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Other Short Communication Abstracts

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Supplementation of unsaturated fats (UFA) in the food of dairy cows has been a significant trend to improve the quality of milk for human consumption. The aim of this study was to determine the effect of dietary UFA on gene expression in the mammary gland tissue of dairy cows via microarray analysis. Twenty-eight Holstein lactating cows were randomly assigned to 4 UFA-enriched concentrates based on linseed, soybean, and rapeseed oil, and a proportional mix of them all. After 23 days (Period I), all cows were switched to a non-UFA-enriched concentrate for 27 days (Period II). On the last day of each period, a biopsy of mammary tissue of each cow was taken for subsequent gene expression determination. The model included UFA source, period (associated to UFA level), and the interaction between UFA source and period, as fixed effects, and cow within pen as a random effect. Period was considered a repeated factor. Results indicated down-regulation of gene expression related to defense and inflammatory responses when cows were fed with UFA-enriched concentrates, as well as pathways related to innate immunity including chemokines and the complement pathway regulator SERPING1. Conversely, up-regulation was found for genes associated with major histocompatibility complex. Gene expression was not affected by UFA source in the concentrates. Changes observed in the expression of immune- and inflammation-related genes in response to UFA supplementation suggests that dietary UFA can influence the immune characteristics of the mammary gland through the production of cytokines and the differential regulation of the functional properties of immunocompetent cells. Present results demonstrate that the use of microarrays permits a better understanding of the effects of UFA diet supplementation on defense mechanisms in the udder, thus helping to develop nutritional conditions that optimise udder health and improve the resulting quality of milk of dairy cows.

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IS*621* profiling as an epidemiological tool of bovine and human O26 enterohaemorrhagic *Escherichia coli*

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A total of 18 copies of IS*621* were identified on the chromosomes of two bovine and two human O26 enterohaemorrhagic *Escherichia coli* **(**EHEC) strains after sequencing. Primers located upstream and downstream (outside <OUT>_ F and OUT_R primers) of each IS*621* insertion site were designed to detect the presence or absence of IS*621* in 11 bovine and human O26 EHEC strains including the four sequenced ones (= detection PCR). Eight to 14 copies of IS*621* were detected in each strain with four copies present in all strains. Subsequently multiplex PCRs were designed with different combinations of OUT_ primers and with one IS*621* inside (IN_) primer (OUT_F/IN_R sets and OUT_R/IN_F sets) to amplify either end of each copy (= typing PCR). The typing PCRs were tested on the same 11 strains and results were compared with those of the detection PCRs: 2 IS*621* copies gave highly different results; 3 IS*621* copies gave comparable results, but were present in all 11 strains; 13 IS*621* copies gave comparable results and were not present in all 11 strains. These 13 copies were finally chosen as targets of two final multiplex PCRs using corresponding combinations of OUT_F/IN_R or OUT_R/IN_F primers respectively (= profiling PCR). The two profiling PCRs were at first tested on the 11 O26 EHEC strains with results in agreement with those of the detection and typing PCRs. When compared the results of the two profiling PCRs were identical, but for one human O26 EHEC strain showing different results for two insertion sites: positive results with one set of primers and negative results with the other set. The reasons of non-agreement between the results of the detection, typing and profiling PCRs may be various: mismatches in primer sequences, truncation of IS copies by some genomic deletion, genetic rearrangements at IS insertion sites, etc. Nevertheless the two IS*621* profiling PCRs may represent useful epidemiological tools that are now being tested on more bovine and human O26 EHEC, EPEC (enteropathogenic *E. coli*) and also non-EHEC/EPEC, strains.

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