

## Characterisation of metabolites by 1D <sup>1</sup>H NMR in drip samples of lamb with confinement odour (#102)

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### Introduction

New Zealand exports more than 340 ton of lamb meat to 110 countries every year corresponding to around 40% of the global market. On rare occasions lamb meat displays "Confinement odour" (CO), which is an unpleasant smell observed immediately after the package is opened. While the CO dissipates quickly, consumers can easily mistake it for a sign of meat spoilage, even though the meat is microbiologically safe and wholesome to eat (Reis et al., 2016). The etiologies of confinement odour in lamb meat is not yet fully understood, and we hypothesize that metabolites present the drip samples as result of bacterial growth can contribute to better understanding of the production of CO. Thus the aim of this study was to measure metabolites profile in drip by Nuclear Magnetic Resonance (NMR) spectroscopy, in order to better understand the CO phenomenon in lamb meat on a molecular level.

### Methods

Individually vacuum packed commercial lamb legs with shank on were obtained from two commercial processing plants. Samples were submitted to various regimes of temperature/storage conditions as previously described by Reis, Reis, Mills, Ross, & Brightwell (2016) to generate a range of storage conditions prone to produce CO as well as the absence or presence of persistent odour (PO). Drip was sampled and stored at -80°C until analysis. 400 µL of drip was thawed and mixed with 800 µL ice-cold acetonitrile/methanol/ acetone (1:1:1) to precipitate the proteins. Following centrifugation, the supernatant was collected and the solvent evaporated. 1D NOESY NMR spectra were acquired on the reconstituted extracts on a Bruker Avance 700 MHz NMR spectrometer, using a 5 mm cryoprobe. D<sub>2</sub>O was used as a lock solvent and DSS as a chemical shift reference and internal standard for quantification. 1D <sup>1</sup>H NMR spectra were processed and metabolites quantified using the Chenomx NMR Suite Professional 7.7 software (Chenomx Inc., Edmonton, Canada). Canonical Partial Least Square (CPLS) was applied to investigate the association of the detected metabolites with presence of CO, visual assessment of meat, processing plant, pH and bacterial counts. The data analysis was carried out using the MixOmics package for R.

### Results

In this study we quantified 57 metabolites in drip samples. CPLS was applied to identify the association of the concentration of these metabolites with meat attributes including: pH, visual appearance, bloom, bacterial count, amount of drip and confinement odour, Reis et al. (2016). According to the

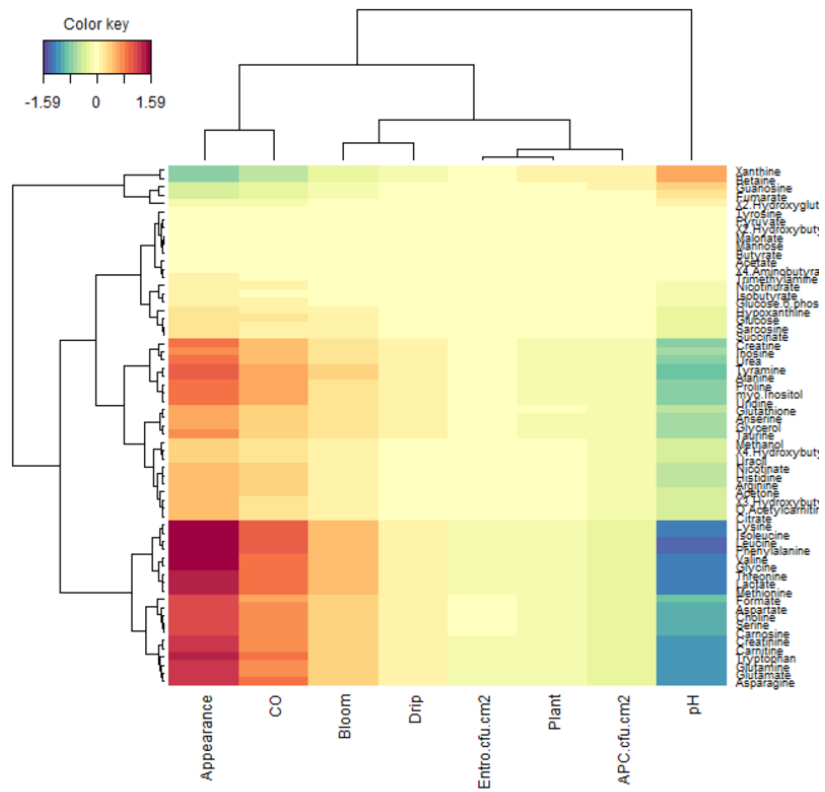
heat map of component 2 from CPLS (Fig. 1), the colours of the pixels indicated high positive correlation (red), high negative correlation (blue) or no correlation (yellow) between meat parameters and metabolites. The columns were ordered according to similarity among metabolites as assessed by hierarchical cluster analysis and expressed by the dendrogram on the top. This results show high positive association between confinement odour and metabolites associated to amino acid metabolism, while negative association is observed between these metabolites and pH. This could suggest that bacterial population has shift from use of glucose as carbon source to amino acids. These results are in alignment with the association between confinement odour and production of volatiles investigated by Reis et al. (2016).

### Conclusion

In conclusion, the CO phenomenon can be correlated with some metabolites indicative of bacterial population.

### References

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**Figure 1**  
 Correlation analysis of drip metabolite concentration data and various meat properties. Appearance: visual evaluated by a panel (Gribble et al., 2014); CO: confinement odour measured by three panellists; bloom: fresh cherry-red appearance after the package was open; drip: volume of drip from the meat; Entro: Enterobacteriaceae count; APC: Aerobic bacteria counts; pH: meat pH when the package was open.

## Notes