



Kikuyu is a perennial pasture species commonly grown in NSW for livestock production.

It is classified as a C4 grass meaning it is adapted to warm or hot conditions. Kikuyu is fast growing and produces more dry matter – of higher quality – than other C4 grass varieties.

However, there’s still a lot to learn about Kikuyu, including understanding the cause of Kikuyu poisoning – a risk for livestock producers.

Kikuyu poisoning

Cattle deaths and illness officially linked to Kikuyu poisoning are rare but have been recorded in NSW over the past 20 years.

Kikuyu poisoning, or toxicity, is frequently associated with specific environmental conditions and new growth following heavy rain fall, often after a summer drought or prolonged dry conditions.

Cause

The compound or mechanism that makes Kikuyu

Unlocking the potential of Kikuyu

Dairy UP’s P1 project aims to unlock the potential of Kikuyu pastures used by NSW dairy farmers. P1 is a suite of five projects that collectively explore new management options to grow and utilise more Kikuyu over summer and increase the productivity of Kikuyu-based pastures.

P1a: Remote pasture management using advanced sensing technologies

P1b: Antinutritional Factors (toxicity)

P1c: Genetic Diversity of Kikuyu

P1d: Carbon on NSW dairy farms

P1e: Nutritional Value.

This document provides an update on P1b: Antinutritional Factors (toxicity).

toxic to cattle under these conditions is unknown. Kikuyu toxicity is difficult to research because of the unpredictability and rarity of Kikuyu poisoning. The only definitive way to determine if cattle have Kikuyu poisoning is a combination of the history, clinical signs, and specially looking for damage to the forestomach (necropsy findings).

Specific signs linked to Kikuyu toxicity include dehydration, sham drinking (trying to drink but unable), abdominal pain, unsteady gait, drooling and death. But not all cattle suffering from Kikuyu poisoning present with these signs. In some instances, animals may recover, although they will not be as productive as before, given the damage to the digestive system.

Some affected cattle are reported as Kikuyu toxicity cases; however, many remain



unreported, with their illness blamed on other causes or not investigated.

Project aim

DairyUP researchers wanted to find out why Kikuyu can become toxic, so dairy farmers can use the grass with confidence.

Providing clarity around Kikuyu toxicity would help dairy farmers and their understanding of the issue as well as inform future grazing management practices and research.

Ultimately, project findings could be used to develop new Kikuyu varieties that are less susceptible to toxicity events, diagnostic tests to evaluate pasture safety, in-field preventative treatments and treatments for affected cattle.

Benefits

Although Kikuyu poisoning is infrequent, it remains a risk and can prevent dairy farmers from unlocking all the benefits of Kikuyu.

Understanding the underlying reason for Kikuyu poisoning would enable dairy farmers to manage their herds and pastures with increased confidence. There would also be more assurance using Kikuyu as a feed option – potentially providing more homegrown feed alternatives year-round.

Kikuyu poisoning also affects beef cattle. Sheep and goats can also be affected, although they are less susceptible. Therefore, any findings could benefit Australia's entire livestock sector.

On-farm monitoring

The team collected and analysed grass and soil samples from properties across NSW. An average sample of grass from a paddock contains hundreds of microbial species and thousands of secondary metabolites.

Samples from unaffected farms provided a normal "baseline" for reference and comparison with "toxic" Kikuyu.

Dairy UP researchers from the NSW Department of Primary Industries and Regional

Development's Elizabeth Macarthur Agricultural Institute and the University of Sydney visited the farms affected by the following suspected Kikuyu poisoning events:

- 2018-19: Hunter Valley
- March 2024: Bega (unconfirmed).
- April 2024: Hunter Valley

Farmers on affected farms gave their observations of Kikuyu poisoning.

Samples were collected from the reference and affected farms and analysed for fungal and bacterial communities (microbiome analysis).

A technology called metabolomics was used to examine samples from the reference and affected farms. Metabolomics gives a "fingerprint" of the many compounds present in a grass sample. Researchers were able to identify potentially toxic compounds by comparing compounds in the database from the baseline and affected farms.

Findings

Metabolites: The team identified 7 metabolites that were consistently abundant in the leaf and stems from toxic samples but low or absent in the baseline samples.

Fungi: Samples from toxic pastures appeared to have less diversity and richness of fungi in the leaf and stem tissue. However, five fungi were more abundant in the toxic samples. Two of these are being further investigated as potential causes of kikuyu toxicity.

Greenhouse trial

In addition, PhD student, Vivien Tan set up a greenhouse trial to create the environmental conditions that are understood to precede Kikuyu toxicity. The trial pots contained soil collected from farms with a history of toxicity cases. It included three varieties:

- Whittet, the most common commercial Kikuyu cultivar
- a drought resistant variety in development
- a drought-tolerant variety in development.



She examined how the different varieties and their associated microorganisms, including fungi, respond to the greenhouse conditions to identify what role genetics plays in Kikuyu toxicity or if potentially toxic microorganisms flourish under these conditions.

An additional pot trial was undertaken with the addition of *Fusarium torulosum*, a fungus frequently found in affected Kikuyu pasture. The trial investigated how its abundance is affected by a drought/re-water cycle, which typically precedes a Kikuyu toxicity event. This fungal species is known to produce two metabolites known to cause stomach lesions in laboratory rats.

Findings

Microbiome: The fungal community was similar across the three varieties indicating there is no genetic effect.

There was also little difference in overall fungal community composition between the control and drought treatment pots. However, the fungal community composition was significantly impacted after the re-watering. This suggests that the microbiome is more responsive to extreme

wet conditions than dry conditions.

When *Fusarium torulosum* was added, there was no significant difference in *Fus. torulosum* abundance between the control and reduced-watering treatments. Results showed a significant reduction in *Fus. torulosum* abundance after a week of re-watering following the treatments. This indicates that *Fus. torulosum* abundance is not favoured by conditions associated to toxicity.

Collaborators

The P1b project is a collaboration between Dairy UP, University of Sydney and the NSW DPIRD.

Read more

Tan et. Al. 2025 Effect of drought on microbiome community and metabolite profiles in kikuyu.

[ADSA abstract.](#)

More info

Project lead

Barbara Brito

NSW DPIRD

barbara.britorodriguez@dpiird.nsw.gov.au

Delivery organisations



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