



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 toxicity – a risk for livestock producers.

Kikuyu toxicity

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 rainfall, often after a summer drought or prolonged dry conditions.

Cause

The compound or mechanism that makes kikuyu 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 specifically looking for damage

Unlocking the potential of Kikuyu

Dairy UP's PI project aimed to unlock the potential of Kikuyu pastures used by NSW dairy farmers. PI was a suite of five projects that collectively explored new management options to grow and utilise more Kikuyu over summer and increase the productivity of Kikuyu-based pastures.

PI a – Kikuyu: Remote monitoring

PI b – Kikuyu Investigating toxicity

PI c – Kikuyu: Developing new varieties

PI d – Kikuyu: Carbon on NSW dairy farms

PI e – Kikuyu: Nutritional value

This document is the final update on PI b – Kikuyu: Investigating toxicity.

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, to help find ways to prevent or manage it.

Providing clarity around kikuyu toxicity would



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 reasons for kikuyu poisoning would give dairy farmers more confidence using kikuyu as a feed option – potentially providing more homegrown feed alternatives year-round.

Any findings could benefit Australia's entire livestock sector. As well as affecting dairy and beef cattle, kikuyu poisoning can also affect sheep and goats, although they are less susceptible.

Key findings

Findings from this research weaken the evidence for *Fusarium torulosum* as the primary cause of kikuyu toxicity. Although this fungus was previously found in affected pasture, our results suggest other plant or microbial compounds may

be involved.

This work provides a foundation for future diagnostic tools and evidence-based pasture management strategies to help reduce toxicity risk.

Supporting findings:

- Kikuyu variety strongly influenced plant metabolite profiles, suggesting some cultivars may carry lower toxicity risk.
- Seven compounds were consistently elevated in leaf and stem samples from toxic pastures, making them strong candidate biomarkers of toxicity.
- Re-watering after drought triggered greater biological change in kikuyu grass than drought alone.
- *Fusarium torulosum* declined after re-watering and was not consistently associated with toxic pastures.
- One fungal species was consistently elevated in toxic pastures and warrants further investigation.

More info

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Research and results

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 and historically affected farms provided a reference “baseline” for comparison with samples collected during active or suspected kikuyu toxicity events.

Dairy UP researchers 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 collected from the reference and affected farms were 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 identified potentially toxic compounds by comparing compounds in the database from unaffected and affected farms.

Findings

Several fungal species were significantly more abundant in toxic samples. One fungal species was consistently elevated across leaf, stem and soil samples from toxic pastures. It is now being investigated further as a potential contributor to kikuyu toxicity.

Importantly, *Fusarium torulosum* – a fungus frequently found in affected kikuyu pasture – was not significantly enriched in toxic pasture samples. This fungal species is known to produce metabolites that can cause stomach lesions in laboratory animals.

Metabolites: The team identified seven metabolites that were consistently elevated in both leaf and stem tissue from toxic samples but low or absent in the unaffected and historical samples. These compounds are considered the strongest candidate biomarkers or potentially toxic compounds identified in the project to date.

Fungi: Samples from toxic pastures appeared to have less diversity and richness of fungi in the leaf and stem tissue.

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 drought and re-watering conditions. The aim was to determine whether genetic background influences the fungal microbiome or plant chemistry associated with kikuyu toxicity risk.

An additional pot trial involved inoculation with *Fusarium torulosum* to investigate how its abundance is affected by a drought/re-water

cycle, which typically precedes a kikuyu toxicity event.

Findings

Fungi: There was also little difference in overall fungal community composition between the control and drought treatment pots. However, the fungal community composition changed significantly following re-watering. This suggests rehydration has a much greater impact on the microbiome than drought conditions alone.

Genotype also influenced some fungal communities, particularly in root and soil samples, while plant genotype was the strongest factor influencing metabolite profiles.

When *Fusarium torulosum* was added, there was no significant difference in *Fus. torulosum* abundance between the control and reduced-watering treatments. Its abundance declined significantly after re-watering following drought treatment. This suggests the conditions associated with kikuyu toxicity do not favour proliferation of this fungus.

Metabolites: Analysis also showed that kikuyu genotype strongly influenced plant chemistry, with clear differences in the types and abundance of compounds produced by different varieties. Re-watering after drought triggered larger biological changes than drought alone, supporting field observations that toxicity events are most commonly associated with rapid regrowth following drought-breaking rain or irrigation.

Importantly, two metabolites previously linked to *Fusarium torulosum* (wortmannin and butanolide) were not detected in the pot trials.

Together, the findings weaken the evidence for *Fus. torulosum* as the primary cause of kikuyu toxicity and suggest other plant or microbial compounds may be involved.

Collaborators

The PI b project was a collaboration between Dairy UP, University of Sydney and NSW Department of Primary Industries and Regional Development's Elizabeth Macarthur Agricultural Institute (DPIRD- EMAI).



Read more

[PIb final report](#)

Tan et Al. 2025 Effect of drought on microbiome community and metabolite profiles in kikuyu. [ADSA abstract.](#)

Delivery organisations



Department of Primary Industries and Regional Development



Partner organisations



Additional program supporters, collaborations or partnerships

Charles Sturt University | DairyBio | DataGene | Eagle Direct | Entegra
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