Prediction of 24h pH and lamb meat quality parameters in different muscle fibre types using rapid evaporative ionisation mass spectrometry

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Objectives: Accurate prediction of meat muscle quality is an important goal for ensuring that meat is graded for its most appropriate use, improving consumer experience and ensuring maximal return to farmers and meat processors. One of the key predictors of meat quality is pH, with high pH meat generally scoring badly for flavour and colour. Several technologies have been assessed for in-plant measurement of meat quality, though to date most meat processors still use visual inspection when evaluating carcass quality. Rapid evaporative ionisation mass spectrometry (REIMS) is a relatively new tool for direct measurement of samples, producing a fingerprint based on the metabolites and lipids present in the sample within a few seconds of a measurement. REIMS can be easily used on solid samples such as meat (Ross, Brunius et al. 2021) and has been successfully tested in abattoirs for detection of boar taint (Verplanken, Stead et al. 2017).

Materials and Methods: We hypothesised that within the REIMS fingerprint of lamb, there will be detected metabolites that are correlated with meat pH and other markers of meat quality. Because the proportion of high pH meat from New Zealand abattoirs is very low, we developed an exercise stress model to utilise muscle glycogen stores pre-slaughter to produce high pH meat (Lee et al., ICoMST 2022 abstract). Twenty ewe lambs (Coopworth, 6 months old) were divided into two equal groups, with one group kept quietly in pens prior to slaughter, and the other group run with a dog around a paddock for 30 minutes every hour for 4 hours prior to slaughter, simulating normal herding practices (LU-AEC, #2021-01). Lambs were stunned using captive-bolt and slaughtered by throat cutting. Each carcass was dressed and ten different muscles were removed within 30 min of slaughter, and snap frozen in liquid nitrogen for REIMS analysis. Those 10 muscles represented different muscle fibre types (predominantly fast/glycolytic: longissimus lumborum, longissimus thoracis, semitendinosus; slow/oxidative: supraspinatus, infraspinatus; and intermediate: semimembranosus, psoas major, gluteus medius, gracilis; one unknown muscle fibre type: sternomandibulous). REIMS analysis was carried out using a laser-assisted REIMS system in negative ionisation mode, collecting data between m/z 50-1200.

Results and Discussion: REIMS fingerprints clearly differed between different muscles and broadly clustered according to the pre- dominant fibre types. One muscle (sterno-mandibulus) with no defined muscle fibre type clustered with slow/oxidative muscles. This supports earlier work that found that lamb leg muscles readily clustered according to function. REIMS fingerprints differed between exercised and non-exercised lambs for both slow and fast muscle types, though different REIMS features explained the difference in these muscles. Similarly, correlations between observed and predicted 24 h pH and shear force loss were modest when including all muscles (r^2=0.4-0.5), but excellent when only modelling muscles of similar types together (r^2>0.95). Together these results suggest that while all muscles undergo changes in relation to the exercise stress, the impacts are not the same across all muscles, underlining the importance of assessing each muscle individually. Further work on determining if 24 h pH and shear force can be predicted in several muscles based on the REIMS measurement of one muscle will be carried out, along with tentative identification of potential biomarkers of meat quality detected by REIMS.

Conclusions: In this work we demonstrate that REIMS is able to distinguish between different muscles, and that this could be related to muscle fibre type. REIMS is also able to distinguish between muscles of lambs that have been exercised pre-slaughter compared to those who have not. Further work on validating these findings in a new study are underway. REIMS as an example of a direct analysis mass spectrometry method, shows promise as a tool that can combine the depth and detail of mass spectrometry-based metabolomics with the speed that is required for monitoring quality in modern meat processing plants. This project has been fund- ed by the New Zealand Ministry of Business, Industry and Employment Catalyst fund.

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