ANNUAL PROGRESS REPORT
NATIONAL RESEARCH SUPPORT PROJECT – NRSP008
Year Ending 2004
Preliminary Information-Not for Publication
Station: Nevada
Location: Reno, Nevada

I. PROJECT TITLE:

NRSP008: National Animal Genome Research Program

II. COOPERATING AGENCIES AND PRINCIPAL LEADERS:

III. NATURE OF WORK AND PRINCIPAL RESULTS OF YEAR:

Objective 1: *Enhance and integrate genetic and physical maps of agriculturally important animals for cross species comparisons and sequence annotation.*

The Second Generation EST Radiation Hybrid ($RH_{7000rad}$) Map (2035 ESTs).
The Second Generation EST Radiation Hybrid Map confirms > 98% coverage of the human genome. Currently ~ 60 breaks between chromosomes and ~70 breaks within regions of homology have been detected. The 2pt LOD score criterion for creating the 2nd generation porcine EST radiation hybrid map using Carthagene was set at 6. Good statistical support for local gene order was considered to be more valuable than creating large linkage groups and obtaining complete chromosome coverage through a minimum number of linkage groups. This is particularly important in those regions where the human genome sequence is ambiguous.

Radiation Hybrid Mapping Project – $IMpRH_{12000rad.}$
We used Carthagene (http://www.inra.fr/bia/T/schiex/Export/WABI.pdf) to calculate an updated version of the 2nd Generation pig human comparative map (IMpRH7000Rad panel). Carthagene is also the software of choice in developing the $IMNpRH_{12,000\text{-rad map.}}$ Markers that introduced new homologies to the comparative map are reevaluated based on their multipoint linkage assignment (using the IMpRH mapping tool), rather than on their 2pt LOD value. These maps will be transferred to the FTP site as they become available. An Excel file (Complete Info for 2035 ESTs.xls) containing all pertinent information (annotation, primers, location in HGS build 29, mapping information) is also available from the FTP site. All vectors generated by our group are public and will continue as such as markers are assigned. Build 35v1. of the HGS is the version of the human sequence upon which we are building the comparative map. BLASTN comparisons against the contig assembly and dbEST have been completed. BLASTP comparisons of the dataset against the CCBC protein database set and nrNCBI db are continuous.
We have currently assigned a total of 2774 ESTs to all chromosomes on the $IMNpRH_{12,000\text{-rad}}$ panel. A total of 1918 (94% 2035 ESTs) ESTs on the $IMpRH_{7000rad}$ map have been assigned to the $IMNpRH_{12,000\text{-rad}}$ map. The location of these ESTs is currently being finalized and will be available on our web sites (www.toulouse.inra.fr/lgc/lgc/, http://www.ag.unr.edu/ab/standard.htm), shortly. To date, 791 microsatellite primer pairs (from the original 7,000rad framework map; Hawken et. al. 1999) have been assigned to the $IMNpRH_{12,000\text{-rad}}$ panel in duplicate (or triplicate, as necessary). We are currently optimizing 316 and typing 100 ms primer pairs. An additional 28,992 (EST) sequences in our database (CCGB-biodata, University of Minnesota), are available to develop primer pairs in addition to the 677 BAC primer pairs (of ~2,600) in our laboratory (courtesy Jon Beever, UICU). Figure 1 illustrates the comparative map of SSC12 - HSA17 *circa* January, 2005.

IV. APPLICATION OF FINDINGS:

V. WORK PLANNED FOR NEXT YEAR: Complete typing of the $IMNpRH_{12,000\text{-rad}}$ panel; this includes ~10,000 ESTs, ~1000 ms, and initiate typing of ~2,600 BAC end primer pairs ordered on the $IMpRH_{7000rad}$ panel.

VI. PUBLICATIONS: