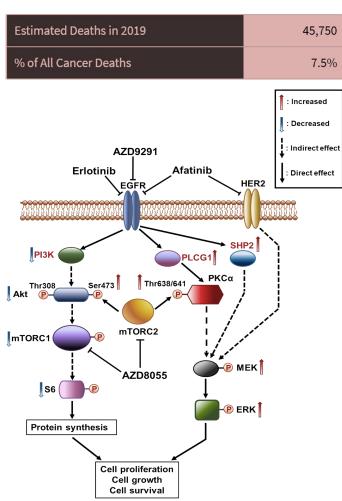


"To examine the combinatorial therapeutic effects of EGFR inhibitor and mTORC2 inhibitor for treatment of pancreatic cancer"

Paulomi Modi, Henry Vo, Celise Robertson, Xiaolian Gao Department of Biology and Biochemistry, University of Houston, Houston, Texas

Background

Statistics for pancreatic cancer deaths



Problem

- Pancreatic cancer is one of the most lethal cancer types that is associated with low survival rate and late diagnosis.
- Despite the highly progressive and aggressive nature of the disease, limited treatment options available for pancreatic cancer.
- Treating pancreatic cancer with a more molecularly targeted, precise approach based on the relevant signaling pathway and protein activities holds great potential to be clinically beneficial to the patients.

Objectives

- Treat cancer cells with a combination of mTORC2 and EGFR inhibitors.
- Observe the cell proliferation using MTT assay and confirm the results with western blot analysis.
- Determine the synergistic effect of drug combination for therapeutic purposes

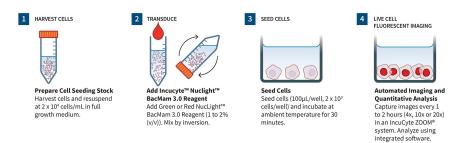
Materials and Methods

Cell Culture and addition of inhibitor

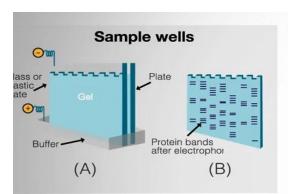
- BxPC-3 cells were seeded into a 96-well culture plate (8,000 cells in 100 µL of media per well) and allowed to growovernight.
- The next day, the media was removed and fresh media containing the inhibitor ofinterest was added to each well atdefined concen-
- DMSO and media without inhibitor (nodrug) were used as the controls.

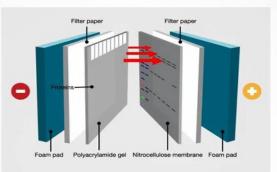
MTT assay

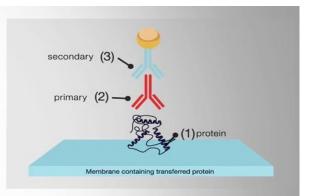
- · After 48 hours of incubation, MTT agent (Thiazolyl Blue Tetrazolium Bromide) was added and incubated for 3.5 hours
- Absorbance was measured spectrophotometrically at 570 nm and 620 nM wavelengths using the Molecular Devices SpectraMax Plus 384 Microplate Reader.



Western Blot







1. Separate proteins by gel electrophoresis

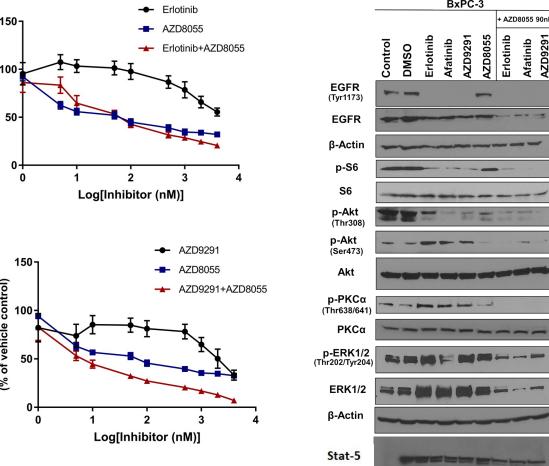
2. Transfer proteins from the gel to a solid support

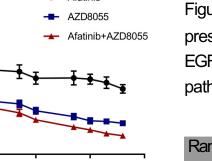
3. Detect Where we use antibodies specific to the target protein to visualize the protein of interest.

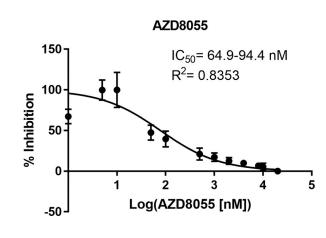
We used the conventional western blot to validate the endogenous protein expression in different EGFRitreatments. Such validation methods are specific and reliable but suffer from being low-throughput and time consuming.

Our future studies therefore aim to improve our peptide library design by utilizing other high-throughput proteomic technology such as mass spectrometry to experimentally validate all those known peptide-protein interactions of interest.

Results







Log[Inhibitor (nM)]

Figure. The data shown above is obtained from MTT assay. It is presented here as normalized %inhibition versus log (concentration [nM]).

IC50 values and SDswere acquired by fitting the data to a sigmoidal curve. GraphPad Prism v.7 software was used to obtain the datacurve.

							+ AZC	8055	90nM
	Control	DMSO	Erlotinib	Afatinib	AZD9291	AZD8055	Erlotinib	Afatinib	AZD9291
EGFR (Tyr1173)	-	-				-			
EGFR	-	-		-	-	_	-		=
β-Actin	-	-	_	_				-	-
p-S6			-		-		_		
S6		-	_	_	_	_	_	_	-
p-Akt (Thr308)			-	Street,	17	-	-	-	
p-Akt (Ser473)	-	-	-	-	-	-	-	-	-
Akt	•	-	-	-	-	-	-	-	-
p-PKCα (Thr638/641)	-			-	_	-			
ΡΚСα	1	-	-	-	-	-	-		-
p-ERK1/2 (Thr202/Tyr204)	-	-	100	F		-	-	- 6	
ERK1/2	1	=				-	-		-
β-Actin	-	_	_	_	_	_	-	-	-
Stat-5		-			-	-	-	-	

Figure. Western Blot data collection for expression of various proteins. Suppression of EGFR/Akt/mTORC1 and mTORC2/PKCa/ERK pathways can be observed with various

Range of combina- tion index	Description
<0.1	Very strong syner- gism
0.1-0.3	Strong synergism
0.3-0.7	Synergism
0.7-0.85	Moderate synergism
0.85-0.9	Slight synergism
0.9-1.1	Nearly additive
1.1-1.2	Slight antagonism
1.2-1.45	Moderate antago- nism
1.45-3.3	Antagonism
3.3-10	Strong antagonism
>10	Very strong antago- nism

Total Dose [AZD9291+AZD8055]	Effect		C	Cl Value		
5.0	0.579		0	0.07522		
10.0	0.6	0.603		0.07375		
50.0	0.7	0.740		.02036		
100.0	0.7	55	C	0.03347		
500.0	0.8	0.826		0.06678		
1000.0	0.850		0	0.09366		
2000.0	0.885		0	.10187		
4000.0	0.9	34	0	.06077		
8000.0	0.9	79	0	.01140		
10000.0	0.9	75	0	0.02033		
Total Dose [Afatinib + AZD8055] nM		Effect	(CI Value		
5.0		0.581	().06316		
10.0		0.554	C).30448		
50.0		0.656).04944		
100.0		0.681	0).04011		
500.0		0.761	0	0.00821		
1000.0		0.775	(0.00875		
2000.0		0.807		0.00372		
4000.0		0.823		0.00318		
8000.0		0.848		0.00148		
10000.0		0.855		0.00119		
Total Dose [Erlotinib+AZD8055]		Fa		CI Value		
5.0		0.338		185.990		
10.0		0.421		22.0276		
50.0		0.570		0.90654		
100.0		0.616		0.39534		
500.0		0.730		0.03159		

[Erlotinib+AZD8055]	Га	Ci value
5.0	0.338	185.990
10.0	0.421	22.0276
50.0	0.570	0.90654
100.0	0.616	0.39534
500.0	0.730	0.03159
1000.0	0.745	0.03462
2000.0	0.779	0.01672
4000.0	0.810	0.00873
8000.0	0.840	0.00485
10000.0	0.852	0.00372

Figure. Drug synergy was determined by calculating the combination index (CI) and fraction affected (Fa) at different concentrations using the Chou and Talalay method and CompuSynsoftware.

Conclusion

MTT cell proliferation data represented with the Q curve shows a significant decrease in cell viability when treated with the combination of EGFR and mTORC1/ mTORC2inhibitors. The EGFRinhibitors cause a reduced downstream regulation of Pl3K/Akt/mTOR signaling by inhibiting the EGFRphosphorylation. Afatinib is shows inhibitions of EGFRand HER2. Erlotinib and AZD9291 only inhibit EGFR.AZD8055 (mTORC1/mTORC2 inhibitor) that prevents the growth pancreatic cancer cells in combination with EGFRinhibitors (Erlotinib, Afatinib, AZD9291). Combinatorial treatment with EGFRi(Erlotinib, Afatinib, or AZD9291) and mTORi (AZD8055) improved anti-proliferative effects on BxPC-3 cell as compared to EGFRitreatment alone. This combination is shown to be synergetic by Chou and Talalay method, showing high synergetic drug combination at and above IC50.

National Cancer Institute, https://seer.cancer.gov/statfacts/html/pancreas.htmlhttps:/ www.essenbioscience.com/en/protocols/incucyte-cell-count-proliferation-assay-general-pr/ Vo, Henry et al. "Proteomic profiling of SH2domain-containing proteins and cellular signaling pathways using microfluidic peptide microarray", 2019 Molecular and proteomics, in revision. https://cf-images.us-east-1.prod.boltdns.net/v1/static/3663210762001/1b05f085-bfff-4275-bdaf-50add67d7cb5/fbc3d820-f8c5-4dfa-b62b-de2eeb54d5e5/1280x720/match/image.jpg