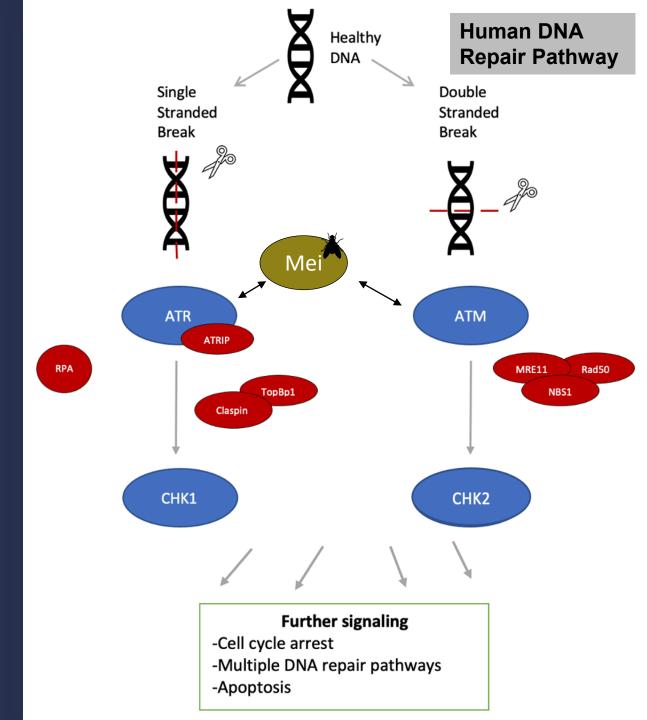
Results – Summary

Resolution of Data Collected

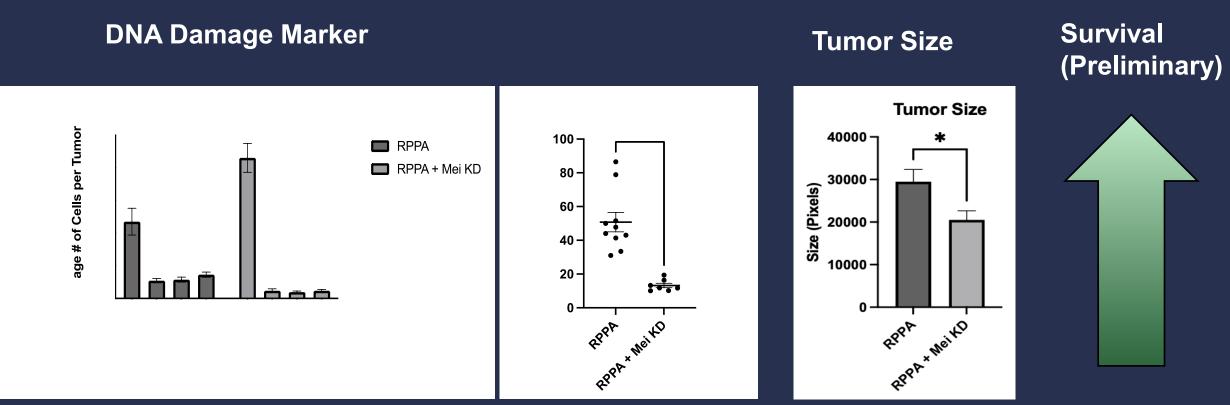
	Gene knock down in RPPA background											
	Mei	Tefu	Grp	Lok	Blm	UAS P53	Nbs	Mus 304	Mus 101	Mre11	RPA-70	Claspin
Senescence Marker Activity			?	1								
DNA Damage Marker Activity	↓ (large)	↓ (small)	ſ	1								
Tumor Size	\downarrow	-	-	?	-	-						
Survival (Preliminary)	Ţ	ſ	↑ *	\downarrow	Ţ	ſ	Ţ	ſ	Ţ	↑	Ţ	Ţ

Mei/ATR

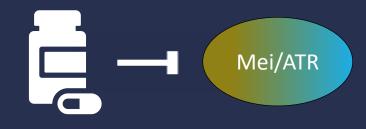




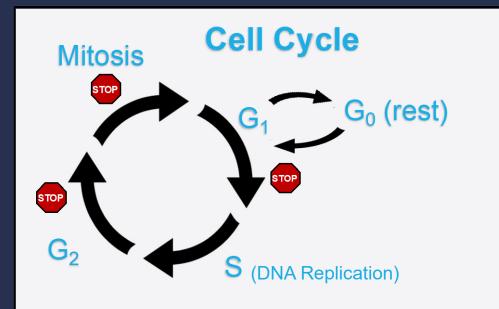
Results – Mei/ATR

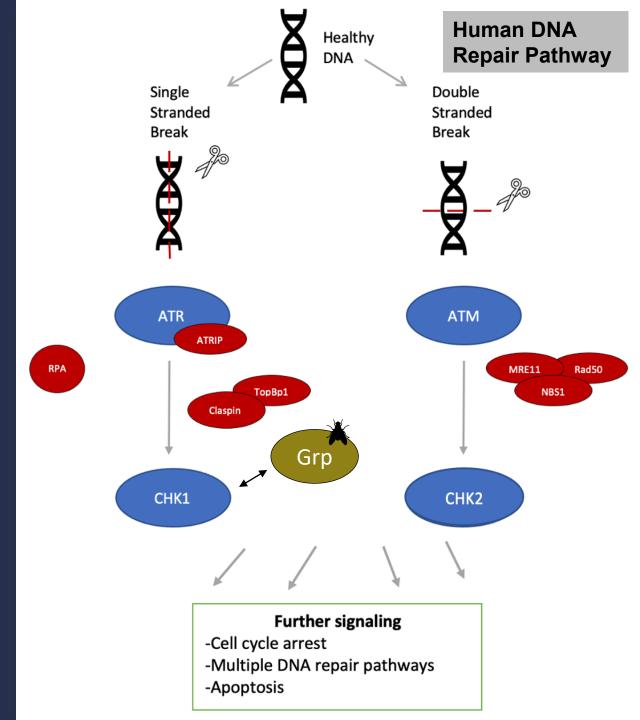


Conclusion: Decrease in activity of Mei/ATR might preferentially harm/limit tumor cells via some mechanism involving DNA Damage Detection



Grp/CHK1



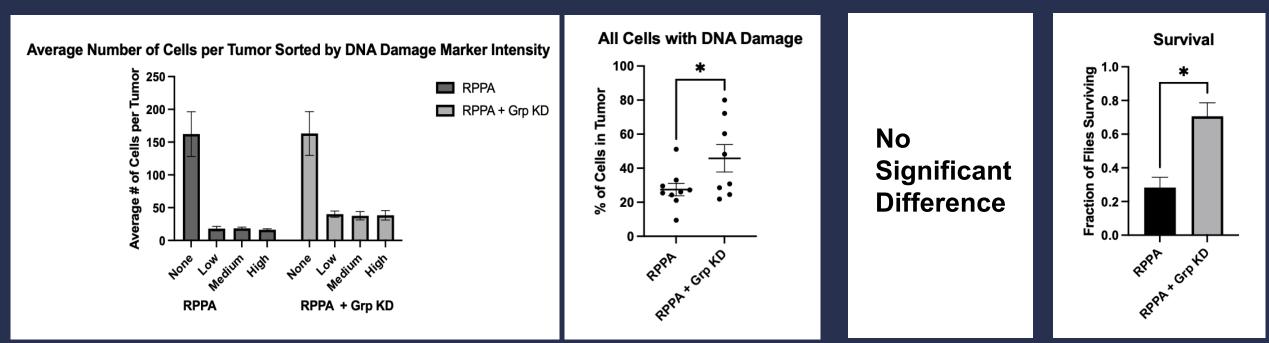


Results – Grp/CHK1

DNA Damage Marker

Survival

Tumor Size



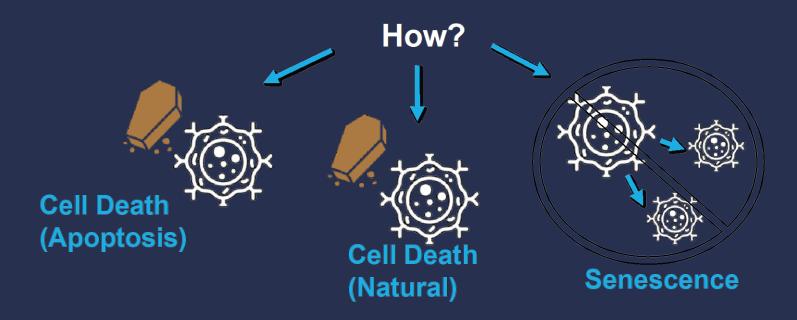
Conclusion: Decrease in activity of Grp/CHK1 enhances survival through some mechanism involving DNA Damage



Discussion - Survival

•Decrease in DNA Repair Gene Expression = Increased Survival

Gene Knockdown	Mei	Tefu	Grp	Lok	Blm	UAS P53	Nbs	Mus 304	Mus 101	Mre11	RPA-70	Claspin
Survival (Preliminary)	1	1	↑ *	\downarrow	1	1	1	1	1	1	1	Ţ



Closing Remarks – Why is this important?

- 1. Actionable targets for anti-cancer drugs
- 2. Screening in unique backgrounds
- 3. Better understanding of cancer
- 4. Broader applications



Acknowledgements

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