

**ABSTRACTS**  
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**SYMPOSIA AND ORAL SESSIONS**

**Ancillary Scientists Symposium: Conservation of Avian Genetic Resources: Current Opportunities and Challenges**

**1 Historical and contemporary issues related to genetic conservation.**  
J. Hodges\*, *Compuserve, Mittersill, Austria.*

Genetic conservation and natural selection worked together over long evolutionary periods. A change occurred about 12,000 years ago during the Neolithic or Cultural Revolution when domestication of animal and bird species placed selection and conservation in human hands. After that, stockbreeders' selection was slow, phenotypic, localized and based upon small populations. Subsequent human global migrations with livestock increased biodiversity within domesticated species and between human cultures. The need for active genetic conservation has grown since the advent of intensive agriculture, the discovery of genetics and the recent genetic revolution. Today mono-systems, scale, global reach, manipulations of genotypes and individual genes make humanity directly responsible for the loss of biodiversity. In the West the era of sustainable integrated communities of people, domestic animals and birds has gone. Today public decisions are based on emerging scientific options and economic values. The basic relationship between the natural world and *Homo sapiens* has changed. The food chain in which livestock and birds are now disposable resources is a major locus of this change. *H. sapiens* is the dominant and exploitive species with vast power. Prospective genetic technologies open a vista of redesigned animals and birds violating the genetic principles of natural selection, ignoring the evolutionary time scale and breaching the historic boundaries of life leading to new levels of potential catastrophe and tragedy. It is simplistic to think that technical conservation of genes and traits is the solution. The issues go far deeper. The need for genetic conservation exists only because mankind behaves with ruthless self interest. The urgent issue is whether society having such awesome power will squander or conserve historic human civilization with its values of community, restraint and sustainability? As scientists in the food chain we need to broaden our world view. Our current values and our definitions of progress are placing genetic resources at risk and are also eroding the civilized history, identity and dignity of *Homo sapiens*.

**Key Words:** Biodiversity, Boundaries, Civilization

**2 Netherlands approach in animal genetic resource conservation: Poultry perspective.** H. Woelders\*<sup>1,2</sup>, C. Zuidberg<sup>1</sup>, and S. Hiemstra<sup>1</sup>, <sup>1</sup>*Centre for Genetic Resources, Lelystad, The Netherlands*, <sup>2</sup>*Wageningen University and Research Centre, Lelystad, The Netherlands.*

In European countries various governmental, private, and NGO actions are being taken to preserve genetic diversity of livestock species. EU-regulations provide a framework for national support actions and subsidies to conserve rare breeds. Several national governments want to stimulate a market driven use of rare breeds such that these breeds will no longer be endangered (*in situ* conservation), without using structural subsidy measures.

In addition, gene banks are being established for *ex situ* conservation. Cryostorage of germplasm is extremely important as the ultimate security against loss of allelic variation and loss of entire breeds, but also to support breeding schemes for *in situ* populations of rare breeds. For these reasons, the Centre for Genetic Resources, the Netherlands (CGN) is establishing collections of germplasm (largely semen) of a number of livestock species, including poultry. In addition, CGN is active in research on genetic strategies to minimise inbreeding, and on cryobiology to increase the efficiency of cryopreservation.

Our recent work on freezing cock semen was focused on finding a suitable replacement for glycerol (which is contraceptive in the hen) as a cryoprotectant. For reasons of hygiene and sample identification we favoured straw freezing, as opposed to the highly effective pellet freezing method. We have worked on improving the medium composition, have tested various cryoprotectants, and optimised the combination of cooling rate and cryoprotectant concentration. The finally developed freezing method resulted in very good fertility with frozen cock semen. Inseminations twice per week with 0.3 billion sperm per insemination resulted in 97% and 86% fertilized eggs with fresh and frozen semen, respectively. The fertility remained high up to day 9 after the last insemination. This indicates that inseminations once a week would even be sufficient for this frozen-thawed semen.

**Key Words:** Genetic diversity, Poultry semen, Cryopreservation

**3 Avian genetic stocks: The high and the low points from an academia researcher.** M. E. Delany\*, *University of California, Davis.*

Specialized, selected and mutant stocks of poultry including chicken, turkey and Japanese quail, are important tools for research in numerous disciplines spanning agricultural science, basic biology and biomedical research. Genetic resources of poultry, from breeds to mutant lines, continue to support the creation of new knowledge, applied and basic, not only in genetics and genomics, but also in oncology, physiology, behavior, nutrition, and developmental biology, to name a few. However, as most poultry biologists know, stock losses continue unabated, living stock conservation remains the only sure mechanism for sustaining the resources, and conservation is on a case by case basis at the institutions holding the stocks. Visibility and recognition of the problem have definitely improved via the efforts of the Avian Genetic Resources Task Force (Pisenti et al. 1999), and the USDA-ARS National Animal Germplasm Program, and individual scientists (Miller et al. 2004); but at agricultural institutions where most stocks reside, the funding of facilities and staff continues to erode. There is little doubt that stocks will in fact vaporize if the so-called formula funding undergoes reallocation, as is currently under discussion. The significance of our extant poultry research resources is underscored by the availability of the chicken draft sequence wherein great opportunity exists to understand the genetic, molecular and physiologic basis for cellular and organismal phenotypes, through analysis of our unique poultry resources. Indeed, the consideration for a high point of the stocks issue has to be that from Bateson (1902) to Hillier et al. (2004), the chicken has crossed a long and winding road back to the future as a premier genetic model organism. The low point remains unchanged over the last two decades, the consistent news of terminated research lines, the count for 2004 being at least another 20 lines.

**Key Words:** Genetic resources, Poultry stocks, Conservation

**4 Why do we need to conserve what we have? A post-genome sequencing perspective on existing chicken strains.** M. Miller\*, *Beckman Research Institute of the City of Hope National Medical Center, Duarte, California.*

Now that we have the chicken genome, what can we do with the remaining chicken strains? Far more than we could before, particularly if remaining strains and mutant lines are preserved. This is especially true for the possibility of defining genes that influence immunity and host-pathogen interactions. For example, now that significant sequence data are available, work to define which gene or genes within the major histocompatibility complex (MHC) *B* are responsible for the strong genetic influence of the MHC in responses to virus-induced tumors can move rapidly forward. Inbred, congenic and recombinant MHC lines that are still available provide a means of resolving which MHC genes are most influential. Already the comparison of the Red Jungle Fowl MHC haplotype with haplotypes in other strains has revealed hot spots of variability in the form of single nucleotide polymorphisms and insertion/deletions. Indeed, closely related recombinant haplotypes in fully congenic lines differing in Marek's disease responsiveness have targeted a candidate locus for MD resis-

tance. Alleles at this candidate locus will be compared using additional congenic MHC lines differing in MD response. Existing inbred lines and new lines generated from them will be needed to pursue functional interactions among members of multigene families including new families, as well as those in the MHC *B* and *Y* regions. With the genome sequence now available additional lines carrying developmental mutants and loci affecting growth will lead to genetic mechanisms for normal development being defined. Phenotypic characteristics presently mapped to particular linkage groups may now be defined in terms of genes provided that relevant stock remains available. The genome sequence opens the way to moving quickly forward. Defined lines carrying mutations and inbred lines against which alleles can segregate are inherent in the progression of these studies. Further loss of lines will curtail these interesting and important pursuits.

**Key Words:** Genome sequence, Genetic strains, Conservation

**5 Use of genetic strains of chickens in studies of ovarian cancer.** P. Johnson\*, *Cornell University, Ithaca, New York.*

Investigation of basic factors involved in the etiology of ovarian cancer in women has been hampered by the lack of an animal model. Most animals do not spontaneously develop ovarian cancer with the exception of the domestic hen. We have access to two strains of White Leghorn hens (Cornell C and K) which were previously compared with respect to incidence of ovarian cancer. These strains were derived from a similar genetic background and have a different incidence of ovarian cancer at 2 years of age. We repeated this and found that C strain hens which died spontaneously at 2 years of age had greater than 20% incidence of ovarian cancer. In contrast, no tumors were observed in the K strain hens although we have observed tumors in K strain hens at 3-4 years, an onset which is delayed compared to the C strain. To evaluate differences that could be related to the etiology of the tumors, we collected blood samples from different aged hens of the two strains at defined stages of the ovulatory cycle and assessed plasma estradiol and progesterone. Plasma estradiol was significantly higher in the C strain compared to the K strain ( $p < 0.001$ ) at every age while progesterone was not consistently different between strains. Most significantly, ovulation rate was not different between the two strains. We also assessed estradiol production by various compartments of the ovary. Follicles from the C strain hens produced amounts of estradiol not different from that of K strain hens. The difference in plasma estradiol could be attributed to the fact that the ovaries of C strain hens were significantly larger than those of K strain hens both on an absolute basis as well as when expressed relative to body weight. Interestingly, estrogen, when prescribed as estrogen-only replacement therapy for women, has been implicated as a risk factor for ovarian cancer. Although previous workers have characterized ovarian adenocarcinoma in the hen, they have not utilized two related genetic strains of hens with different incidences of the tumor. The use of two strains may reveal an important difference that underlies the differential susceptibility to ovarian cancer.

**Key Words:** Hen, Ovarian cancer, Animal model