

Changes in mixed microbial inoculums to prevent the toxic side-effects in cattle grazing new varieties of *Leucaena*.

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Leucaena leucocephala is a legume fodder crop that grows in tropical and subtropical environments. *Leucaena* provides a high quality feed for cattle boosting liveweight gain both per animal and per hectare, improving profitability for steer turnover by 121% compared with the base scenario of grazing buffel grass (Bowen and Chudleigh, 2018). A number of commercial leucaena cultivars, Cunningham, Peru, Taramba, El Salvadore, and Wondergraze, are used in Queensland. *Leucaena* contains a toxic amino acid, mimosine, which many rumen bacteria can degrade to a toxic metabolite 3-hydroxy-4-(1H)-pyridone (DHP). Productivity from leucaena-pasture can be reduced by DHP-induced depressions in intake. A DHP degrading bacterium, *Synergistes jonesii* was isolated from a mixed bacterial population isolated from a goat from Hawaii (Allison *et al.*, 1992). For over twenty years DAF has provided a mixed bacterial rumen inoculum, containing *S. jonesii*, for cattle grazing Leucaena-pastures, produced in an *in vitro* fermentation system with Cunningham cultivar as the feed source. All of the commercial cultivars are susceptible to attack by psyllid insects, limiting their use in higher rainfall areas - to address this limitation, a commercial psyllid-resistant cultivar, Redlands, was released in 2019. To assess if the leucaena inoculum is impacted by Redland's anti-psyllid, chemical characteristics a series of 30 day *in vitro* anaerobic fermentations were undertaken feeding either Redlands, Cunningham or Wondergraze cultivars. The fermentations were conducted following the method of Klieve *et al.* (2002). Fermentations were started with either cryopreserved leucaena inoculum from a single day of a production fermentation; or day 30 of a Wondergraze or Redlands fermentation. Daily samples were taken and assays set up on days 10, 15, 20, 25 and 30 to monitor the fermentation's ability to break down mimosine, 3,4 DHP and 2,3 DHP. Genomic DNA extracted from daily samples was used in a *S. jonesii* quantitative PCR and for barcoded amplicon sequencing of the 16S rRNA gene V3 -V4 region using the Illumina MiSeq platform.

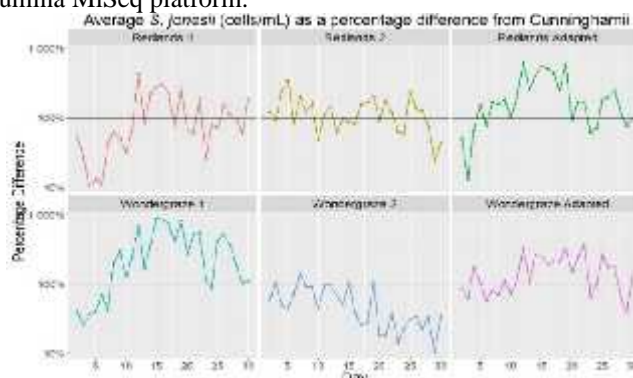


Figure 1. Average *S. jonesii* numbers present in fermentations fed either Wondergraze or Redlands, presented as a percentage difference with *S. jonesii* numbers in Cunningham fermentations set as 100 %.

Compared to the Cunningham fermentations, the Redlands 1 and 2 and Wondergraze 1 and 2 fermentations had an initial drop in *S. jonesii* numbers taking 10 days to build up to similar levels normally seen in Cunningham fed fermentations (Figure 1). The degradation of DHP was also compromised in Redlands and Wondergraze fed fermentations, with one not completely degrading DHP by day 30. Microbial diversity profiling was also used to monitor the effects of feeding different cultivars on microbial populations. These results will help determine if new inoculum formulations are required for cattle grazing different leucaena cultivars to be effective and maximise production benefits.

References

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