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Gene expression in different tissues of lactating cows of differing metabolic type: 1. Comparison of mRNA patterns by the differential display method

M. Schwerin, J. Voigt, J. Wegner, Ch. Kühn, K. Ender and H. Hagemeister

Abstract

Among other factors the nutrient utilization of a cow is influenced by its individual physiological and genetic predisposition. There are large differences within cows in the manner of partition of the nutrients that may affect the size and activity of the individual organs and the whole body composition. High genetic merit dairy cows have a higher potential rate of protein excretion than medium genetic merit dairy cows even when energy and protein intake are equal. Medium genetic merit dairy cows show higher potential rates of protein and fat deposition of the body. This phenomenon was partly explained by the regulatory functions of the hormone insulin (see Brockman and Laarveld 1986; Broucek et al. 1991; Wylie et al. 1998). Additionally, it is widely considered that the somatotropic axis [growth hormone, growth hormone releasing factor and insulin-like growth factor I (IGF-I)], could be involved, as one of the key control and balance mechanisms which regulate the partition of nutrients (Breier and Sauerwein 1995; Schams 1995; Knight 1997). Several studies have provided insights into the physiological action of these and further hormones, transport proteins and enzymes, e.g. the erythrocyte-type glucose transporter, the insulin-responsive glucose transporter or the glycerol-3-phosphate dehydrogenase, and indicate that these molecules may affect nutrient repartitioning and utilization as well as milk yield, growth and fat accumulation (Mathews et al. 1988; Bauman and Vernon 1993; Burton et al. 1994; Girard et al. 1994; Binelli et al. 1995; Zhao et al. 1996; Abe et al. 1997). However, the mechanisms of regulation of most of these processes are insufficiently known.

This paper presents a comparison of mRNA patterns of tissues potentially associated with protein and energy turnover in lactating cows of different metabolic types. The technique of differential display of messenger RNA species originally described by Liang and Pardee (1992), has already been applied as a powerful tool for cloning genes that are differentially expressed in various tissues or under altered conditions in the same tissue (e.g. Liang et al. 1993; Aiello et al. 1994; Li et al. 1994; Nishio et al. 1994). This method was applied to characterize the expression patterns in 12 tissues of three cows with divergent metabolic types (milk type, meat/milk type, and meat type) by the display of differentially and identically expressed cDNA bands. The aims of this exploratory study were first to indicate which of the 12 tissues analysed are mainly involved in trait differentiation according to their differentially displayed mRNA patterns. Secondly, the results of this study represent the prerequisite for the identification of tissue-specific expressed sequence tags in general, and individual or type-dependent differentially expressed sequence tags in particular.