



# Pig Genome Update

## No. 112 July 1, 2012

**The Swine Genome Sequencing Consortium is pleased to announce** that we have reached another significant milestone in the Pig Genome Project. We have completed the manuscript describing the generation, analysis and annotation of a high quality draft reference pig genome sequence. The manuscript has been submitted for publication and is currently under review.

The manuscript entitled "Pig genomes provide insight into porcine demography, domestication and evolution" describes not only the generation and analysis of a high quality draft reference genome sequence of a single domesticated pig (*Sus scrofa*) but also the analysis of 16 other individual genomes including both 10 European and Asian wild boar (*Sus scrofa*) and 6 domesticated pigs. Amongst, the major farmed animal species the pig is unique in as much as the wild ancestors (wild boar from Europe and Asia) from which it was domesticated are still extant. The analyses provide new insights into the demography of wild boar and their subsequent domestication. For example, we have evidence of a deep phylogenetic split between Asian and European wild boar which points to their divergence about 1 million years ago. Our analyses provide further insight in the domestication of the pig in the past 10,000 years as well as the more recent development of specific breeds.

Analysis of the pig genome and its gene content in an evolutionary context has revealed accelerated evolution of genes associated with immune response and olfaction. Olfaction is clearly important to this scavenging animal. The pig is not only an important agricultural species (pork is the most widely consumed meat globally) but also an important biomedical model. The 1000 Genomes project has revealed that humans carry a burden of potential loss of function mutations. Analysis of individual pig genomes has revealed similar mutations. These mutations potentially extend the scope of the pig as a biomedical model. This manuscript represents the efforts of the Consortium and the authors include scientists from over 50 laboratories in 12 different countries. The Consortium is associated with a series of companion papers of which 17 are currently under review, revision or in press in BMC journals with a further 5-10 in draft (kindly provided by Alan Archibald on behalf of the Swine Genome Sequencing Consortium).

**The International Society of Animal Genetics (ISAG) 2012 Conference in Cairns, Australia** on July 15-20<sup>th</sup> is around the corner. They have an exciting scientific program planned with excellent plenary speakers, workshops and poster sessions, and of course, a truly outstanding location. The theme of the ISAG 2012 conference is "Quantitative Genetics Meets Molecular Genetics" and many of our plenary speakers will reflect this theme. However, the plenary sessions will reflect also a wide variety of other interesting and topical areas in genetics, including gene expression defining phenotypes, ancient DNA analysis of livestock, epigenetics and new technologies. The ISAG conference workshops and symposia will include not only the genomics and DNA testing of specific animal species (e.g. cattle, sheep, goats, birds, pigs, horses, dogs, cats, fish), but there will be also dedicated workshops on animal genome sequencing, immunogenetics, forensics, genetic diversity, epigenetics and comparative genomics. For more information, please see: <http://www.isag.us/2012>. Please join us for a fantastic conference (Provided by Cindy Bottema on behalf of the 33rd ISAG Organizing Committee).

**NRSP-8 rewrite is progressing well.** The NRSP-8 is scheduled to end in September of 2013, so if it is to continue, it must be revised and resubmitted for review by NIFA and the Experiment Stations again this year. The approximate deadline is this September for submitting the revised project. New draft objectives for NRSP-8 and a draft have been circulated. All members of NRSP-8 may receive requests for input into the new proposals. Please respond promptly, as we're on a tight deadline and this will be a huge help to the writing teams. A special thanks to Tom Porter and the writing team for leading this effort.

**SNP chip update.** An Illumina low density SNP panel is currently in production through GeneSeek Inc. The chip will include close to 10,000 SNP and will be available around the end of August (kindly provided by Jeremy Walker).

**Upcoming meetings** (see: <http://www.animalgenome.org/pigs/community/meetings.html>)

33rd International Society for Animal Genetics Conference in Cairns, Australia on July.15-20, 2012. For details see <http://www.isag.us/2012/>

American Society of Animal Science (ASAS), Dairy Science (ADSA), and Canadian Society of Animal Science (CSA) Joint Annual Meeting in Phoenix, AZ on July 15 – 19, 2012. For details see <http://www.jtmtg.org/2012/>

PAG-XXI/NRSP-8 will be January 12-16, 2013, for details see <http://www.intlpag.org/web/>

Gordon Research Conferences: Quantitative Genetics & Genomics, Genetics of Complex Disease, February 17-22, 2013, Galveston, TX for details see <http://www.grc.org/programs.aspx?year=2013&program=quantgen>

PAG Asia to be held in Singapore, March 2013. For details see <http://www.intlpag.org/web/>

**Items for *Pig Genome Update 113*** can be sent to me by no later than September 15 please.

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