

Landmark Study Finds Industrial Chicken Breeds Seriously Lack Genetic Diversity

February 19 2009

(PhysOrg.com) -- Commercial chicken breeds used to produce meat and eggs around the world have lost at least half of the genetic diversity once present among their ancestors, according to a study conducted by an international team of researchers that includes a UC Davis animal scientist.

The study is the first experimental analysis of genetic diversity for an entire agricultural commodity. It raises concerns over whether the genetic diversity of commercial flocks is sufficient to deal with future challenges.

The global poultry industry produces more than 40 billion birds for meat and eggs annually and has grown rapidly during the past 50 years, leading to intensive selection for traits such as size and egg production. As the industry has become more concentrated in a smaller number of firms, inbreeding and loss of genetic diversity have increasingly become concerns.

“The results of our analysis reaffirm the importance of maintaining a healthy genetic reservoir for chickens, as well as all other food-producing animals, through preservation and conservation,” said Mary Delany, chair of the UC Davis Department of Animal Science and co-author on the study. The findings were published in the Nov. 3, 2008, issue of the *Proceedings of the National Academy of Sciences*.

“It is crucial that breeders be able to readily access the genetic resources

that will enable our flocks to cope with new and recurring diseases, environmental changes, new flock-management practices and even changes in consumer preference,” Delany said. “Biotechnology has great potential to introduce beneficial traits without sacrificing other genetic gains,” she said.

Using the sequence of the chicken genome, published in 2004 based on a UC Davis inbred chicken line called the Red Jungle Fowl, the researchers used a method called single nucleotide polymorphisms or SNP to measure biodiversity among existing chickens. They sampled DNA from more than 2,500 chickens, more than half from commercial flocks, and checked for gene variations that were present in the larger population but missing from the commercial breeds.

The study was led by Hans Cheng of the U.S. Department of Agriculture. Other collaborators on the study were from Purdue University; the University of Alberta, Canada; the Beijing Institute of Genomics; Wageningen University, Netherlands; Cobb-Vantress Inc., Arkansas; Hendrix Genetics, Netherlands; and Illumina Inc., California.

Provided by UC Davis

Citation: Landmark Study Finds Industrial Chicken Breeds Seriously Lack Genetic Diversity (2009, February 19) retrieved 3 May 2024 from <https://phys.org/news/2009-02-landmark-industrial-chicken-lack-genetic.html>

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