Widespread expression of the bovine Agouti gene results from at least three alternative promoters.

In wild-type mice, it is well known that Agouti is only expressed in skin where it controls the banded-hair phenotype. As a first step to investigate the physiological role of Agouti in cattle, we isolated the corresponding gene and studied its expression pattern. We found no evidence of coding-region sequence variation within and between eight breeds representing a large panel of coat colour phenotypes. We detected by northern hybridization two Agouti mRNA isoforms in brain, heart, lung, liver, kidney, spleen and a third in skin. We characterized the full-length Agouti transcript in skin and isolated the 5' UTR of two mRNAs expressed in the other tissues. The three mRNAs have the same coding region but differ by their 5' untranslated regions. Upstream regulatory sequences display two alternative promoters involved with the broad expression in tissues other than skin. Interestingly, these sequences are highly homologous to upstream sequences of the orthologous human (76-85% identity) and pig (82-86% identity) ASIP genes. In addition to its potential role in pigmentation (as seen in mice), we suggest that bovine Agouti could be involved in various physiological functions. Furthermore, the significant homology between cattle, pig and human regulatory sequences indicate that these orthologous genes are regulated alike. Lastly, since the 5' UTR of many eukaryotic mRNAs are physiologically relevant, their impact on bovine Agouti mRNA performance is discussed.

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