



Plant & Animal Genomes XII Conference

January 10-14, 2004
Town & Country Convention Center
San Diego, CA

Poster: Genome Sequencing & ESTs

P58

ANNOTATION OF *Bos indicus* FUNCTIONAL GENOME

Luis Felipe P Silva¹, Erika C Jorge¹, Lilian G Zaros¹, Mateus Patricio¹, Saul C Leite¹,
Luciana Correia de A Regitano², Marcia Cristina de S Oliveira², Antonio C Silveira³, Luiz R
Furlan³, Luiz L Coutinho¹, AEG FAPESP⁴

¹ ESALQ/USP, Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil

² EMBRAPA-Sudeste, Rodovia Washington Luiz Km 234, São Carlos, SP, 13560-970, Brazil

³ UNESP, Dist. Rubião Jr, s/n, Botucatu, SP, 18618-000, Brazil

⁴ FAPESP, R. Pio XI, 1500, São Paulo, SP, 05468-901, Brazil

The main goal of this project is to discover genes that can be used to generate new technologies and products to overcome the hurdles faced by the beef cattle industry. To this end, an expressed sequence tag (EST) project was initiated to sequence 100,000 valid *Bos indicus* transcripts. The sequencing is being conducted by the AEG group (Agronomical & Environmental Genomes) with financing from FAPESP and Central Bela Vista. Twenty six animals were slaughtered at different ages to construct fifteen cDNA libraries pooling mRNA from several tissues: hypothalamus, pituitary, adipose tissue, skeletal muscle, liver, skin, lymph node, ovary, uterus, prostate, epididymis, seminal vesicle, adrenal gland, bone marrow, mammary gland, small intestine and abomasum. Five prime end sequencing of 7,296 clones yielded 5,272 with PHRED>20 over 140 bp, with an average read length of 660 bp. The average insert length was 1369 bp. Clustering and assembly of ESTs database resulted in 3,726 unique sequences with 589 clusters (assembled with 2,135 ESTs) and 3,137 singletons. Comparative analysis against the protein database on GenBank (blastx) identified 3,497 unique sequences with similarity to the database, and 1,143 sequences with no match (Evalue>1⁻⁵). An EST pipeline was developed using a relational database manager, to process and functionally annotate sequences using Gene Ontology, and automatically detect polymorphisms. The EST database will be used in microarrays to identify genes regulating important traits, such as sexual precocity, resistance to parasites, and beef tenderness. This resource will also be useful to identify polymorphisms related to economic traits.