



# POULTRY GENOME NEWSLETTER 2004

Issue No. 4

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## PAG XIII & NAGRP/NC-1008 Meeting

PAG-XIII will be **January 15-19, 2005** at the usual spot, the **Town and Country Hotel, San Diego, CA**. See [www.intl-pag.org/](http://www.intl-pag.org/) for a schedule and registration information. **The abstract deadline is Friday, October 1;** submit at [www.intl-pag.org](http://www.intl-pag.org). Registration is \$475 before Nov. 1 for those from non-profit organizations and \$650 for industry participants, with fees going up by \$100 after Nov. 1 and another \$100 on-site. Student registration is \$275/\$325/\$375, respectively. A weekend rate (Fri.-Sun. only) is available at \$250/\$300/\$350. Among others, Nobel Laureate **Rich Roberts** from New England Biolabs and **Bill Haseltine** from Human Genome Sciences are scheduled to give plenary lectures. **The NC-1008 Multistate Research** project committee will meet concurrently, as will the **National Animal Genome Research Program, NRSP-8**. **Chris Ashwell**, chair for NRSP8-Poultry, and **Doug Foster**, chair of NC-1008, will co-organize the meeting, scheduled to start at 1:40 pm on Saturday, January 15. Applications are again being accepted as part of the registration process from interested graduate students for the **Neal A. Jorgensen Student Travel Award for Poultry** (\$525 travel award and complementary registration). Limited partial travel assistance will be available for NRSP-8 poultry committee members or members of their labs. Please contact the coordinators asap if interested.

## WASHINGTON FUNDING UPDATE:

The **2005 NRI competitive grants program** has been announced ([www.reeusda.gov/nri/](http://www.reeusda.gov/nri/)). **Deadline dates are now Dec. 3, 2004, for Animal Protection and Animal Reproduction; May 17, 2005, for Animal Growth and Nutrient Utilization; and June 15, 2005, for Animal Genomics, Animal Genome Reagent & Tool Development and Functional Genomics of Agriculturally Important Organisms.** (However, the 2005 Functional Genomics competition may be cancelled in favor of adding next year's funds to the available pool for the 2004 proposals yet to be reviewed.) Total 2005 NRI funding remains uncertain, but is recommended at \$180M in the Agriculture Appropriations Bill passed by the House and at \$183M in the Bill recently marked up in Senate Committee. Either would be an increase over the \$165M available for 2004, but, typically, the NRI budget is reduced prior to final passage. In addition, the Senate language requires that 20% of the budget go to integrated programs and 10% to AREA (Ag. Research Enhancement Awards) grants. More disturbing, the Senate Committee Bill includes the following language: **"The Committee notes the substantial increase in public and private sector research related to genomics, genetics, and other breakthrough biotechnology developments. However, this shift in emphasis has resulted in a decline in classical research in the animal and plant sciences. The Committee encourages the Department, especially in the establishment of priorities within the National Research Initiative, to give consideration to research needs related to classical plant and animal breeding."** It's unfortunate that the Senate committee fails to recognize that genomics and genetics form a continuum with "classical breeding".

In other NRI news:

Reviews of the 2004 Animal Genomics grants will take place in mid-November, so the grants themselves will be fortunate to begin within calendar 2004.

**Surprisingly and unfortunately, the Animal Genome Reagent & Tool Development program that has been very successful is now scheduled to end after the 2005 year.** Those who are concerned about this decision may wish to contact Dr. Anna Palmisano, Deputy CSREES Administrator for Competitive Programs ([apalmisano@csrees.usda.gov](mailto:apalmisano@csrees.usda.gov)) and/or Dr. Brad Fenwick, Chief Science Advisor, CSREES-NRI ([bfenwick@csrees.usda.gov](mailto:bfenwick@csrees.usda.gov)).

### USDA Animal Genomics Workshop

The USDA held an **Animal Genomics Workshop** on September 22-23. Scientists representing both ARS and CSREES were invited to participate, with the objective being **“To identify critical infrastructure needs in the post-genome sequencing era of domestic animal genomics, specifically for research communities working with cattle, sheep, swine, and poultry.”**

**Dr. Joseph Jen, USDA Undersecretary for Research, Education and Extension**, acted as host and was able to attend most of the meeting, as did many members of the **National Science and Technology Council Interagency Working Group on Domestic Animal Genomics**, chaired by Dr. Jen and including representatives from NIH, NSF, DOE and other Federal agencies with genomics interests. Immediately following the Workshop, a small group of Workshop participants (representing various species) was invited to meet with the Interagency Working Group to summarize conclusions from the Workshop and respond to questions.

Among the consensus conclusions of the overall Workshop were:

1. There's still a lot to do in terms of genome sequencing. In particular, strong support was expressed for swine genome sequencing and targeted sequencing and/or finishing of other genomes.
2. Tools and reagents are more important now than ever, including access to high throughput technology and instrumentation and continued non-hypothesis-driven research. Thus, there was uniform disappointment in cancellation of the USDA Tools and Reagents program (see above).
3. Animal genomics informs all aspects of animal science and should be considered an integral part of these domains in terms of grant review and research support.
4. Domestic animal genomics research is potentially of great value to the missions of NIH, NSF, etc., because of the huge populations and genetic diversity it studies, along with the opportunity to bridge the genetics to the wealth of physiology, pathology, nutrition and general phenotypic biology that is already known about or yet to come from these species.
5. Related to item 4., it is critical that animal resources in terms of populations, lines, germplasm, and tissues be preserved and expanded via appropriate support mechanisms.

## CHICKEN GENOME SEQUENCE UPDATE

As most readers know, the **Washington U. Genome Sequencing Center** (WUGSC) and the **National Human Genome Research Institute** released the draft chicken genome sequence on March 1, 2004. The sequence derives from a single (female) UCD001 inbred Red Jungle Fowl.

**Using the Sequence.** The sequence, along with a variety of viewing options and analytical tools, can be accessed at three different browsers: the UCSC Chicken Genome BrowserGateway, (<http://genome.ucsc.edu/cgi-bin/hgGateway?org=Chicken&db=0&hgsid=30948908>); the NCBI Chicken Genome Resources, (<http://www.ncbi.nlm.nih.gov/genome/guide/chicken/>); and the EBI's Ensembl Chicken Genome Browser, ([http://www.ensembl.org/Gallus\\_gallus/](http://www.ensembl.org/Gallus_gallus/)). For bulk searches or more complex queries, you may also want to try Ensembl's Ensmart system at [http://www.ensembl.org/Multi/martview?species=Gallus\\_gallus](http://www.ensembl.org/Multi/martview?species=Gallus_gallus). See also the WUGSC chicken site at <http://genome.wustl.edu/projects/chicken/>. It's important to understand that the draft sequence is just that, a draft. If you access your gene(s) of interest, you may find that it includes one or more short stretches of unknown sequence (-NNNNNNN-) or you may find it's missing an exon or two. (Errors in assembly of sequence blocks ("contigs") or chromosome assignment appear to be relatively few, but gaps are more common.) A considerable portion (5-10%) of the sequence contigs are of uncertain location and are placed in the "chromosome unknown" pool. Similarly, there are also smaller pools of sequence contigs that are assigned to a chromosome, but whose location and/or orientation within that chromosome's sequence cannot be assigned with confidence (e.g., GGA1\_random for chromosome 1). As described previously, funds are being sought for generating a "finished" or nearly finished sequence of the chicken genome. Prospects for a "pre-finishing" stage remain hopeful, but still uncertain, at this time.

**Domestic chicken sequences and chicken SNPs.** Through the efforts of **Bin Liu** and **Gane Ka-Shu Wong** and others at the **Beijing Genome Institute** and elsewhere, 0.25X whole genome shotgun sequence sets have been obtained from each of a White Leghorn, a broiler, and a Silkie genome. Since the 6.6X draft sequence is from a Red Jungle Fowl, comparison of these three to it and to each other generated 2.8 million single nucleotide polymorphisms or SNP. This work will be published as a companion to the genome sequence paper, and the data can be accessed at <http://chicken.genomics.org.cn/index.jsp> or the UCSC or Ensembl browsers. This work should be a major contributor to the future of poultry and agricultural genetics.

**BAC Contig Physical Map, ChickFPC and ChickAce.** The WUGSC BAC contig physical map, based on over 133,000 BAC fingerprints is comprised of about 260 contigs, nearly 80% of which have been anchored to the genetic linkage/chromosome map. This map provided an essential companion to the sequence assembly process. For information on how to access the BAC contig map and use this information, go to the browsers listed under "Using the Sequence" or see more information at the end of this newsletter on **The BAC Page**.

## ON THE ROAD AGAIN. UPCOMING MEETINGS:

Advantages of Agriculturally Important Species as Biomedical Models, October 29-31, 2004; Kellogg Center, Michigan State University, East Lansing, MI. See [www.adsbm.msu.edu](http://www.adsbm.msu.edu).

Ninth DISCOVER Conference on Food Animal Agriculture. "Protecting and Managing Animal Genetic Resources for Future Generations: The Next Steps", November 2-5, 2004, Cheyenne, Wyoming. See [www.adsa.org/discover/](http://www.adsa.org/discover/) for further information.

Plant and Animal Genome XIII, joint with NC-1008 and NAGRP annual meetings, Jan. 15-19, 2005, Town & Country Convention Center, San Diego, CA. See [www.intl-pag.org/](http://www.intl-pag.org/).

Symposium on Integration of Structural and Functional Genomics (14<sup>th</sup> Annual Growth Factor and Signal Transduction Conference), September 22-25, 2005, Iowa State University, Ames, Iowa. See [www.bb.iastate.edu/~gfst/homepg.html](http://www.bb.iastate.edu/~gfst/homepg.html)

### CHICKEN CHIPS, ESTs and cDNAs

A 13K chicken spotted cDNA glass slide array is still available from the Array Facility at the Fred Hutchinson Cancer Research Center, FHCRC. A similar resource is available at **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](mailto:genomics@fhcrc.org). **NAGRP Coordination funds have been used to make a small number of free test arrays available to NAGRP members. Additional sets have been secured; contact [dodgson@msu.edu](mailto: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 <ftp://milano.fhcrc.org/ArrayLab/chicken13k/tech.report/>.

**Affymetrix, Inc.** is moving forward with a synthetic oligo "chicken chip" that could be available late this year. Preliminary estimates are that the chip would target 42,000 mRNA sequences (chicken plus a limited number of chicken pathogens) with 16 probe pairs/sequence. Suggestions or comments can be sent to **David Hanna** ([David.Hanna@affymetrix.com](mailto:David.Hanna@affymetrix.com)) of Affymetrix.

The **BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA sequencing project** (mentioned last issue) has announced the public availability of an enlarged set of (full length) chicken cDNA sequences finished at the Sanger Institute. 16212 cDNAs have passed quality control and are available from EMBL/Genbank. A (large) file with all 19076 finished cDNA sequences is also available at <http://www.sanger.ac.uk/Users/mdr/chicken>.

### 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. New Population Tester Kit primers have been obtained, so we now have these both fluorescent labeled or not, depending on your needs. If interested, contact: ([dodgson@msu.edu](mailto:dodgson@msu.edu)) or ([hcheng@msu.edu](mailto:hcheng@msu.edu)), describing your desired use.

## THE BAC PAGE!

The **chicken BAC library** constructed at Texas A&M 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 sub-libraries are available, email [dodgson@msu.edu](mailto:dodgson@msu.edu). **Pieter de Jong** (Children's Hospital of Oakland Research Institute) has made a chicken BAC library with ~195 kb inserts (CHORI-261: ~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, see [www.chori.org/bacpac/](http://www.chori.org/bacpac/). **Coordination funds have been used to purchase several sets of CHORI-261 chicken BAC filter arrays and a set can be provided on request while supplies last. A limited number of the turkey CHORI-260 arrays have also been purchased are available on request.** Pieter's group has also constructed a **fosmid library** using the same source DNA. If interested, contact BACPAC at [www.chori.org/bacpac/](http://www.chori.org/bacpac/).

**BAC Contig Physical Map; ChickFPC and ChickAce.** As noted above, the WUGSC BAC contig physical map, based on over 133,000 BAC fingerprints is comprised of about 260 contigs, nearly 80% of which have been anchored to the genetic linkage/chromosome map (Wallis et al., in press). The mapping effort has been led by **Wes Warren** and **John Wallis** at WUGSC with assistance from **Jan Aerts** and **Martien Groenen** of Wageningen U. and others. The Wageningen group has also developed the **ChickFPC** browser in AceDB format at <http://www.bioinformatics.nl/gbrowse/cgi-bin/gbrowse/ChickFPC>, allowing one to search the map beginning with a known gene, marker, or BAC. Similarly, BAC locations denoted by BAC end sequences can be found on other sequence browsers noted above. At ChickFPC, BACs from the TAMU libraries have the prefix JB, JE, or JH for the *Bam*HI, *Eco*RI and *Hind*III insert libraries, respectively. CHORI-261 BACs have the prefix JA. White Leghorn BACs from the Crooijmans et al. library (*Mammalian Genome* 11: 360-363, 2000) have the prefix bW. See also the overall Wageningen **ChickAce** chicken genome mapping database with emphasis on linkage, cytogenetic, radiation hybrid and BAC contig maps as well as mapping information for phenotypic traits such as QTL at <https://acedb.asg.wur.nl/>.

**Your gene/marker of interest may already have BACs identified that contain it!** See our list of over **910 different genes and markers that have now been placed on over 7800 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>.

### 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 December 15 for the next issue.

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