

**Gene expression analysis as a tool for the investigation of the physiological and genetic background of metabolic and growth traits in cattle**

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Gene expression analysis can provide information on the genetic determination of metabolic and growth traits and as well on the regulation of physiological pathways underlying these traits. Our investigations were performed in the Charolais and the German Holstein breed serving as founder breeds for an F2-resource population. The breeds differed substantially regarding tissue development and nutrient partitioning, thus representing divergent metabolic types of cattle. The investigation of differences in gene expression in twelve tissues by differential display revealed genes/ESTs differentially expressed in the two breeds and enabled identification of physiological pathways putatively involved in trait differentiation. About 30% of the identified ESTs did not show significant matches to any entry in public genome data bases. Differential expression of the identified genes/ESTs was verified by Real-time PCR expression analysis. Further characterization of these genes/ESTs by Radiation hybrid mapping and mutation analysis provided information to assess the differentially expressed genes/ESTs as functional candidate genes for metabolic and growth traits. Furthermore, these genes/ESTs identified by a comprehensive approach are also included into parallel expression studies of targeted genes of known functional relevance to complement physiological studies of tissue development and nutrient partitioning.