



POULTRY GENOME NEWSLETTER 2004

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Best Wishes for the Holiday Season and a Happy New Year to All!

Although the Chinese calendar indicates 2004 to be the Year of the Monkey, 2004 will also be the **Year of the Chicken** (one year early, chicken is really 2005). As described below, **the complete sequence of the chicken genome is anticipated early next year** and many additional strides are being made in avian biology. (Admittedly, the chimpanzee draft sequence will also soon be done, so maybe it's still the Year of the Monkey, but then there's the dog, and the zebrafish, and the cow and ?) This issue of the newsletter is appearing slightly early due to the avalanche of chicken genome news.

Chicken Genome Sequence: Impact and Applications - Meeting Report

This meeting, organized by **AviGenics, Inc.** and the **U. of Georgia** was held Nov. 13-14, 2003 in Atlanta, GA. The program began with **Wes Warren, Martien Groenen, Bin Liu** and **Jerry Dodgson** describing progress in completing the physical map and draft genome sequence of the chicken (more below), as well as SNP development. Talks were presented on telomere biology, bioinformatics and functional genomics by **Mary Delany, Dave Burt** and **Larry Cogburn**. The relationship of the sequence/genome to disease was reviewed by **Robin Morgan, Hans Cheng, Ton Schat** and **Hyun Lillehoj**. **Rob Etches** and **Mark Leavitt** discussed projects for transgenic chicken-based biotechnology. **Frank Milward, Stewart Bauck, Jim McKay,** and **Milton Boyle** provided the perspective of breeders and vaccine companies, and **Jean-Marie Buerstedde** discussed B cell development and the DT40 cell line. Two workshops aimed at envisioning future outcomes followed. Workshop A was led by panelists **Martien Groenen, Dave Burt, Bin Liu** and **Hans Cheng** on **Structural and Functional Genomics**. Workshop B was led by panelists **Shane Burgess, Kirk Klasing,** and **Bertrand Pain**, chaired by **Muquarrab Qureshi**, with the topic of **What's Next?**

A major focus of Workshop A was the need to obtain funding (estimated at \$2M) to allow the **Washington U. Genome Center** to complete "**pre-finishing**" of the draft chicken genome sequence. The primary purpose of pre-finishing is to close gaps, extend the size of sequence contigs and enhance overall quality. This provides a much more valuable and reliable product for end users. [A crude analogy would be if the sequence is viewed as a book, pre-finishing would be going from an unbound collection of thousands of loose-leaf pages to an ordered and bound manuscript.] Pre-finishing at this stage is very cost-effective, as the clone libraries remain readily available for automated re-sorting. **If not done now, the required sequence enhancement will be up to local user groups (using grant funds) or, less likely, a genome sequencing center would have to remount the whole chicken sequence effort at a later date. Either of**

these options would be much more costly, less accurate and less timely. It should also be noted that, given the low density of repeats in the chicken genome, a pre-finished chicken sequence may be nearly equal in quality to a finished mammalian genome (e.g., mouse). Pre-finishing would bring the total genome coverage for chicken up to ~8X, about what's now expected for dog and cow. **Efforts are being made to rally industry support to persuade USDA to fund the pre-finishing costs for the chicken genome.** (Sequencing costs to date have been borne solely by NIH.)

Another major focus was the genome sequence as an "enabling tool" that will allow high throughput proteomic analysis, SNP genotyping, and studies of gene expression and function. The potential is there to determine (some of) the source of the genetic variation that's contributed to the remarkable progress made by breeders using quantitative genetics. However, many of these new technologies are costly, and it's unclear how individual poultry scientists (or companies) can afford to utilize them fully.

A third theme of the meeting was that the sequence should attract more interest in use of the chicken as a model for cell and molecular biology. The chicken has a great deal to offer as a model for nutrition, growth, development, disease resistance and other aspects of human biology. Both agricultural and medical applications should ensue from the chicken sequence. For this "unification" to occur, it's important that advances be made in manipulating the chicken genome both in cell lines and in transgenics.

A more detailed summary of the program, abstracts and other aspects of the meeting can be found at <http://www.avigenics.com/symposium1.htm>. Thanks to **Yashwant Deo** and **Bob Ivarie** of Avigenics for hosting the meeting and to **Muquarrab Qureshi** and **Ronnie Green** for support from USDA-CSREES and USDA-ARS. Thanks also to **Janet Fulton** whose notes on the workshops contributed to this report.

Livestock Genomes - Meeting Report

Texas A&M University and the **Baylor Human Genome Sequencing Center** hosted the **Livestock Genomes: Sequence Annotation and Informatics Challenges** Meeting at the Del Lago Conference Center near Houston, TX on Oct. 5-7, 2003. **Richard Gibbs** gave the keynote address and made a strong push for the development of SNP maps. He also made the interesting observation that worldwide sequencing capability is such that about 6 draft mammalian genome sequences (or 15 avian genomes) could be produced annually. As the meeting title implies, there was extensive discussion about the prospects for bioinformatic support for domestic animal genome sequences. As usual, we will mostly be depending on "the kindness of strangers" (e.g., Ensembl, NCBI, UC Santa Cruz and others). There were updates on the bovine sequence and the chicken sequence, as well as those of the dog, pig, macaque, and honeybee. **John McPherson**, among others, discussed what these "emerging" genomes can learn from the experiences of the human genome sequencers, and the meeting ended with a workshop session on "**The Road Ahead**". As part of the workshop, **Leif Andersson** made the point that no other animal species have been phenotyped and selected so intensively as our agricultural animals, and thus there is much to be learned in basic and medical biology from our research. He used his crosses of wild boar x domestic pigs and, more recently, Red Junglefowl x White Leghorn chickens as examples of how fascinating insights will come from unravelling the genetic changes that have been made during the domestication process. Thanks to **Dave Adelson** and his colleagues at Texas A&M and Baylor for organizing this very interesting meeting.

CHICKEN GENOME SEQUENCE REPORT

The Washington U. Genome Sequencing Center (WUGSC) recently projected completion of raw sequence reads for the draft genome sequence by about Dec. 8, and the >6X assembly is being processed as this is being written. The full assembly should be done by year's end. Following a brief period of quality control review, this assembly will be released to bioinformatics groups for analysis and public access (e.g., Ensembl, <http://www.ensembl.org/> and UCSC, <http://genome.ucsc.edu/>; see also the WUGSC site: <http://genome.wustl.edu/projects/chicken/>). A paper is being prepared (for *Nature*) to describe the sequence and its primary attributes. This is expected to appear in the first half of 2004. The WUGSC BAC contig physical map, based on over 133,000 BAC fingerprints (out of 188,369 runs) is comprised of about 280 contigs, two-thirds of which have been anchored to the genetic linkage/chromosome map (see The BAC Page below). The map should be submitted for publication and become publically available in January. A test 5.2X sequence assembly covered about 1 billion base pairs (~97% coverage) with 41% GC content. This included 73 Mbp of interspersed repetitive sequence or ~7%. (Note that some repeats may have been mistakenly merged at this stage and that tandem repeats are under-represented, so the total genome is expected to be 1.1-1.2 Gbp with a somewhat higher repeat content and probably higher %GC.) Thanks to **Richard Wilson, Wes Warren, LaDeana Hillier and all the other WUGSC Staff**, past and present, who've produced the chicken genome sequence. As of Dec. 12, the NCBI Trace Archive (<http://www.ncbi.nlm.nih.gov/Traces/trace.cgi?>) contains 11,524,114 chicken sequences or over 3.8% of the total Archive.

PAG XII & NAGRP/NC-1008 Meeting: See you in San Diego!

PAG-XII will be held **January 10-14, 2004** at the usual location, the **Town and Country Hotel, San Diego, CA**. See www.intl-pag.org/. Registration is also available on-line at the site. Questions can be directed to Scherago Int'l at 212-643-1750 x20 or email pag@scherago.com. **The NC-1008 Multistate Research project committee that replaces NC-168 will meet concurrently, scheduled to begin at 12:45 pm on Saturday, January 10 (Bill Muir, personal communication)**. See <http://www.intl-pag.org/12/12-poultry.html> for the program. **The National Animal Genome Research Program, NRSP-8, will also meet concurrently** with PAG-XII. The NAGRP business meeting will be on Monday evening. Congratulations to **Melissa Schreiweis** of Purdue University, this year's recipient of the **Neal A. Jorgensen Student Travel Award for Poultry!**

WASHINGTON UPDATE:

The **NRI competitive grants program has finally been announced** (see www.reeusda.gov/nri/) with significant changes from previous years. Most important, deadline dates have been changed such that **Animal Protection (includes former animal health programs) and Animal Reproduction deadlines are Jan. 9, 2004 and those for Animal Genomics, Animal Genome Reagent & Tool Development and Functional Genomics of Agriculturally Important Organisms are June 15, 2004**. Total 2004 NRI funding remains uncertain, but was set at \$165M in the conference report of the Consolidated Appropriations Bill passed by the U.S. House and scheduled to be taken up by the Senate in January. New, multi-institutional special programs have been added to the '04 RFA, and it's unclear how much these will detract from typical individual investigator-based awards. Funding limits have also increased, most often to a total of \$500,000 (varies depending on program). The indirect cost limit remains at 19% of total grant funds but may increase to 20% after the Bill passes.

ON THE ROAD AGAIN. UPCOMING MEETINGS:

Plant and Animal Genome XII, joint with NC-1008 and NAGRP annual meetings, Jan. 10-14, 2004, Town & Country Convention Center, San Diego, CA. See www.intl-pag.org/. See above.

British Society of Animal Science Annual Meeting, April 5-7, 2004, York University. See www.bsas.org.uk/meetings/annual.htm.

Second International Chicken Genome Workshop, Stowers Institute for Medical Research, Kansas City, MO. Tentative dates: April 23-24, 2004. For information contact Olivier Pourquié at OLP@Stowers-Institute.org.

XXII World Poultry Conference, June 8-12, 2004, Istanbul Turkey. Email WPSA2004@WPSA2004.org. For scientific matters contact Servet Yalcin, Yalcin@ziraat.ege.edu.tr

Poultry Science Association Annual Meeting (joint with American Dairy Science Assoc. and American Society of Animal Science), July 25-29, 2004, St. Louis, MO. See www.fass.org/2004 for further information.

ISAG 2004, 29th International Conference on Animal Genetics, Sept. 11-16, 2004, Surugadai Campus, Meiji University, Tokyo, JAPAN. See <http://www2.kobe-u.ac.jp/~isag2004/>.

CHICKEN CHIPS, ESTs and cDNAs

A 13K chicken spotted cDNA glass slide array is now available from the Array Facility at the Fred Hutchinson Cancer Research Center, FHCRC. This is the result of combined efforts of FHCRC (**Jeff Delrow** and **Paul Neiman**), the U. of Delaware (**Joan Burnside**), GSF, Munich (**Jean-Marie Buerstedde**) and the Roslin Institute (**Dave Burt**). A similar resource is being made available by **ARK-GENOMICS** at the Roslin Institute (<http://www.ark-genomics.org/resources/chicken.html>) for those outside the U.S. FHCRC arrays are available at \$150 per array. Email requests to genomics@fhcrc.org. NAGRP Coordination funds have been used to make a small number of free test arrays available to NAGRP members. Contact dodgson@msu.edu if interested. A technical report describing details of the construction and use of the arrays and the source of the cDNAs spotted can be downloaded from <http://milano.fhcrc.org/ArrayLab/chicken13k/tech.report/>.

Larry Coghurn at the U. of Delaware has also produced two systems-wide chicken microarrays: a metabolic/somatic (10K) and a neuroendocrine/reproductive (8K) system array. These are being used for transcriptional profiling in tissues of divergently-selected broiler chickens. See <http://udgenome.ags.udel.edu/~coghurn/> to view the data and learn more about these arrays.

A joint project between the U. of Manchester (UMIST, **Simon Hubbard**, **Stuart Wilson**, and **Paul Boardman**) and the Sanger Institute (**Jane Rogers**) is sequencing full length chicken cDNA clones (goal of 10,000) using both UMIST and other libraries. If you haven't already, I suggest you check out the BBSRC ChickEST Database at <http://www.chick.umist.ac.uk/>.

POULTRY MICROSATELLITES

Microsatellite primer kits: Information on chicken microsatellite primer pairs can be found at <http://poultry.mph.msu.edu/resources/microkits.htm>. A version of a framework primer kit (with 147 well-spaced microsatellite marker primer pairs) called the "Comprehensive Mapping Kit #7" is available. Only this and the Population Tester Kit, designed for the rapid testing of the suitability of populations and/or chicken microsatellites for a given application, are still

available, as demand has waned in recent months. If interested, contact: (dodgson@msu.edu) or (hcheng@msu.edu), describing your desired use of primers.

THE BAC PAGE!

The **chicken BAC library** constructed at Texas A&M by **Hongbin Zhang** and colleagues, using (a female of) the UCD001 Jungle Fowl line as its DNA source, consists of over 115,000 BACs (~39,400 each in three sublibraries with *Bam*HI, *Eco*RI and *Hind*III partial digest inserts, called TAM31, TAM32, and TAM33, respectively; Lee et al., *Animal Genetics* 34: 151; Ren et al., *Genome Research* 13: 2754). Filter sets with 36,864 BACs from the *Bam*HI and *Hind*III sublibraries are available, email dodgson@msu.edu. A requirement for receiving a free filter set is that the user agree to provide the name of the probe used and clone locations (for the list described below), so all users can benefit from coordination resources. Alternatively, filter sets can be obtained directly from GENEfinder Genomic Resources (<http://hbz.tamu.edu>) at the cost of preparing them. In either case, once your clone of interest is identified, individual clones can be obtained for a fee from GENEfinder. Contact **Felipe Santos** at contact@bac-center.tamu.edu to purchase BACs. **Pieter de Jong** (Children's Hospital of Oakland Research Institute) has made a **chicken BAC library with ~195 kb inserts (CHORI-261)**, using the same UCD001 source DNA. CHORI-261 has ~73,700 BACs for ~12x haploid genome coverage. Pieter has also generated a **turkey BAC library (CHORI-260)** using DNA from an inbred Nicholas Turkey Breeding Farms bird. If interested in either library and/or filter arrays, see www.chori.org/bacpac/. **Coordination funds have been used to purchase a limited number of CHORI-261 chicken BAC filter arrays and a set can be provided on request while supplies last.** Pieter's group has also constructed a **fosmid library** using the same source DNA. If interested, contact BACPAC at www.chori.org/bacpac/. If you want to isolate single genes or small linked gene families, it may be easier to use a fosmid library (inserts ~45 kb) than to dissect your gene from a large BAC.

Your gene/marker of interest may already have BACs identified that contain it! We've recently updated our list of over **720 different genes and markers that have now been placed on over 5700 specific BAC clones** from the TAM31, TAM32, TAM 33 and CHORI-261 libraries. These are listed at <http://poultry.mph.msu.edu/resources/Resources.htm#bacdata>. These data provide the platform for assembly of the physical map and sequence of the chicken genome (see above) in addition to being a useful resource for those who wish to obtain BAC clones of their gene/region of interest.

PUT YOUR ITEM OF INTEREST HERE

We're happy to include items of general interest to the poultry genetics community in this Newsletter. Please email your contributions to us by March 15 for the next issue.

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