

## Research consortium to sequence turkey genome

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Turkeys. Image: Curtis Novak

An international consortium of researchers has begun an effort to sequence the genome of the domesticated turkey, Meleagris gallopavo. The genome sequence will be obtained using the Roche GS-FLX<sup>TM</sup> sequencing platform and the recently launched Roche GS FLX Titanium PicoTiterPlate device and reagents.

The new upgrade to the Roche GS-FLX sequencing system permits more than 1 million individual sequencing reads to be generated for each sequencing run with an average read length of 400 base pairs. The turkey genome will be assembled using shotgun fragments and short and long



paired-end reads. The assembled genome will be compared with the chicken genome sequence to examine similarities and differences in genome organization.

Otto Folkerts, associate director of technology development at the Virginia Bioinformatics Institute (VBI) at Virginia Tech, remarked: "The pilot phase of this project will rapidly establish a two-fold shotgun coverage of the entire turkey genome using the Roche GS-FLX sequencing technology at the Core Laboratory Facility at VBI. This sequence will be of immediate interest to various stakeholders and will be the starting point for our longer-term objective to sequence more than 95 percent of the turkey genome." He added: "The funding for this pilot phase was provided by the consortium members. In 2009, we plan to seek federal and industry support for the full sequencing effort."

The turkey genome sequence will offer considerable benefits to academic and private sector researchers interested in this commercially important source of food. According to the National Turkey Federation, turkey was the fourth most popular choice of "meat protein" for consumers in the United States in 2007. An estimated 271 million turkeys will be raised in 2008.

Ed Smith, professor in the Department of Animal and Poultry Sciences at Virginia Tech, commented: "The turkey genome sequencing effort is a community-driven project. Some of the leading researchers behind this initiative met recently at VBI to participate in a Turkey Genome Sequencing Consortium Mini Symposium. We are very fortunate and excited to have some of the leading practitioners in poultry science and comparative genomics committed to this sequencing effort."

The genome sequence and genomic resources that will be developed from the project should provide turkey breeders with tools needed to improve commercial breeds of turkey for production traits such as meat



yield and quality, health and disease resistance, fertility, and reproduction. Rami Dalloul, assistant professor of poultry immunology in the Department of Animal and Poultry Sciences at Virginia Tech, remarked: "Having the turkey genome sequence at hand will help uncover disease-resistance and immune-related genes that can then be targeted to improve our understanding of disease development in the context of host-pathogen interactions. Such discoveries will help direct our efforts to enhance the turkey immune competence and develop new, more effective disease-prevention strategies." Comparative genomics in avian species, especially as it relates to determining the function of the chicken genome sequence, will also be facilitated by the availability of the turkey genome. Kent Reed, Associate Professor of Veterinary and Biomedical Sciences at The University of Minnesota, commented: "We have learned much from studies that compare the genetic map of turkey genome with the chicken whole genome sequence. This effort will not only provide information on the turkey genome, but will benefit the chicken genome sequence as well."

The turkey genome sequence will enable the integration of other turkey research tools and resources, such as genetic linkage and cytogenetic maps, expressed sequenced tags, predicted genes and proteins, regulatory regions, and other resources. It will also serve as a platform for development of future tools, such as high-throughput gene expression arrays and high-density genetic marker maps based on single nucleotide polymorphisms.

Tim Harkins, marketing manager for genome sequencing at Roche Applied Science, commented: "We are pleased to see that the continuous improvements in sequencing technology, and reductions in cost per Mb of genome sequenced, enable smaller groups of academic scientists to take on the sequencing of larger eukaryotic genomes. This is another example of the tremendous impact the GS-FLX sequencing technology is making on the academic community."



The consortium will be instrumental in the collective annotation of the first assembly of the turkey genome as well as future versions of the sequence. The assembled and annotated genome sequence will be made freely available to the global research community and will be publicly released to GenBank.

Jerry Dodgson, professor of microbiology and molecular genetics at Michigan State University, remarked: "The time is right to sequence the turkey genome. The sequence of the chicken genome is known and continues to be refined. The scientific community has established many of the experimental resources that make this project feasible." He added: "Pyrosequencing on the Roche GS-FLX platform and assembly of the sequence using the publicly available chicken sequence as a reference represents a very cost-effective approach to deliver the turkey genome sequence rapidly to the wider scientific community."

David Burt, professor in the Department of Genomics and Genetics at the Roslin Institute and Royal (Dick) School of Veterinary Studies, United Kingdom, commented: "Having both the chicken and turkey genome sequences will enable, for the first time, the comparison of the information contained in two bird genomes. This will allow us to look for similarities and differences in the coding and non-coding portions of the genomes."

Bruno Sobral, executive and scientific director of VBI, noted: "This project showcases how VBI's capabilities contribute to the development of world-class research initiatives, such as this state-of-the-art sequencing project. We are excited to make our capabilities available to Virginia Tech researchers, the wider scientific community, and other partners as part of this innovative, collaborative sequencing initiative."

Source: Virginia Tech



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