

**Project number:** 6192  
**Funding source:** Science Foundation Ireland (SFI)

**Date:** Dec, 2018  
**Project dates:** Sept 2011 - Aug 2014

## An examination of the molecular control of nutrient digestion and absorption in the gastrointestinal tract of cattle undergoing compensatory growth



### Key external stakeholders:

Livestock industry, Animal nutrition and feed companies, Universities, Veterinarians, AI industry, Department of Agriculture, Food and the Marine, Irish Cattle Breeding Federation (ICBF).

### Practical implications for stakeholders:

- In animals undergoing compensatory growth there was evidence for prioritization of recovery of rumen and gastrointestinal tract tissues ahead of other tissues/organs examined, during the re-alimentation period.
- The structural integrity of the rumen may be compromised following a period of dietary restriction, however this is quickly reversed upon re-alimentation during compensatory growth
- Genes and pathways involved in digestion and metabolism, cellular growth and differentiation as well as immune function and cellular detoxification were the most affected molecular processes during both dietary restriction and subsequent compensatory growth.
- Genes identified as differentially expressed will be further interrogated for potential use as molecular biomarkers for the selection of cattle with a greater propensity to display compensatory growth.

### Main results:

- Rumen epithelial genes involved in ketogenesis, pyruvate metabolism and cellular structure were affected by dietary restriction and subsequent re-alimentation in cattle, suggesting an effect of dietary restriction and compensatory growth on rumen epithelial function through altered integrity of the rumen wall.
- The rumen epithelial transcriptome was affected by both dietary restriction and subsequent compensatory growth through alterations to the expression of genes involved in processes including gene transcription and protein folding, cellular interactions and organization as well as immune function.
- The jejunal epithelial transcriptional profile was affected by both dietary restriction and subsequent compensatory growth through alterations to the expression of genes involved in processes including digestion and metabolism; cellular growth and differentiation; and immune function and cellular detoxification.
- Genes identified as altered during compensatory growth may be targeted for the identification of genetic variants for the selection of animals to display enhanced compensatory growth. This information could contribute to national and international genomically assisted selection breeding programmes for the selection of cattle with a greater propensity for compensatory growth.

### Opportunity / Benefit:

Key genes contributing to compensatory growth have been identified which may serve as molecular biomarkers for the selection of greater compensatory growth potential in cattle. Further investigation of these genes including their regulatory regions is warranted, this is in addition to the requirement to evaluate the DNA sequences of these genes in cattle varying in compensatory growth potential, which would aid in the discovery of genetic variants. Following appropriate validation, these genetic variants could be utilized as molecular biomarkers for enhanced compensatory growth in cattle.

## Collaborating Institutions:

UCD

**Teagasc project team:** Prof. David Kenny (PI)  
Dr. Sinead Waters  
Ms. Emma O'Shea  
Dr. Kate Keogh  
Dr. Paul Cormican  
Dr. Matt McCabe

**External collaborators:** Dr. Alan Kelly (UCD)

### 1. Project background:

In beef production systems, feed costs represent the largest variable cost accounting for up to 80% of the cost of production. Consequently any method that would reduce feed costs would be advantageous to the profitability and sustainability of the production system. Compensatory growth is a naturally occurring process whereby animals can display greater growth rates and enhanced feed efficiency upon re-alimentation following a prior period of dietary restriction. The incorporation of compensatory growth into beef production systems is common practice worldwide but particularly in pastoral based production systems such as in Ireland, where there is an opportunity to reduce overall feed costs by rebalancing feed demand from times of the year when feed is expensive (i.e., winter period) towards times when feed is cheap and plentiful (i.e., during the grazing season). Additionally during re-alimentation induced compensatory growth animals display improved feed efficiency. However although extensively utilized worldwide, knowledge of the underlying biological control contributing to compensatory growth is lacking, particularly in components of the body directly involved in digestion and metabolism. Evaluations have been made in relation to the physiological control regulating compensatory growth as well as in relation to nutrient partitioning. Studies have shown that the gastrointestinal tract, particular the reticulo-rumen complex are largely affected by both dietary restriction and subsequent compensatory growth through alterations in the size and weight of these organs. A greater understanding of the molecular control of compensatory growth may provide essential information to the discovery of DNA-based biomarkers which could be incorporated into genomic selection breeding programs to select animals that display enhanced genetic potential for compensatory growth following a prior period of dietary restriction. Furthermore a greater knowledge of the molecular mechanisms controlling compensatory growth may also be useful for the selection of animals that are more feed efficient. The aim of this project was to elucidate the molecular mechanisms controlling the expression of compensatory growth in cattle, focusing on components of the gastrointestinal tract, namely the rumen and jejunum.

### 2. Questions addressed by the project:

- What was the effect of restricted feeding and subsequent compensatory growth on rumen epithelial function?
- What effect does restricted feeding and subsequent re-alimentation have on the rumen epithelial transcriptome?
- Is the jejunal epithelial transcriptional profile altered in response to feed restriction and subsequent re-alimentation induced compensatory growth?

### 3. The experimental studies:

The objective of the first study was to examine the effect of an industry-typical period of feed restriction (125 days) and a subsequent period (55 days) of re-alimentation induced compensatory growth in Holstein-Friesian bulls to rumen epithelial function through an evaluation of transcript abundance of genes involved in pyruvate metabolism, ketogenesis, metabolite transport, cellular structure, growth and volatile fatty acid activation in rumen epithelial tissue.

1. The objective of the second study was to examine the differential expression of rumen epithelial genes in Holstein-Friesian bulls following a period of restricted feeding (125 days) and subsequent compensatory growth (55 days of re-alimentation) using RNAseq technology.
2. The aim of the third study was to examine the molecular control of compensatory growth in jejunal epithelium tissue of Holstein Friesian bulls following a period of feed restriction (125 days) as well as a period of re-alimentation induced compensatory growth (55 days) using RNAseq technology.

#### 4. Main results:

- Rumen epithelial genes involved in ketogenesis, pyruvate metabolism and cellular structure were affected by dietary restriction and subsequent re-alimentation in cattle, suggesting an effect of dietary restriction and compensatory growth on rumen epithelial function through altered integrity of the rumen wall.
- The rumen epithelial transcriptome was affected by both dietary restriction and subsequent compensatory growth through alterations to the expression of genes involved in processes including gene transcription and protein folding, cellular interactions and organization as well as immune function.
- The jejunal epithelial transcriptional profile was affected by both dietary restriction and subsequent compensatory growth through alterations to the expression of genes involved in processes including digestion and metabolism; cellular growth and differentiation; and immune function and cellular detoxification.
- Genes identified as altered during compensatory growth may be targeted for the identification of genetic variants for the selection of animals to display enhanced compensatory growth. This information could contribute to national and international genomically assisted selection breeding programmes for the selection of cattle with a greater propensity for compensatory growth.

#### 5. Opportunity/Benefit:

Key genes contributing to compensatory growth have been identified which could be harnessed following appropriate validation to identify molecular biomarkers for the selection of greater compensatory growth potential in cattle. Further investigation of these genes including their regulatory regions is warranted, this is in addition to the requirement to evaluate the DNA sequences of these genes in cattle varying in compensatory growth potential, which would aid in the discovery of genetic variants. Following appropriate validation, these genetic variants could be utilized as molecular biomarkers for enhanced compensatory growth in cattle.

#### 6. Dissemination:

Main publications:

O'Shea, E., S.M. Waters, K. Keogh, A.K. Kelly and D.A. Kenny. 2016. Examination of the molecular control of ruminal epithelial function in response to dietary restriction and subsequent compensatory growth in cattle. *J. Anim. Sci. Biotech.* 7(53).

Keogh, K., S. M. Waters, P. Cormican, A.K. Kelly, E. O'Shea and D.A. Kenny. 2017. Effect of dietary restriction and subsequent re-alimentation on the transcriptional profile of bovine ruminal epithelium. *Plos One.* 12(5):e0177852.

Keogh, K., S. M. Waters, P. Cormican, A.K. Kelly and D.A. Kenny. 2018. Effect of dietary restriction and subsequent re-alimentation on the transcriptional profile of bovine jejunal epithelial cells. *Plos One.* 13(3):e0194445.

Popular publications:

O'Shea, E., S.M. Waters, A.K. Kelly, P. Cormican, K. Keogh and D.A. Kenny. The effect of feed restriction and realimentation on the transcriptome of bovine jejunal epithelium. Proceedings of the British Society of Animal Science 2014, Nottingham, 29th and 30th April, p90.

Keogh, K., S. M. Waters, P. Cormican, A.K. Kelly and D.A. Kenny. 2016. Response of bovine jejunal transcriptome to dietary restriction and subsequent compensatory growth. Proceedings of the European Association of Animal Production 2016, Belfast, 29<sup>th</sup> August to 2<sup>nd</sup> September.

Keogh, K., S. M. Waters, P. Cormican, A.K. Kelly, E. O'Shea and D.A. Kenny. 2016. Transcriptional profile of bovine rumen papillae in response to diet restriction and re-alimentation. Proceedings of the European Association of Animal Production 2016, Belfast, 29<sup>th</sup> August to 2<sup>nd</sup> September.

#### 7. Compiled by: David Kenny and Kate Keogh