

Pig Genome Update No. 51 November 1, 2001

New pig microsatellite diversity primers are available. This set of primers was made in response to requests and suggestions concerning pig diversity research and selected from markers across all 19 pig chromosomes. These were suggested by several people and should work nicely to study diversity in different breeds. There are a total of 50 pairs of primers, half of each primer pair is labeled with one of the three fluorescent dyes (TET, HEX, and 6-FAM) in 5,000 pmole amounts. These primers were produced by Research Genetics. To date, there are 11 sets of primers covering a total of 559 microsatellite markers that have been made available through the USDA/CSREES Pig Genome Coordination Program. More information on all sets of primers can be found at the web site: http://www.genome.iastate.edu/resources/fprimerintr.html. A Java graphic view of fluorescent primers sets for microsatellite markers has been created showing the relative linkage location (http://www.genome.iastate.edu/resources/PrimerOnChr.html). A click on the marker name in this graphic viewer will send a query to the PigBase database and fetch detailed information on this marker. In addition, there are a limited number of bags of the previous set X of primers still available. For additional questions, please contact me (https://www.genome.iastate.edu) or Dr. Yuandan Zhang (ydzhang@iastate.edu).

A new public porcine expressed sequence tagged (EST) database, a set of tools for EST analysis and web query tool for public access to this database have all been developed. A consortium of five institutions (Iowa State University, University of Missouri-Columbia, University of Iowa, University of Nebraska and the National Center for Genomic Resources) is developing extensive expressed sequence and mapping data for cDNAs expressed in all major female reproductive tissues. A total of 14,602 EST sequences derived from 20 libraries (estrus or gestation for whole embryo, anterior pituitary hypothalamus, ovary, uterus and term placenta) has been produced and submitted to GenBank. Nucleotide similarities between the pig ESTs and human genes were determined by BLAST analysis against 92,152 human UniGene sequences. A number of PERL scripts were written for parsing the BLAST output and integrating it with a) human gene maps, b) the PigBase database and c) pig-human comparative map information. LocusLink, UniSTS and radiation hybrid (RH) map location were used to order the putative human orthologs of pig ESTs on human chromosomes. The pig-on-human comparative maps and homology between pig and human chromosomes were then used to predict EST assignments on pig chromosomes. For further information, please see the database which is comprised of a number of tables covering the EST profile, alignment similarity (between pig ESTs and human UniGene and between pig ESTs and pig genes/loci sequences), human ortholog and information on cytogenetic, linkage, and RH locations. Interactive web querys can be made by the public through using the EST database query interface (http://pigest.genome.iastate.edu/). It is likely that public EST data will be added to generate a more diverse pig EST database. Visualized web presentation of putative human homology and predicted pig maps of the pig ESTs is also in progress.

September 11 and a personal reflection. It is impossible for civilized people not to shocked and saddened by the wholesale destruction of lives and property by terrorists. It is likely that like me, you may know someone who lost a loved one, but even if this is not the case we have all been touched by the tragic and criminal recent events. For your own personal health, take time to make a special effort to be with family and friends and to work at reclaiming the important things in life. Help others and find a minute to smile and offer a friendly hand.

Are you going to San Diego for PAG?? Please see www.intl-pag.org/pag for more information. Dr. Francis Collins, "Czar" of the Human Genome Program at NIH, has agreed to give one of the plenary talks. Other speakers include Ralph Greenspan on behavioral genetics, Tom Blumdell on structure and function of the proteome, Steve Brown on ENU mutagenesis in mice and Eric Green on comparative genome sequencing. Several changes are on tap for next year. PAG-X will again be at the Town & Country Convention Center in San Diego, CA, next year running from Sat., Jan. 12, through Wed., Jan. 16. The PAG-X meeting will include plant, animal and agricultural microbe genomics all in one meeting. Also it is planned that a weekend-only registration rate (\$175) is available in addition to the usual student (\$225), non-profit (\$425 early/\$525), and industry (\$550 early/\$650) for full week registrations. Registration badges will be required to participate in any workshop. As is the usual case the swine committee will be meeting on Sunday January 13 of the meeting. Jon Beaver, chair, has planned interesting swine sessions. Please have your graduate student apply for the Neal Jorgensen Travel Award for Swine before November 1 by sending a cover letter and abstract to Max Rothschild at mfrothsc@iastate.edu.

Upcoming meetings (for more details see: http://www.genome.iastate.edu/community/meetings.html)

Plant and Animal Genome X January 12-16, 2002 at the Town and Country Convention Center, San Diego, CA. For information please contact D. Sherago, Sherago International at darrins@scherago.com.

International Society of Animal Genetics, Göttingen, Germany, August 11-15, 2002. See http://www.gwdg.de/~bbrenig/ISAG2002.html for further information.

7th World Congress of Genetics Applied to Livestock Production, August 19-23, 2002, Montpellier, France. See http://www.wcgalp.org for more information.

Additional items can be found at: http://www.agbiotechnet.com/calendar/index.asp.

Items for *Pig Genome Update 52* can be sent to me by no later than December 10 please.

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cc: Dick Frahm, CSREES and Caird Rexroad II, ARS Paid for by funds from the NRSP-8 USDA/CSREES sponsored Pig Genome Coordination Program.