CASE STUDY:
GENOMICS

Research Question

Can we identify mutations associated with high level methicillin resistance in Staphylococcus aureus (MRSA)?

Our Approach

We re-sequenced two S. aureus genomes and performed single-nucleotide polymorphism (SNP) analysis. SNPs were identified in the gdpP and ftsE genes. Both of these may contribute to antibiotic resistance and are being further investigated.

'The service by the Genomics Core was excellent. It was much faster and more efficient than our previous experience using a commercial company. It was invaluable to have access to the expertise of scientists in the Core when doing the sequencing and bioinformatic analysis.'

Dr Jim O'Gara
UCD

CASE STUDY:
GENOMICS

Research Question
Can RNAseq be used to gain a more complete and accurate picture of the bovine transcriptome? Can we avoid or reduce pooling of early bovine embryo samples in our experiments?

Our Approach
We carried out RNAseq experiments involving 150 individual bovine samples. The experiments encompassed early embryo development, cervix tissue in peri-oestrus period, endometrium during early pregnancy and theca and granulosa tissue of the ovarian follicle during the stages from selection to luteinisation. Many of the tissues were poorly characterised from a transcriptomic point of view and some, such as early embryo stages, presented additional problems of low sample quantity.

'The early availability of RNAseq technology and the support available in library preparation, including early access to new protocols, was critical in our ability to switch to the RNAseq technology for our gene expression experiments.'

Professor Alex Evans
UCD Reproductive Biology Research Cluster

Dr Paul McGettigan
postdoctoral fellow

GENOMICS

CORE TECHNOLOGIES
at UCD Conway Institute
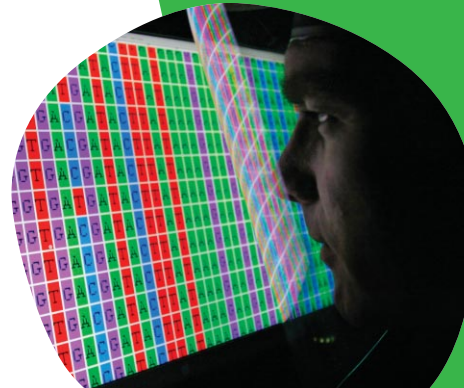
Research Question

Can we establish the transcriptomic profile of renal epithelial cells exposed to the profibrotic cytokine transforming growth factor beta (TGFB1) as an in vitro model of renal fibrosis?

Our Approach

Human kidney epithelial cells (HK-2) were stimulated with TGF-β1 and three independent experiments gave rise to six samples for RNA-Seq analysis. We identified 2027 differentially expressed genes using RNA-Seq and then validated the responses of several genes in our *in vitro* model using TaqMan Real-Time PCR. Subsequent promoter analysis of transcription factor binding sites in the TGF-β1 responsive gene set allowed us to predict the activation of multiple transcriptional networks, including NFκB.

'The use of the Genomics Core is an invaluable service for our research into the mechanisms underlying renal fibrosis. In particular, as part of our RNA-seq experiment, we received considerable advice from staff on the design and execution of these experiments.'

Professor Catherine Godson, *UCD*

Dr Eoin Brennan, *postdoctoral fellow*

CORE TECHNOLOGY:
GENOMICS

OUR EXPERTISE:

Offering genomics solutions to academic and commercial clients in a customisable range of services at each stage of the research pathway; from experimental design to final publication.

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Register your interest here:
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