

Cross-species comparison of hepatic sex differences identified in transcript profiles

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Sex-related differences in body composition and onset of metabolic disease, might be related to differences in the metabolism of carbohydrates and lipids. More knowledge concerning sex differences in fuel metabolism and the mechanisms behind this might therefore help us to understand why women to some extent are protected against metabolic disorders and cardiovascular disease. We have recently described the utility of gene arrays to identify sex-related gene products in rat liver. Here we have extended this initial study to include sex-dependent transcript profiles from rat, mouse and human liver. The online software DAVID was used to classify the obtained profiles into functional groups. Regardless of species, 15% of the genes represented on the arrays were expressed and roughly 15% of those were sex-differentiated. Some interesting functional groups were identified, such as lipid metabolism, insulin signaling and immune responses. Within these functional groups of transcripts, specific genes with a sex-differentiated expression in all three species were identified. It seems likely that sets of genes from specific metabolic pathways may be regulated in a coordinated manner. Identification of promoter sequences and cis-regulatory elements shared by this set of co-regulated genes might lead to the characterisation of commonly used transcription factors and upstream signalling pathways.