



## Transcript profiling of expressed sequence tags from semimembranosus muscle of commercial and naturalized pig breeds

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**ABSTRACT.** In general, genetic differences across different breeds of pig lead to variation in mature body size and slaughter age. The Commercial breeds Duroc and Large White and the local Brazilian breed Piau are ostensibly distinct in terms of growth and muscularity, commercial breeds are much leaner while local breeds grow much slower and are fat type pigs. However, the genetic factors that underlie such distinctions remain unclear. We used expressed sequence tags (ESTs) to characterize and compare transcript profiles in the semimembranosus muscle of these pig breeds. Our aim was to identify differences in breed-related gene expression that might influence growth performance and meat quality. We constructed three non-normalized cDNA libraries from semimembranosus muscle, using two samples from each one, of these three breeds; 6902 high-quality ESTs were obtained. Cluster analysis

was performed and these sequences were clustered into 3670 unique sequences; 24.7% of the sequences were categorized as contigs and 75.3% of the sequences were singletons. Based on homology searches against the Swiss-Prot protein database, we were able to assign a putative protein identity to only 1050 unique sequences. Among these, 58.5% were full-length protein sequences and 17.2% were pig-specific sequences. Muscle structural and cytoskeletal proteins, such as actin, and myosin, were the most abundant transcripts (16.7%) followed by those related to mitochondrial function (12.9%), and ribosomal proteins (12.4%). Furthermore, ESTs generated in this study provide a rich source for identification of novel genes and for the comparative analysis of gene expression patterns in divergent pig breeds.

**Key words:** Expressed sequence tags; Muscle; cDNA library; Ham; *Sus scrofa*