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Effect of fatty acids and epigenetic modifications on immune cells functions*P. Lacasse, C. Ster, N. Vanacker and A. Roostaee**AAFC-Sherbrooke R&D Centre, 2000 College, J1M 0C8, Sherbrooke, QC, Canada; pierre.lacasse@agr.gc.ca*

Cows undergoing energy deficit have a weakened immune system and are at greater risks of infection. Negative energy balance usually occurs during the transition period in high-yielding dairy cows, but also occurs in cows under acute stress that are unable to eat the required amount of feeds. Our recent researches have indicated that high blood non-esterified fatty acid (NEFA) concentrations impair lymphocyte and neutrophil functions. This research program improves our understanding of the mechanism by which NEFA affects cow immune cell functions. A better understanding of the mechanisms involved in the NEFA-induced immunosuppression, may enable the development of approaches to reduce immunosuppressive effects of NEFA. Beyond changes in immunity related to the nutritional status, there are variations between individuals. There are a growing number of evidences that suggest that environment, including intra-uterine environment, can affect animal phenotype several years later. This phenomenon may be related to the regulation of transcription by epigenetic modifications of the genome, such as DNA methylation and histone acetylation. Our work shows that immune functions are particularly affected by epigenetic modulations. This open-up an exciting new field of research.

Study of the MaSC/progenitors committed to the development of the bovine mammary gland*L. Finot, E. Chanat and F. Dessauge**INRA, UMR 1348 PEGASE, 16 Le Clos, 35590 Saint-Gilles, France; laurence.finot@inra.fr*

Milk production is highly dependent on the extensive expansion of the mammary epithelium which largely occurs during puberty. Within the mammary epithelium, the Mammary Stem Cells (MaSC) and their progeny play a key role in driving the development of the future functional mammary gland. Later, these cells contribute to regenerate the secretory epithelium in order to ensure future lactations. To elucidate the epithelial cell lineage involved in the establishment of the functional gland, we investigated the MaSC/progenitors populations in the bovine mammary tissue at various physiological stages. We used flow cytometry to phenotype epithelial cells on the basis of CD49f and CD24 expression in animals at three contrasted physiologic stages: puberty (heifers of 17 months of age), lactation (multiparous cows producing 35 kg of milk) and drying off (cows at 6 years after drying off). Comparison of the cytometric profiles highlighted the presence of a distinct epithelial population of CD49^{low}CD24^{pos} cells at puberty (23.7%±3.6) which substantially decreased in the others stages (4.1%±1 at lactation and 6%±1 at drying off). These CD49^{low}CD24^{pos} cells had features of a dual lineage, with luminal and basal characteristics (CD10, ALDH1 and keratin 7 expression) and were considered to be early common progenitors. The MaSC fraction was recovered in the sub-population of CD49^{high}CD24^{pos} cells. When cultured *in vitro* (in a 3D culture system with matrigel), these cells formed mammospheres, a functional property of MaSC. At puberty, total mammary cells contained 2.8%±0.3 of MaSC. This proportion of MaSC was significantly reduced at lactation (1.1±0.3%) and at drying off (0.4±0.3%). Further phenotypic characterization of the CD49^{high}CD24^{pos} cells showed that they expressed CD10 and keratin 14 at any stages. This in-depth characterization of the epithelial sub-populations at various physiological stages provide new insights into the epithelial cell hierarchy in the bovine mammary gland from puberty to drying off.