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Feeding the Next Generation Dairy Cow

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BULLETIN BOARD ABSTRACTS

Optimising the temporal distribution of dietary protein in early lactation dairy cows

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During the first two to three weeks of lactation (fresh period), dairy cows experience negative protein balance when requirements for maintenance and milk production exceed intake, and amino acids are mobilised from body tissue. As well as providing substrate for immediate milk protein synthesis, extra amino acids supplied at this time may promote mammary cell proliferation and/or influence nutrient partitioning, exerting effects beyond the fresh period. Previous research demonstrated that abomasal infusions of casein increased milk protein yield during the fresh period, with this difference potentially persisting into later lactation. However, this effect has not been translated into practical feeding strategies for implementation on commercial dairy farms using representative UK diets. We hypothesise that milk protein yield and nitrogen use efficiency in early lactation (defined for the purpose of this experiment as the first 49 days) will be higher when, for a given amount of dietary protein provided in early lactation, a higher proportion of that protein is offered during the fresh period. Forty multiparous Holstein-Friesian cows (blocked into two cohorts of 20 based on calving date) will be paired at calving and allocated within pair to one of two dietary treatments for the first 49 days of lactation. Treatment A (control) is a total mixed ration (TMR) formulated to contain 172g CP/kg DM. Treatment B comprises two TMRs formulated to contain 222g CP/kg DM (offered from day 1 to 14 of lactation) or 156g CP/kg DM (offered from day 15 to 49 of lactation). Using predicted dry matter intake, total intake of CP during the experiment is calculated to be the same for both treatments. Measurements are individual dry matter intake, milk yield and composition, body weight, body condition score and body fat and muscle depth (assessed by ultrasound). The first cohort of 20 cows have completed the experiment. The pattern of milk urea concentration throughout the experiment mirrored dietary CP concentration, confirming different patterns of protein consumption, as planned. Data analysis, and work with the second cohort of cows, is in progress.

The faecal phenotype: Can faeces be used to assess efficient starch provision?

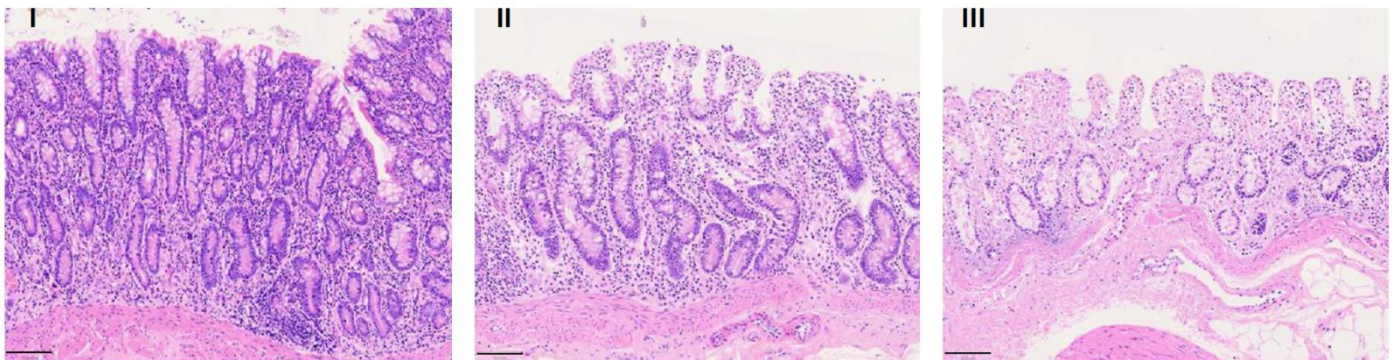
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In many farming systems, diets containing large proportions of rapidly degradable carbohydrates in the form of high-starch cereal grain are fed to meet energy requirements for efficient production. However, the over-supply of, or rapid transition to, high-starch diets can result in digestive diseases such as ruminal acidosis and sub-acute ruminal acidosis. The challenge posed by such diets causes anatomic, microbial, proteomic, and transcriptomic changes throughout the gastrointestinal tract (GIT), along with variable systemic effects. These changes have been well characterised in the proximal GIT, however, there is a paucity of data from cattle describing the impact in the distal GIT. This work aims to characterise the faeces of cattle fed diets with inefficient starch levels. First, by evaluating the effect of feeding commercial diets containing variable grain inclusions on caecal mucosa morphology and immune cell distribution and second, by assessing the impact these diets have on faecal chemistry. Caecal tissue was obtained immediately post-slaughter from 30 beef animals from 3 fattening systems

offering diets containing grain inclusions of 0%, 50%, or 90% (n=10 each group) of the total ration. Tissue samples were processed and stained with chemical and immunogenic stains before being digitally scanned and examined via digital pathology software. Faecal samples were collected at the point of defecation from commercial beef and dairy cattle fed diets of varying starch inclusions and subjected to starch, pH and lipopolysaccharide (LPS) measurements. Morphological characterisation of the caecal mucosa revealed a reduction in mucosal integrity and loss of normal mucosal structure with increasing dietary grain (Figure 1). The two grain-based systems resulted in caecal inflammation. The proportion of immune cells in the mucosa and mucosal tissue exhibiting signs of cell death was significantly higher in the high-grain-fed animals. Faecal pH was lower, whilst faecal LPS and starch were higher in beef cattle fed grain-based as opposed to grass-based diets. However, faecal starch levels reduced with increasing time from defecation within pats. We conclude that feeding grain during the fattening period results in pathological changes in the caecum and measurable changes to the faecal environment, which requires prior knowledge of the defecation time before interpretation.

Figure 1: Assessment of tissue morphology from cattle fattened on diets containing 0% (I), 50% (II), and 90% (III) grain inclusion; I) a representation of tissue structure score 1; II) a representation of tissue structure score 2; III) a representation of tissue structure score 3. Scale bars in Figures 1 I, II, and III represent a length of 100 μ m.



Using existing on-farm monitoring systems to identify positive welfare

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UK consumers have an interest in dairy cattle welfare, with 93% of respondents to a study saying they would pay more for good dairy welfare. Allowing pasture access to dairy cows gives increased opportunity for expression of natural behaviour as well as improving health and consumers may consider it an indicator of “happy cows”. The ability to use technology already on-farm for management purposes (predominantly oestrus/illness detection) to understand more about an animal’s welfare in an automated way, would not only allow farmers a better understanding of their herd health and dynamics, but could provide a verifiable and non-biased indicator of positive welfare.

Qualitative behaviour assessment (QBA) was carried out on four farms and QBA metrics examined in relation to sensor outputs. On each farm, 20 animals were randomly scored by one member of staff, giving 160 data points (80 housed and 80 at pasture). Sensor data from leg-mounted accelerometers were collected during housing and at pasture for lying times and step count. Principal components analysis (PCA) was used to analyse QBA data in R using parallel analysis. Animals at pasture displayed more positive behaviours, with PCA scores indicating positive behaviours for 67.5% of cows (Figure 1). In comparison, PCA scores for housed cows showed 61% negative behaviours (Figure 1). Some sensor data, particularly step count and lying time, correlated strongly with cattle location. Data showed significantly greater "clustering" of lying times at pasture, with pasture cows lying for more similar amounts of time compared to when housed. This was attributed to lying synchrony. The potential for cows to all lie down at the same time, due to increased lying space at pasture, allows cows to exhibit similar behaviours compared to when housed. Behavioural synchrony, such as lying and feeding synchrony, has been shown to be a positive welfare indicator for cattle. A smaller spread of QBA scores was also noted at pasture, potentially also suggesting higher levels of synchrony. The potential for an automated link between farm management sensor data and positive cattle welfare is the subject of continuing work.

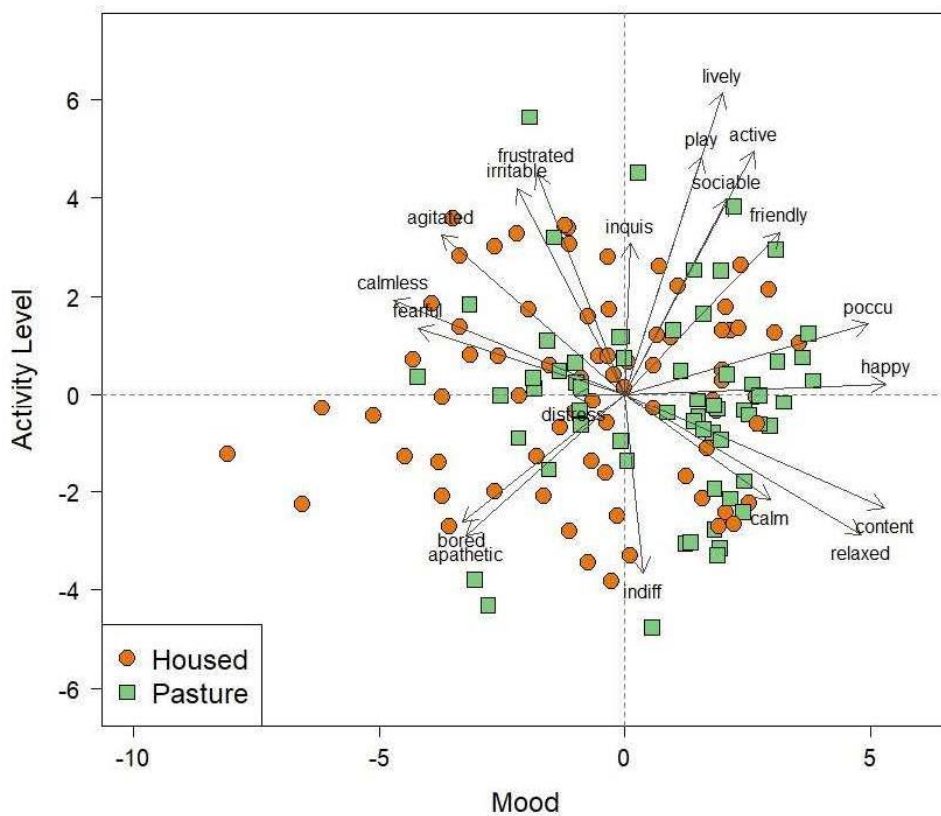


Figure 1: Principal components analysis (PCA) output depicting the Qualitative Behaviour Assessment (QBA) scores for animals housed and at pasture for four UK farms. Each data point shows an individual cow (n=160) PC scores, where the x-axis refers to overall PC1 score (mood – negative to positive) and y-axis shows PC2 score (activity level: active to less active) and individual QBA behaviour descriptors.

The development of organoids for precision lab-based studies of livestock diseases

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Infectious diseases are a major contributor to production and economic losses in dairy farming worldwide. However, the lack of *in vitro* tools for studying livestock health and disease in detail has hampered progress. The development of three-dimensional cell culture systems representative of tissues from animals of veterinary interest is accelerating research that seeks to address specific questions tied to animal health. In terms of their relevance and complexity, these *in vitro* models can be seen as a midpoint between the more reductionist single-cell culture systems and more complex live animals. Organoids, in particular, represent a significant development due to their organised multicellular structure that more closely represents *in vivo* tissues compared with other cell culture technologies. Recently, we have developed gastrointestinal organoids from ruminants and demonstrated their application in infectious disease models in the laboratory. In the context of dairy research, we have been working on the development of ruminant mammary organoid culture. We have demonstrated the ability to successfully propagate and differentiate mammary organoids in the laboratory and have characterized a basal epithelial cell structure within the organoids. We anticipate that these mammary organoids will be a valuable tool for detailed mastitis studies in the future, in particular for investigating host-pathogen interactions with a view towards identifying novel targets for disease intervention.