

Project number: 5665
Funding source: DAFF (RSF 06/0409)

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Localisation of milk production and tuberculosis resistance genes in cattle.



Key external stakeholders:
Scientific community

Practical implications for stakeholders:

This study has identified potential regions of the genome associated with milk production and susceptibility to bovine tuberculosis in Holstein-Friesian dairy cattle which can be used to help in identifying the mutations in the genome that are actually causing the differences in production and disease susceptibility among animals.

Main results:

- Regions of the genome were identified to be associated with milk production, corroborating previous international results on genome wide association studies as well as research on candidate genes undertaken by Teagasc.
- Regions of the genome were found to be associated with susceptibility to bovine tuberculosis.

Opportunity / Benefit:

Preliminary knowledge on the regions of the dairy cow genome associated with milk production and bovine tuberculosis. This information can be used in the search for the causative mutations affecting milk production and disease susceptibility

Collaborating Institutions:

Trinity College Dublin, University College Dublin, Department of Agriculture Food & Fisheries, Irish Cattle Breeding Federation

Teagasc project team: Dr. D. P. Berry
External collaborators: Prof. Dan Bradley (Project Leader), TCD
Dr. Simon More, UCD
Dr. Margaret Good, DAFF
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1. Project background:

There is currently a lack of information about the genomic regions that affect susceptibility to bovine tuberculosis (TB). Herd- and animal-level incidence of TB is approximately 5.0 and 0.2% in Ireland, respectively with an estimated control cost of €80 million per annum – this is unsustainable. Reduced genetic susceptibility of TB in Irish cattle will increase our competitiveness internationally. Increasing our knowledge on genomic regions associated with milk production, especially in grass based systems of milk production, will also be useful for scientists to help understand the biological mechanism underpinning genetic differences in milk production.

2. Questions addressed by the project:

Are there regions of the genome associated with milk production and bovine tuberculosis?

3. The experimental studies:

- The data used to determine if regions of the genome were associated with milk production came from 914 Holstein-Friesian AI bulls with progeny in Ireland and genotyped using the Illumina Bovine50 Beadchip. The variable of interest was milk production.
- The data used to identify possible regions of the genome associated with bovine tuberculosis were estimated breeding values for tuberculosis on 323 Holstein-Friesian AI sires with progeny that underwent a tuberculin test in Ireland. These estimated breeding values were generated in a previous project.
- Genome wide associations were undertaken on all data using genotype data on up to 50,000 genetic markers and different statistical approaches.

4. Main results:

- Regions of the genome were identified to be associated with milk production, corroborating previous international results on genome wide association studies as well as research on candidate genes undertaken by Teagasc.
- Regions of the genome were found to be associated with susceptibility to bovine tuberculosis.

5. Opportunity/Benefit:

Preliminary knowledge on the regions of the dairy cow genome associated with milk production and bovine tuberculosis. This information can be used in the search for the causative mutations affecting milk production and disease susceptibility

6. Dissemination:

No technology transfer occurred during this project because of the potential intellectual property associated with the results

Main publications:

Finlay, E.K., D.P. Berry, B.R. Wickham, E.P. Gormley, and D.G. Bradley. 2011. A Genome Wide Association Scan of Bovine Tuberculosis Susceptibility in Holstein-Friesian Dairy Cattle. *PLoS One*. (Submitted).

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