

Effects of milk replacer composition on gut and lung health and performance in veal calves

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Introduction Various stressors have an impact on health and disease susceptibility of fattening veal calves. Transport, environmental and husbandry changes have an impact on the health of calves and especially on the occurrence of infectious diseases in the first 10 weeks of age. Respiratory diseases and pneumonia account for the major disease burden from arrival to 6 weeks after arrival at a veal farm. At time of birth the immune system is immature and has to develop in the following period of life. It is well-known that commensal microbiota in the gastrointestinal tract shape the immune system of the intestine in the post-natal period and modulates the competence of the system in later life. The commensal bacteria not only regulate the local mucosal defences against intestinal pathogens, but also regulate immune responses at extra-intestinal sites such as the lungs. The microbiota population in the intestinal tract is considered to be determined by early post-natal colonization and by diet composition. In the present study the effect of changes in the composition of milk replacer (CMR) on microbiota composition and immunological development in the gut and lungs of veal calves is studied. Here, we compare the effects of a plant based CMR (pCMR) to a milk/dairy protein based CMR (mCMR) on gut and lung health parameters as well as on zootechnical performance of veal calves.

Materials and Methods First the effects of CMR composition on overall health of calves, the mucosal and immune system of the lung and small intestine and the microbiota composition in the gut of thirty young calves from 1 to 49 days of age were evaluated. Effects of CRM on the immune system and health parameters were assessed by daily health recordings, repeated analysis of haematological parameters, immunological and functional assays on bronchoalveolar fluid (BALF) cells (FACS analysis, phagocytose assays and oxygen radical formation measurement) and lung pathogen detection in BALF by PCR. After euthanasia on day 49, necropsy was performed and samples taken from lung and jejunal tissue for histological and molecular analysis (microarray and PCR) and from jejunum digesta for microbiome analysis. Subsequently, in a second study the effects of CMR composition on health parameters and production characteristics were studied during a whole production cycle. One hundred calves were followed during 196 days and health recordings, production parameters as well as lung and gut inspection at the slaughterhouse were used to compare the long term effects of both CMRs. BALF was collected and analysed similar to the first study.

Results The microbial populations in the jejunal digesta were significantly affected by the two different diets. The diversity of the microbial population, expressed as Shannon diversity, was higher in pCMR compared to the mCMR fed calves. The comparison of the bacterial populations in the jejunum demonstrated that the species composition was significantly different between both treatments. Intestinal gene expression was also affected by the CMR: expression of the investigated mucin genes muc-1, muc-2 and muc-5 were upregulated in calves on pCMR. Whole genome expression analysis indicated that genes involved in immunological/inflammatory pathways were upregulated in jejunal tissue of calves from the pCMR group. No histological differences were observed in small intestinal tissue between both groups.

Composition of CMR also induced changes in the lungs. Gene expression analysis of lung tissue and BALF showed significantly higher gene expression levels for TLR-5, IL-6, cyclooxygenase-1 and proliferation marker p53 in the lungs of mCMR fed calves. In BALF cells, increased levels of TLR-5 and IL-6 were observed at day 42 in the mCMR fed group. No functional changes in phagocytosis capacity of BALF nor in base line production of radical oxygen species were found both groups. Occurrence of clinical disease was not different between treatments.

The performance study showed body weight and body weight gain of calves fed mCMR were significantly higher than of pCMR fed animals. At slaughter the mean body weight was 3.6 kg higher in the group fed mCMR. Feed conversion was significantly lower in the group fed with mCMR from day 0 - 126. No differences with regard to medical treatments were observed between both groups. Slaughterhouse recordings showed that both groups had a similar profile of lung lesions, the majority being mild. A more detailed analysis of 20 calves per group showed that in 40 to 60 % of the animals pneumonia related lesions were found. Data on gene expression in lung tissue obtained at slaughter showed, in agreement with results of the first study, that expression of TLR-5, IL-6 and P53 was higher in mCMR fed calves.

Conclusions Composition of CMR not only change microbiota diversity and composition in the gut and gene expression in small intestinal tissue, but also affects immunological development of the lungs. Early life differences in dietary protein sources in CMR induced differences in the immune system in the lungs as reflected by a higher expression of the pathogen recognition receptor TLR-5 in lung tissue and alveolar cells at 49 and 196 days after the introduction of the experimental diets. Together with the functional activity of alveolar cells, a potential positive effect of mCMR on the immune system is suggested, but its functional significance is unknown so far. These effects might be induced by the changes in diversity and composition of the microbiome in the jejunum. Together, these contrasts in lung and gut development might lead to changes in health supporting capacity of veal calves related to diet composition. No effects of diet composition on the occurrence of general disease manifestations, especially respiratory disease, and required medical treatment were observed. Further investigations on the influence of CMR composition on the intestinal microbiome and the local and systemic immune system are required to understand the mechanisms involved and to exploit the knowledge for improved health management. Via manipulation of diet composition at early age, health benefits can be achieved in relation to modulation of intestinal and respiratory diseases.