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Effect of step-wise dry-ageing and trimming on the metabolite profiles of dry-aged bull beef (#286)

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Introduction

Dry-ageing of beef has been extensively studied in the last decade, but the metabolite profile remains relatively unknown. Several amino acids (tryptophan, phenylalanine, valine, tyrosine, glutamate, isoleucine and leucine) have been reported to be more abundant in the dry-aged beef than the wet-aged [1]. Post-ageing trimming is a common practice to remove the dry and discoloured surface which results in a great loss. The combination of dry-ageing with wet-ageing as a step-wise dry-ageing process has been reported to produce equivalent and/or improved qualities in beef compared to dry-ageing alone [2]. Mass spectrometry-based metabolic fingerprinting using Rapid Evaporative Ionization Mass Spectrometry (REIMS) [3] was carried out to investigate the difference in the metabolite profiles arising from the different ageing methods and trimming practices.

Methods

Bull beef striploins were dry-aged using water-permeable ageing bags (TUBLIN® 10, Denmark) at a chamber set at 2 °C, 0.5 $m.s^{-1}$ air velocity and 75% humidity. Ageing treatment 1 (T1, n=6) used a step-wise dry-ageing method with 7 d of dry-ageing, followed by 14 d of wet-ageing, and ageing treatment 2 (T2, n=11) used straight dry-ageing for 21 d. Approximately 5 mm of the dry surface was trimmed from both T1 and T2. Untrimmed samples from T2 (n=5) was used to determine the impact of trimming. Samples were taken from three different positions; silver skin, trim (1 cm of the surface) and the centre of the meat sample for metabolomic profiling by REIMS on Waters Xevo® G2 QToF (Waters Corp., UK). The meat surface was electrosurgically cut with an electronic surgical knife (depth 5 mm × length 3 cm, five replicates per sample and sampling position) with 15 W power setting. The aerosol produced from the samples was analysed in negative ion mode with the mass range of 50−1500 m/z. The accurate mass of detected ions was measured and used to tentatively identify the chemical identity of the ions. Identification, mass peak integration, and normalisation against total abundance were performed using Progenesis QI (Waters, UK) and differences between methods and sampling sites determined using Orthogonal Projection to Latent Structures-Discriminant Analysis (OPLS-DA) (SIMCA, Umetrics, Sweden). OPLS-DA models were considered to be of interest if the Q2 score for predictability was >0.2. The mass peak areas between treatments were compared using one-way ANOVA with t-test to separate the means at $P<0.05$.

Results

A clear separation was observed between T1 and T2 with Q2 value of 0.852 suggesting that the current model was robust with good predictability towards data matrix (Fig 1a). Out of 1704 metabolites that were detected and tentatively identified (mainly amide derivatives of amino acids and lipids, sulphur-containing compounds and monosaccharide/sugar alcohol), approximately 11%, were significantly ($p<0.05$) more abundant in T1 than T2 (Table 1). This may have resulted from the metabolism of lipids and proteins by bacteria or fungus (yeast) in T1 during wet-ageing process. About 29% of metabolites from glycerophospholipid metabolism and/or lipid peroxidation, proteolysis (glutamate) and tyrosine metabolism (tyramine), were significantly ($p<0.05$) more abundant in T2 than T1.

Sampling position affected the metabolite profiles of dry-aged beef. Metabolites found from silver skin differed from that of the meat centre and the trim (Fig.1b) with a Q2 value of 0.401 suggesting an acceptable prediction was made in current data matrix. Metabolites from proteolysis and amino acids metabolism differentiated the metabolite profiles of silver skin from the meat centre. Only 6% of metabolites were significantly different ($p<0.05$) between the trim and the centre of meat. Meat centre was dominated by lipid metabolites. A higher level of beef flavour enhancing compounds (glutamate, glutamine and histidine) was found on the trim compared to the meat.

Conclusion

Metabolomic profiling in this study indicated that the step-wise dry-ageing may result in different metabolite profiles compared to dry-aging alone. Current metabolite profile of straight dry-aged beef may have resulted from metabolism of microorganisms and lipid oxidation. Further, trimming after dry-ageing may result in loss of several compounds that contribute to the flavour of dry-aged beef.

Acknowledgement

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References

[1] Kim, Y. H. B., et al. 2016, *Meat science*, 111: 168-176.; [2] Kim Y. H. B. et al. 2017, *Meat Science*, 123:57-63. [3] Balog, J., et al. 2016, *Journal of Agricultural and Food Chemistry*, 64(23): p. 4793-4800.

Notes

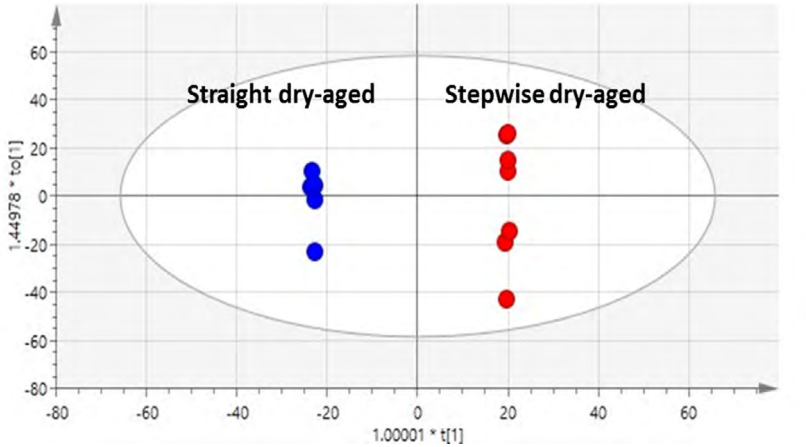

Fig 1.
OPLS-DA score plots of straight dry-aged beef vs. step-wise dry-aged counterparts.

	Putative compounds	Fragments (m/z)
Stepwise dry-ageing *vs.* Straight dry-ageing		
Higher in stepwise dry-ageing (T1, p<0.01)	2-Methyl-1-methylthio-2-butene	137.0
	Glycinamide	221.1
	Arachidonoyl amine	340.2
	Hexoses/Inositol	201.0
Higher in straight dry-ageing (T2, control, p<0.05)	Phosphatidylcholine/ Phosphatidylethanolamine	764.5
	Glycerophosphates	765.5
	Glutamate	128.0
	Tyramine/m-tyramine	410.2
Silver skin *vs.* Meat		

Table 1
Putative metabolites abundant in dry-aged sample with significant change between treatments.

Notes

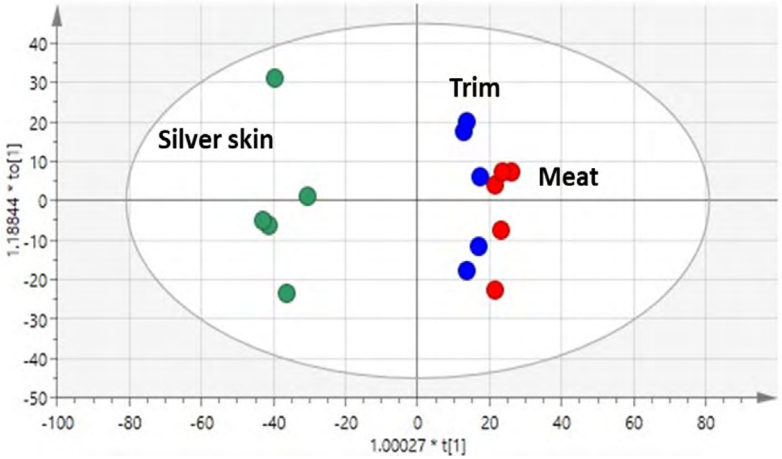

Fig 2.
OPLS-DA score plot of three sampling positions of straight dry-aged beef samples.

Notes