



### Diagnosing scours and respiratory diseases in calves

Scours and respiratory diseases are common causes of death in young dairy calves. On-farm, affected calves are often treated based on symptoms without identifying the microbes involved.

This project investigated the occurrence of viruses, bacteria and parasites in NSW dairy herds. It identified a much wider range of microbes than is routinely included in standard diagnostic tests. Some microbes associated with disease were also commonly present in healthy calves. The results suggest the presence of a microbe alone does not determine disease risk. Pathogen load, calf age and farm management practices also influence whether disease occurs.

The findings provide new insights to support future improvements in diagnosis, treatment and disease prevention strategies. They also provide a foundation for improved disease surveillance, including earlier identification of new or emerging

### Unlocking the potential of cows

Dairy UP's P2 project aimed to unlock the potential of dairy cows to achieve their genetic potential under NSW conditions.

P2 was a suite of seven projects that collectively explored ways to profitably increase both productivity and wellbeing in commercial settings.

- P2a: Cattle Longevity
- P2b: Early Alerts
- P2c: Milk as a Diagnostic Tool
- P2d: Diet and Heat Load
- P2e: Calf husbandry
- P2f: Infectious Diseases ('Infectome')
- P2g: Heifers early calving

This document provides a final update on P2f: Infectious Diseases.

disease-causing strains that may affect the dairy industry.

This project was closely linked with Dairy UP's P2b project – Early Alerts.

### Benefits

Earlier and more accurate identification of the microbes causing disease may help improve treatment decisions, reduce unnecessary antibiotic use and support efforts to minimise antimicrobial resistance.

Although this work focussed on NSW dairy calves, the diagnostic approaches developed may have broader application across Australian dairy regions. This may become increasingly important as extreme weather events and environmental change alter patterns of infectious disease.



## Research approach

The research team used an approach called “metagenomics” to identify bacteria and viruses circulating in NSW dairy calves. Metagenomics analyses all genetic material in a sample and compares it with sequence databases of all known organisms to sort out which organism is present in the samples.

This knowledge may help improve future diagnostic testing and inform future treatment decisions. This work involved visiting farms, collecting samples and laboratory sequencing.

A second part of the study investigated *E. coli*, one of the most common causes of infection in animals and humans, including the different genetic types present in calves and the occurrence of antimicrobial resistance.

In early 2023, the team received an additional \$434k in funding from the Australian Research Council’s Linkage scheme. This funding expanded work on microbial surveillance and helped build the knowledge base needed to improve future diagnostic tools for calf diseases.

### On farm samples

The Dairy UP team visited 72 dairy farms from all NSW dairying regions to collect nasal and faecal samples from calves up to 7 weeks old, including all sick calves and up to 10 healthy calves. In addition, samples were collected from up to 10 cows that had calved within the past 50 days.

Participating farmers were also asked to fill in a survey to gain insights into relevant management practices such as management of colostrum, bedding materials, nutrition, and calf rearing management. Survey responses were received from 52 of the farms.

### Sequencing

About 1900 nasal and rectal swabs were collected on the collaborating farms. These samples were sequenced to identify specific ‘strains’ of the microbes present.

## Key results

Many of the microbes detected were also present in healthy calves, showing that the presence of a pathogen alone does not necessarily mean it is

causing disease. The findings suggest factors such as pathogen load, calf age and farm management practices also influence whether calves become sick.

### Viruses

#### Rotavirus

An important finding was that Rotavirus A was found on almost all farms including some with vaccination programs.

The dominant genotypes were G6 and G10, which are both included in currently available vaccines. We need to further investigate if there are genetic differences within the genotype that may compromise the vaccine efficacy.

#### New viruses

The study also identified a range of viruses that were not previously thought to be common on NSW dairy farms. Here are some examples.

- The relatively recently discovered Kobuvirus was present on most of the farms tested.
- Adenovirus (not usually tested by labs) was present on half of all farms.
- Rhinitis A and Rhinitis B were commonly detected in calves with respiratory disease.

In addition, Pestivirus was found on 17 different farms.

The team prepared a series of [fact sheets](#), collating current knowledge about 11 diseases for farmers and vets.

### Bacteria

The team often detected genes known to be used by bacteria to cause disease. These genes are commonly found in *E. coli* and *Campylobacter* (associated with scours).

Most farms had *Mycoplasma*, but Mannheimia, Moraxella and Pasteurella were the bacteria most often associated with respiratory disease.

Bacterial disease patterns differed markedly between farms, highlighting the importance of management practices such as hygiene, colostrum management, calf housing and stocking density in disease risk.

### Parasites

The study identified several parasites associated with scours in calves, including Cryptosporidium



(“Crypto”), Entamoeba, Giardia and Coccidia, demonstrating the diversity of microbes involved in calf scours.

## Implications of findings

### Rotavirus

While the findings support routine vaccination for rotavirus, logistical issues can compromise its effectiveness and farmer confidence in the value of investing in vaccination.

Vaccinated cows pass antibodies to their calves through colostrum. An annual booster, given about six weeks before calving is required to ensure maximum colostrum antibody levels. This vaccine is sold in multi-dose vials with a limited shelf life once opened. This can pose a challenge in year-round calving herds where only a small number of cows calve each week. The cost per dose becomes prohibitive if the whole vial can't be used before expiry. The alternative is to use all the doses, which involves vaccinating some cows outside of the optimum timing.

This dataset provides a foundation for evaluating whether currently circulating virus strains are sufficiently similar to vaccine strains to provide adequate protection — a key question given that vaccine mismatch can substantially reduce efficacy.

### Salmonella

In the past, Salmonella has been considered an important microbe in calf scours and respiratory disease but Salmonella was only identified in one sample. Detection of Salmonella was rare in our study (preweaned calves), and with the methods used.

### Pestivirus

Pestivirus A is known to be an important virus in cattle. This virus was found on 17 farms in the study, with most possessing the 1c genotype, some with the 1a and 1b genotypes. The presence of even a single clinically sick animal should not be ignored, as it may signal a persistently infected animal circulating within the herd. A single case carries the risk of significant economic losses due to reproductive failure, calf mortality, immunosuppression leading to increased respiratory disease and overall ill-thrift,

resulting in chronic production losses such as reduced milk production and increased culling rates.

### Diagnostics and antimicrobial resistance

Scours is recognised as having multiple causes and not all of the potential pathogens are covered by the scours vaccine.

The findings also highlight limitations of current diagnostic approaches that test for only a small number of pathogens. Future diagnostic tools may need to consider pathogen load, calf age and farm-specific management practices when interpreting results.

The project established a baseline for monitoring antimicrobial resistance in disease-causing bacteria on Australian dairy farms, supporting future surveillance and antimicrobial stewardship efforts.

## PhD students

Two PhD students enrolled at the University of Technology Sydney (UTS) are working on the project.

[Zain Ul Abedien](#)

[Aleksandra 'Ola' Stanczak](#)

## Collaborators

The P2f project was a collaboration between researchers from Dairy UP, UTS, NSW DPI Elizabeth Macarthur Agricultural Institute, Scibus and the 72 participating dairy farms.

## Read more

### Fact sheets

[Bovine Norovirus factsheet](#)

[Bovine Parechovirus factsheet](#)

[Bovine Picornaviruses factsheet](#)

[Bovine Rhinitis A & B factsheet](#)

[Bovine Toravirus Breda factsheet](#)

[Bovine Adenovirus factsheet](#)

[Bovine Enterovirus factsheet](#)

[Bovine Giardiasis factsheet](#)

[Bovine Hunnivirus factsheet](#)

[Bovine Kobuvirus factsheet](#)

[Bovine Nebovirus factsheet](#)

[Bovine Pestivirus infection](#), NSW DPI primefact sheet



### Journal articles

Brito Rodriguez et al., *Next-generation detection in bovine respiratory and enteric diseases: metagenomic and amplicon sequencing insights into microbial diversity.* [Frontiers in Veterinary Science, Volume 13 2026.](#)

### Abstracts ADSA meeting, 2025

- Brito et al, The enteric and respiratory viral diversity of calves in health and disease – a state-wide study.
- Kida et al, Genetic diversity of Bovine Rotavirus in Dairy Calves with and without diarrhoea in New South Wales, Australia.
- Abedien et al, Microbial diversity in dairy calves: an insight of the resistome and virulome in health and enteric disease.
- Brito et al, Untargeted meta-transcriptomic methods to characterize the enteric

infectome of calves with and without diarrhea.

- Brito et al, Expression of virulence factors and antimicrobial resistant genes in total RNA sequenced from rectal swabs from diarrheic calves.
- Brito et al, The respiratory infectome of dairy calves characterized by a total RNA sequencing approach.

### P2 final report

### Project lead

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#### Delivery organisations



Department of Primary Industries  
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