



Epigenetic Modulation of Ovarian Cancer Cells

Mr Jaydip Raut

ST7/ Research Fellow

Derby Teaching Hospitals NHS Foundation Trust
School of Medicine, University of Nottingham



Objective

- Recap what do we know already
- Understand Epigenetics in cancer
- Analyse the design, methods and results
- Discuss future works



What do we know so far

- A common feature of Cancer is:
 - high acid load in the tumour microenvironment
- To counteract cancer cell uses no. of mechanisms
 - Family of two pore domain potassium (K⁺)channels
- Previous studies have proven increased expression of voltage gated and K₂P in Ovarian cancer.



Epigenetics and Cancer

- Epigenetics is the study of mechanism that alter gene expression without changing the primary DNA nucleotide sequence.
- Several different types
 - DNA methylation,
 - histone modifications



DNA Methylation and Cancer

- Normally,
 - 80% of all nucleotides are found to be methylated in mammalian genomes.
 - Rest 20%, CpG islands remain hypomethylated.
- In Cancer,
 - the CpG islands are more methylated
 - Rest of the genome, are hypomethylated.



Hypothesis

Epigenetic modulation in ovarian cancer cells maintained in altered microenvironment affects cancer cell proliferation through pH-sensitive membrane proteins that include K^+ channels.

Aim

- Establish the relation between low pH_e and high pH_i and pharmacologic epigenetic modulation of SK-OV-3 cell lines.
- To investigate the level of expression of K^+ channels in cancer cells after epigenetic modulation
- Selection and designing of gene specific primers compatible for bisulphite converted genomic DNA.



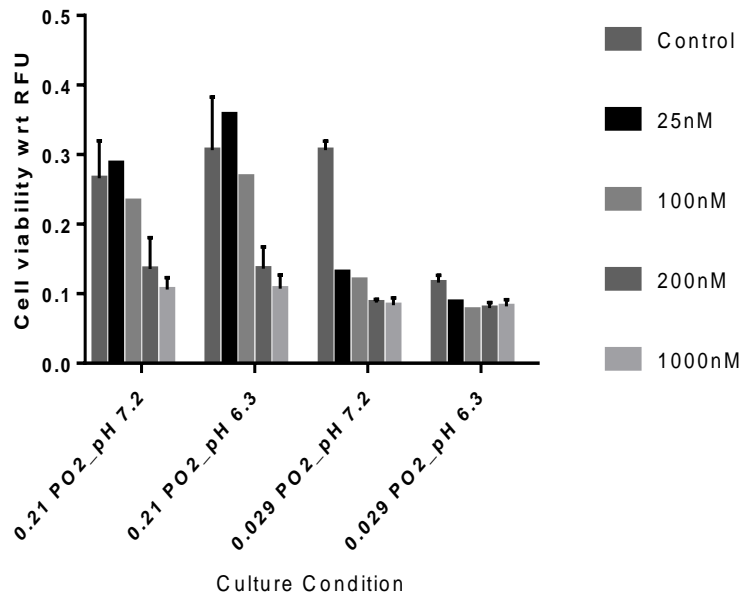
Design: Methods and Materials

- Proliferation of SKOV3 cells at pH_e 6.3 and pH_e 7.5 is assessed after exposing them to epigenetic modulation
 - 5-Azacytidine
 - Zebularine
 - Trichostatin -A
- Mechanism of action

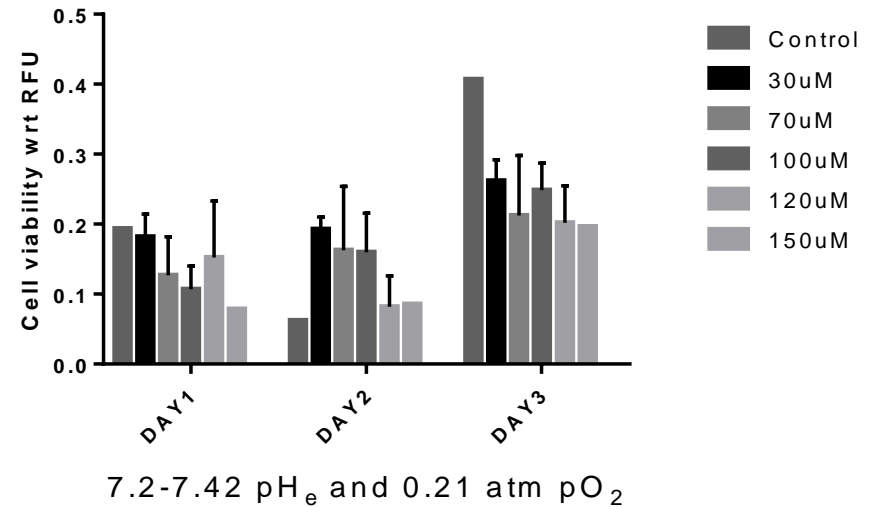


Results

TSA_Day3_Cell viability



Zebularine_Day123_cell viability



Relative Gene expression of K⁺Channel in presence and absence of ZEB





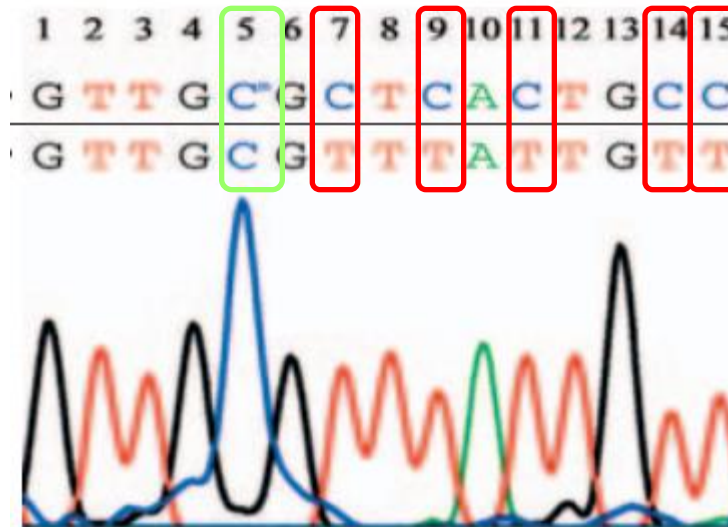
Further Works

- Detection of CpG islands adjacent to promoter region of *KCNK9*, *KCNK17*, *KCNK10* genes coding for TASK3, TALK2 *and* TREK2.
- Designing two sets of primers (compatible to Bisulphite conversion) for nested PCR reactions.



Bisulphite Treatment and conversion

- DNA with epigenetically modulated ($C^m pG$) was processed.
- The methylated cytosine remains intact.
- Unmethylated cytosines were completely converted into uracil following bisulfite treatment
- Detected as thymine following PCR.





The University of
Nottingham

Derby Teaching Hospitals 
NHS Foundation Trust

Any questions?



Summary

- K2P channels are overexpressed in Ovarian cancer
- Epigenetic modulation alters their expression
- Does the modulation alter the methylation status of the promoter region?



Acknowledgement

- Dr Raheela Khan
- Dr Christina Tufarealli
- Mr Ujjal Bose
- Mr Viren Asher
- Mr Anish Bali