

Project number: 6019

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An examination of the physiological and molecular control of compensatory growth in cattle



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:

- Cattle displayed accelerated growth upon re-alimentation following a prior period of dietary restriction, growing at 1.8 times the rate of their non-restricted counter-parts.
- Cattle undergoing compensatory growth had lower feed conversion ratios indicating greater efficiency in these animals during re-alimentation.
- Genes and pathways involved in metabolism, cellular growth and division and energy production were the most affect 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:

- Cattle displayed accelerated growth upon re-alimentation following a prior period of dietary restriction, growing at 1.8 times the rate of their non-restricted counter-parts. Additionally, cattle undergoing compensatory growth had lower feed conversion ratios indicating greater efficiency in these animals during re-alimentation.
- Genes and pathways involved in metabolism, cellular growth and division and energy production were the most affect molecular processes during both dietary restriction and subsequent compensatory growth.
- Genes identified as differentially expressed during subsequent 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 beef cattle.

Opportunity / Benefit:

Key genes have been identified which may serve as molecular markers for compensatory growth. Further investigation of these genes including their regulatory regions is warranted. The use of next-generation sequencing technology, to examine the sequence of DNA from cattle varying in compensatory growth potential would aid in the discovery of DNA variants, which following appropriate validation, could be exploited as potential molecular markers for enhanced compensatory growth and feed efficiency in cattle.

Collaborating Institutions:

UCD
AFBI

Teagasc project team: Dr. Sinead Waters (PI)
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1. Project background:

Feed represents the single largest variable cost in livestock production and can account for up to 75% of the costs of beef cattle production. Therefore, any method that could reduce feed costs and improve overall feed efficiency would be favorable to the profitability and sustainability of the production system. The exploitation of the compensatory growth phenomenon is a common practice in beef production systems worldwide. It is particularly useful in pastoral systems as predominate 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). Studies in Teagasc have clearly shown that moderate feed restriction followed by compensatory growth typically results in increases in net margin in the region of €100 per animal with no negative knock-on effects on carcass output. Additionally, there is evidence for overall improved feed efficiency in animals undergoing compensatory growth. Although information on the physiological control of compensatory growth has been examined previously, primarily through examination of changes in body composition as well as in hormonal and metabolite response, knowledge of the underlying molecular control regulating compensatory growth is lacking. Additionally, due to variation in animal response to both dietary restriction and subsequent compensatory growth, knowledge of the genetic basis for this trait is critical to the future effective exploitation of the trait. An understanding of the molecular mechanisms regulating the expression 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 prior dietary restriction. Furthermore, knowledge of the molecular control of compensatory growth may also be useful for the selection of animals that are more feed efficient and environmentally sustainable. The aim of this project was to elucidate the molecular control of compensatory growth in cattle.

2. Questions addressed by the project:

- What was the effect of restricted feeding and subsequent compensatory growth on animal performance, muscle, fat and linear body measurements and slaughter characteristics?
- What effect does restricted feeding and subsequent re-alimentation have on blood pressure and systemic concentrations of metabolites and metabolic hormones?
- Does the signalling of the somatotrophic axis contribute to the expression of compensatory growth?
- Is the hepatic transcriptional profile altered in response to feed restriction and subsequent re-alimentation induced compensatory growth?
- Is the transcriptional profile of skeletal muscle altered in response to feed restriction and subsequent re-alimentation induced compensatory growth?
- Does insulin sensitivity and signalling contribute to the expression of compensatory growth?

3. The experimental studies:

1. The objective of the first study was to examine the effect of an industry-typical period of feed restriction on feed intake and efficiency, live weight, ultrasonically measured fat and muscle, carcass and non-carcass component growth of Holstein Friesian bulls during both feed restriction and re-alimentation.
2. The objective of the second study was to evaluate the metabolic rate and the response of key metabolic hormones and metabolites associated with feed intake, energy utilisation and growth to restricted feeding and subsequent re-alimentation in cattle, in order to characterise their contribution to the compensatory growth process
3. The aim of the third study was to examine the effect of restricted feeding and subsequent re-alimentation on: (i) pituitary gland sensitivity to synthesise GH, the precursor to IGF-1 through utilisation of a GHRH challenge and (ii) hepatic transcript abundance of component genes of the

somatotropic axis.

4. The objective of the fourth study was to examine the differential expression of hepatic genes in cattle following a period of restricted feeding and subsequent compensatory growth using RNAseq technology.
5. The objective of the fifth study was to examine the molecular control of compensatory growth in *M. longissimus dorsi* tissue of Holstein Friesian bulls following (i) a period of feed restriction (120 days) and (ii) an initial period of re-alimentation (15 days) using RNAseq.
6. The objective of the final study was to (i) assess the pancreatic insulin response to a glucose tolerance test during both dietary restriction and re-alimentation and (ii) examine transcript abundance of genes governing glucose uptake and insulin signalling in skeletal muscle during feed restriction and re-alimentation.

4. Main results:

- Cattle displayed accelerated growth upon re-alimentation following a prior period of dietary restriction, growing at 1.8 times the rate of their non-restricted counter-parts. Additionally, cattle undergoing compensatory growth had lower feed conversion ratios indicating greater efficiency in these animals during re-alimentation.
- Genes and pathways involved in metabolism, cellular growth and division and energy production were the most affected molecular processes during both dietary restriction and subsequent compensatory growth.
- Genes identified as differentially expressed during subsequent 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 beef cattle.

5. Opportunity/Benefit:

Key genes have been identified which may serve as molecular markers for compensatory growth. Further investigation of these genes including their regulatory regions is warranted. The use of next-generation sequencing technology, to examine the sequence of DNA from cattle varying in compensatory growth potential would aid in the discovery of DNA variants, which following appropriate validation, could be exploited as potential molecular markers for enhanced compensatory growth and feed efficiency in cattle.

6. Dissemination:

Main publications:

Keogh, K., Waters, S.M., Kelly, A.K., Wylie, A.R.G. and Kenny, D.A. (2015) 'Effect of feed restriction and subsequent re-alimentation on hormones and genes of the somatotrophic axis in cattle' *Physiological Genomics* 47: 264 - 273.

Keogh, K., Kenny, D.A., Kelly, A.K. and Waters, S.M. (2015) 'Insulin secretion and signalling in response to dietary restriction and subsequent re-alimentation in cattle' *Physiological Genomics* 47: 344 - 354.

Keogh, K., Kenny, D.A., Kelly, A.K., Cormican, P., McCabe, M. and Waters, S.M. (2015) 'Effect of dietary restriction and subsequent re-alimentation on the transcriptional profile of bovine skeletal muscle' *PLoS One* (In review).

Popular publications:

Keogh, K., Kenny, D.A., Kelly, A.K., Cormican, P. and Waters, S.M. (2014) 'Feed restriction and subsequent re-alimentation affect the expression of oxidative phosphorylation genes in skeletal muscle of Holstein Friesian bulls' *Proceedings of the World Congress on Genetics Applied to Livestock Production*, Vancouver, 17th to 22nd August, paper 552.

Keogh, K., Kenny, D.A., Kelly, A.K., Cormican, P. and Waters, S.M. (2014) 'Effect of feed restriction and subsequent compensatory growth on the transcriptional profile of hepatic tissue in Holstein Friesian bulls' *Proceedings of the British Society of Animal Science*, Nottingham, 29th and 30th April, p89.

Keogh, K., Kenny, D.A., Kelly, A.K. and Waters, S.M. (2013) 'Hepatic expression of genes of the somatotrophic axis during dietary restriction and compensatory growth in Holstein Friesian bulls' *Proceedings of the British Society of Animal Science*, Nottingham, 16th and 17th April, p189.

7. Compiled by: Sinead Waters, David Kenny and Kate Keogh.