

Research overview: the impact of animal transport on the health and welfare of beef cattle

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The transport of livestock can have major implications for their welfare, and there is strong public interest and scientific endeavour aimed at ensuring that the welfare of transported animals is optimal. Physical factors such as noise or vibrations; psychological/emotional factors, such as unfamiliar environment or social regrouping; and climatic factors, such as temperature and humidity, are also involved in the transport process. We have conducted a series of animal transport studies from Ireland to Spain, and from Ireland to Italy, using a roll-on roll-off ferry. The overall objective of the studies was to investigate the physiological, haematological and immunological responses of weanling heifers transported to Spain, and of weanling bulls transported to Italy under EU legislation and to evaluate the implications in terms of animal welfare. During these studies, appropriate physiological, haematological and immunological measurements were made on the animals which quantified the effect of transport (by road and sea) on the degree of stress imposed and the performance of the animals in the post-transport period. Physiological, haematological and immunological parameters (including interferon- γ production, cortisol, protein, immunoglobulin, urea, white blood cell numbers and differentials, and haptoglobin) were used to determine the welfare status of animals, before, during and after the respective transport journeys. Age-matched control animals that were blood sampled for the same parameters at times corresponding to the transported animals were retained in Ireland as controls. While transient changes in physiological, haematological and immunological parameters were found in the transported and control animals relative to baseline levels, the levels that were measured were within the normal physiological range for the age and weight of animals that were studied.

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Blood transcriptome response to LPS in pigs

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The aim was to describe immune, hormonal and metabolic responses of pigs to a systemic inflammatory challenge using blood transcriptome. Male pigs of 4 different gonadal statuses were used (intact, surgically castrated, immunized against GnRH, and surgically castrated plus immunized against GnRH, 7-9 pigs per group). Blood samples were collected via jugular catheters at 149 d of age, just before (t-1), and 1, 4 and 24 hours (t1 to t24) after a lipopolysaccharide administration (Escherichia coli O55:B5 serotype LPS, 15 μ g/kg, i.v.). Blood lymphocyte/granulocyte (L/G) ratio was measured, and was maximal at t1 ($P < 0.001$), back to baseline at t4 ($P > 0.1$) and lower than baseline at t24 ($P < 0.001$). Total blood mRNA was extracted and the transcriptome of intact pigs was analyzed using the Agilent 60K microarray. Differential expression among time points was observed for 2,148 annotated single genes (Benjamini-Hochberg adjusted P values < 0.01). The 5 first functional clusters of genes identified with the David software concerned immunity and inflammation, chemotaxis, apoptosis, ion transport, and energy metabolism (209, 196, 185, 127 and 121 genes respectively). Among these genes, 51 were selected to investigate the level of expression in the 4 time points and 4 gonadal statuses by qPCR. The L/G ratio significantly influenced 37 of these genes ($P < 0.05$). Therefore, for all genes, the effects of time, gonadal status and their interaction were analyzed on the residuals of the L/G covariance analysis. The variation along time in response to LPS was confirmed for 43 genes ($P < 0.05$). None of them was affected by the gonadal status. In conclusion, blood transcriptome can be used for investigating LPS responses provided that respective blood cell proportions are known. Furthermore, the innate immune response activated by LPS injection is not sensitive to the sexual status of male pigs.