# Changes in abundance of ruminal bacteria associated with urea level and tannin supplementation in grazing beef cattle

Iorrano A. Cidrini[1]; Yury G. Salcedo[2]; Kênia Alves[2]; Laura F. Prados[3]; Gustavo Rezende Siqueira[3]; Flávio Dutra de Resende[3]

[1]Grant # 2018/00885-6 - São Paulo Research Foundation (FAPESP)- São Paulo; [2]São Paulo State University (Unesp), School of Agricultural and Veterinarian Sciences, Jaboticabal; [3]Agência Paulista de Tecnologia dos Agronegócios (APTA), Colina, São Paulo, Brazil

BOi777
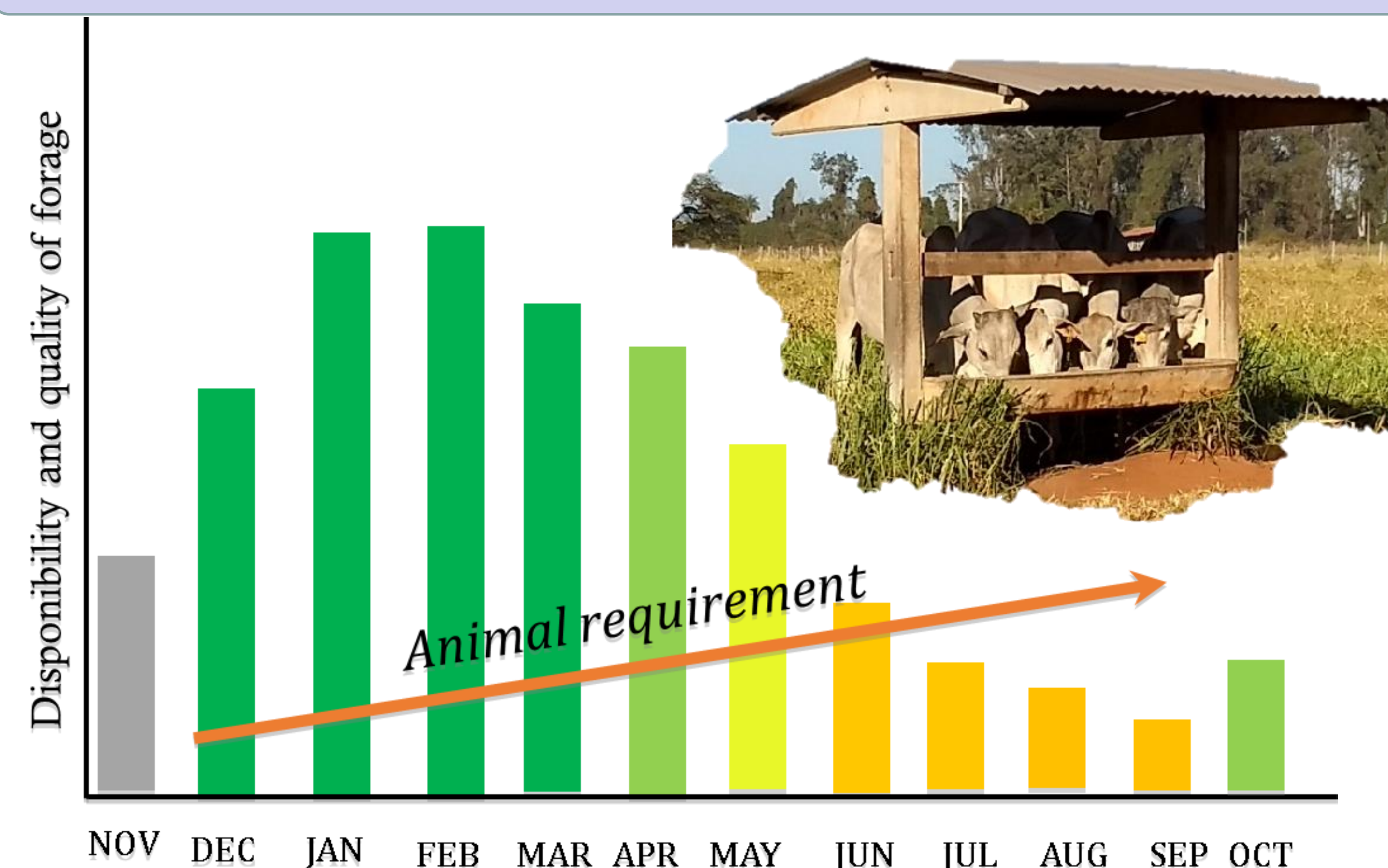
## INTRODUCTION



- Brazilian beef production systems;
- Growing phase:
  - → Dry season – low quality forage.
- Supplement composition – urea inclusion;
- Tannins extract;
- Rumen microbiology.

## OBJECTIVE

- The study was carried out to evaluate the effect of tannins extract (TN) associated to two levels of urea in the supplement of grazing beef cattle on ruminal bacterial abundance.

## MATERIALS AND METHODS

- Four rumen cannulated Nellore steers (293 ± 5.6 kg of BW) in a Latin square 4 x 4 (4 periods of 28 d);

- Steers grazing *Urochloa brizantha* cv. Marandu and were supplemented at 3 g/kg BW with soybean meal, corn, mineral mix and two levels of urea (3% or 5%) associated or not to TN (SilvaFeed-ByPro at 0.7 g/kg);

- LU = low urea without TN; LUT = low urea plus TN; HU = high urea without TN and HUT = high urea plus TN);

- Ruminal samples were collected 3h after supplementation;

- V3/V4 regions of 16SrRNA gene was sequenced;

- Quantitative Insights into Microbial Ecology (QIIME v.1.9.1) were used to filter reads and determine Operational Taxonomic Units (OTUs);

- DESeq2 differential abundance analysis were performed using each steer on LU as control and evaluated by Kruskal-Wallis rank sum test considering statistical significance at P < 0.10.

## RESULTS AND DISCUSSION

**Table 1.** Log2 fold change in abundance of ruminal bacteria associated with urea level and tannin supplementation in grazing beef cattle.

| Taxon | Supplement | | | | P - value |
|---|---|---|---|---|---|
| | LU | LUT | HU | HUT | |
| *Enterorhabdus.spp* | 1.00[a] | 0.208±0.389[c] | 0.784±0.974[b] | 0.579±0.736[bc] | 0.0493 |
| *Streptococcus.spp* | 1.00[a] | 0.608±0.676[b] | 1.352±0.084[a] | 0.478±0.632[b] | 0.0264 |
| *Fusobacterium.spp* | 1.00[a] | 0.698±0.030[b] | 0.988±0.011[a] | 0.601±0.083[b] | 0.0531 |
| *Synergistes.spp* | 1.00[a] | 0.496±0.993[b] | 0.839±0.978[a] | 0.396±0.834[b] | 0.0485 |
| Betaproteobacteria | 1.00[a] | 0.744±0.964[a] | 0.449±0.813[b] | 0.705±0.807[a] | 0.0483 |

*Names in bold and italics indicate class and genera level, respectively. Only taxa present in >80 % of the samples that showed significant change (P < 0.10) for at least one of the analyzed tests are shown.

## CONCLUSION

- In conclusion, TN reduced the ruminal population of important ruminal pathogens bacterial.