



# Globaldiv

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### Editorial - Perspectives for poultry genetic resources

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#### Status

The poultry sector is the most dynamic livestock subsector, with fast genetic improvement, high growth in meat consumption and high levels of vertical integration and concentration. Poultry meat consumption is projected to grow at 2.5% per annum to 2030, exceeding other species (FAO, 2006). Developments in breeding, feeding and housing have enabled an unprecedented increase in production and productivity. Breeding had the biggest contribution at the annual gain in meat and egg production per animal. While commercial poultry genetics, developed from a limited number of breeds during the last century in Europe and North America, well characterized and intensively selected, supply an estimated

67% of global poultry meat production and 50% of global egg production, non-descript local breeds without structured breeding programmes predominate in the small-scale backyard and family poultry sub-sectors which provides up to 90% of total poultry production in some of the least developed countries.

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In such low external input systems with few links to formal markets, broody local breeds with good scavenging behaviour are better adapted than commercial hybrids. In a few cases, hybrids or crossbreds from special breeding programmes selected for adaptive and performance traits outperform local breeds.

FAO's Global Databank contains breed-related information from 182 countries on 16 avian species, with about 2000 breeds in 3505 country-level breed populations. Many breeds have been reported by more than one country; these populations have been linked and are referred to as "transboundary" breeds. 1644 "local", 85 "regional transboundary" and 157 "international transboundary" poultry breeds have been reported (FAO, 2007a). The number of local breeds in a region is influenced by the history of breed formation and the number of breeds that had been developed and described before commercialization of the sector began.

## Threats

Population data - a prerequisite for breeds' genetic management and the assessment of the risk status - are missing in most cases, primarily due to the difficulties involved in monitoring small livestock, and the low importance that governments tend to attribute to poultry. As a result, 36% of reported breeds are of unknown risk status. Out of 2000 reported avian breeds, 9%, mainly chickens and mainly from Europe, are reported to be extinct; this is fewer than in mammalian species (FAO, 2007a). A further 30% of avian breeds are classified as being at risk; this is a higher figure than for mammalian species. The regions with the greatest proportion of their avian breeds classified as at risk are those that have the most highly-specialized/commercial industries. Two additional recent developments may further threaten poultry genetic diversity as a result of the structural changes they bring which may further push local breeds and smallholder production systems out of the market: outbreaks of highly pathogenic avian influenza (HPAI) and increasing feed prices. But in an enabling environment they may also do the opposite by confining smallholders to niche markets and production for home consumption, reducing their propensity to switch to higher yielding exotic breeds. The HPAI related movement controls and banning of exhibitions led to a reduction in the number of breeders and increased inbreeding in some European fancy breeds. However, due to difficulties in data collection, no hard data are available to show that HPAI has directly decreased the number of breeds (EFSA, 2008). If the present increase in feed prices - the major cost of production - continues, commercial poultry with their very good feed conversion ratio may further gain competitive advantage over local breeds. It is therefore timely to take stock of poultry diversity and conservation measures.

Information on poultry conservation programmes is not easy to find, but they are fewer in number than those for large mammalian species. Only 15% of all countries had poultry conservation programmes (*in-vivo* and *in-vitro*). Such programmes cover local populations but also subpopulations of transboundary breeds. Around 25% of chicken breeds and fewer than 10% of the breeds of other species are covered by a conservation programme, with little information available about the efficiency of the



programmes. Half of the reported programmes were run entirely by governments, the others were run in cooperation with the private sector, research groups and NGOs.

Cryoconservation technology for avian species lags far behind that for mammals (Blesbois, 2007). Cryoconserving embryos is not possible for avian species, meaning that the female genome and mitochondrial DNA are not conserved. Moreover, a number of technical problems associated with semen cryoconservation in avian species still have to be overcome. Thus, the efficiency and efficacy of ex situ conservation will depend on advances in reproductive and cryoconservation technology.

It can be concluded that poultry genetic diversity faces a high level of risk, with 30% of reported poultry breeds at risk, a lack of characterization and few structured breeding or conservation programmes, particularly in developing countries.

## Opportunities

In developing countries, the role of poultry, especially chickens, in small-scale farming and the preference of consumers for meat from local birds will support the continued use of many local breeds, thereby reducing the need for direct conservation interventions. In such cases, selection and the gradual improvement of local breeds can increase their production potential, in-step with changes in the production environment, helping to maintain competitive advantages over commercial lines. In industrialized countries, actions such as the new housing regulations in the European Union are changing the production environments, which may have consequences on breeding programmes. Although these regulations have not yet led to a change in the genetic basis of commercial chicken production, research in behaviour in different housing systems has increased.

Poultry are the only group of species with a well-developed hobby and fancy breed segment in parallel to breeds used for food and agriculture. This practice offers opportunities for in vivo conservation, although such breeders focus on exhibition rather than production traits, and the many variations in feathering and colour shown by some breeds should not be taken as an indication of high genetic variability.

Research institutes and universities in North America and Europe try to conserve local breeds, mainly of chicken, and experimental lines that are no longer used (FAO, 2007a). Usually, breeds of specific phenotypes with low population numbers and therefore at risk were included in conservation programmes. In situ conservation of poultry genetic resources is not necessarily dependent on high-tech approaches or facilities, but mainly on breeding skills and recording. Although the technologies are known and software is available to manage small populations, many hobby and fancy breeders will need training in the use of such tools.

Within-breed diversity is large in poultry breeds of all species, due to past and current gene-flow; however, knowledge about genetic diversity is still lacking, even in developed countries. For the most important poultry species, high within-breed diversity means that the diversity of phenotypes between breeds does not fully reflect genetic diversity (Granevitze *et al.*, 2007).



Many conservation decisions to date have been based mostly on between-breed diversity and risk levels based on population figures, often at national level only. Diversity and characterization studies are therefore prerequisites for rational conservation decisions. International research projects such as AVIANDIV and GLOBALDIV are extremely important in this regard, and the need for meta-analysis across countries and regions cannot be over-emphasized.

## Where to go from here?

The Global Plan of Action for Animal Genetic Resources (FAO, 2007b) emphasizes countries' responsibility for the management of animal genetic resources. Characterization, inventories and spatial information are needed for improved management of poultry genetic resources. While commercial breeding will continue, strategic breeding programmes of local breeds are needed to reflect the important role of poultry for food security, rural livelihoods and gender equity. Valuable genetic material should be conserved as a precautionary measure in view of the rapid structural changes affecting the poultry sector and the risks (most notably epidemics) facing avian species kept at high densities all over the world.

High within-breed diversity, especially in chickens, and the relatively large number of transboundary poultry breeds and lines have implications for conservation programmes. The inclusion of breeds from unconnected and distinct geographical locations may increase the between-breed diversity captured in conservation programmes even if no detailed molecular characterization information is available. Breeds that have not been genetically managed and those without closely related populations should be prioritized for conservation programmes. National programmes that ignore closely related and non-threatened breeds elsewhere may lead to suboptimal allocation of funds and conservation efficiency (Simianer, 2005); conservation strategies should, therefore, be developed at supra-national level.

In vitro conservation of local breeds, wild relatives and populations with known specific traits should get a high priority at the global level. Because commercial lines contain a share of the genetic diversity, they should also be included in national cryobanks; the relevant operational protocols would need to be developed.

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## Article of the month - Molecular characterization of genetic diversity in chickens

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Among agriculturally used poultry species, chickens are the most important and provide an important source of human food. The red jungle fowl, which is believed to be the progenitor of the domesticated chicken, has its widest distribution in East Asia, from Pakistan through China, Eastern India, Burma, most of Indo-China, and on the islands of Sumatra, Java and Bali (Crawford, 1990). As in other livestock species, sequence variation in mitochondrial DNA, in particular in the highly polymorphic D-loop region, has been used to study domestication events and relationships in the chicken. Results suggested that several ancestral chicken populations contributed to the maternal genetic make up of the species, which supports the theory of multiple origins of domestic chickens in South and Southeast Asia (Liu *et al.*, 2006; Oka *et al.*, 2007). Since domestication, chickens have been distributed to various countries, continents and cultures. As a result of many years of domestication and breeding, a wide range of chicken breeds exist today. This heterogeneous group of chicken populations encompasses more or less unselected indigenous chickens and ecotypes of various regions in the world, standardized fancy breeds selected for morphological traits and maintained for leisure activities and commercial lines. Furthermore, the chicken also serves as a model organism for studies in biology and agriculture (Siegel *et al.* 2006), and a wide range of experimental lines have been developed for research purposes.

Genetic diversity of chickens has been divided into a limited number of commercial lines on the one hand, and a vast range of non-commercial populations on the other hand. An increasing number of local chicken breeds are under threat of extinction, and valuable genotypes and traits may be at



risk of being lost (Blackburn 2006). To conserve genetic diversity, a comprehensive characterization of chicken breeds collected from around the world is required. Such a survey should include data on population size, geographical locations, production systems to which they have adapted, phenotypic attributes and information about breed history (Tixier-Boichard *et al.*, 2008). However, the wide range of population types, their large phenotypic variation and geographic distribution on the one hand, and the limited or even missing reliable information about genetic features and relationships between them on the other hand, make it difficult to establish efficient measures counteracting the genetic erosion within this species. Molecular markers, therefore, may provide important information that can be used as an initial guide (Weigend and Romanov, 2001).

In the last decade, microsatellites have been most commonly used and successful application of these types of markers in biodiversity studies has been reported for all major livestock species including chickens (reviewed by Weigend and Romanov, 2001; Delany, 2003). In 2004, the International Society for Animal Genetics and the Food and Agriculture Organization published a revised list of 30 microsatellite loci to be used for evaluating genetic diversity in chickens (Hoffmann *et al.* 2004). Several biodiversity studies have been conducted using all 30 or a subset of these recommended loci. The seven most relevant studies are listed in Figure 1.

The number of markers used per study range from 20 to 40 markers, and the number of breeds/populations from five to 65. Most studies focus on breeds from local regions and an analysis including worldwide data is still lacking. For 28 of the 30 FAO-recommended markers, data for around 100 breeds (Fig. 1; 98-135 breeds per marker) are currently published. Moreover, additional studies including Hungarian, West African and Vietnamese breeds are underway and will augment this data set in the near future (personal communication M. Tixier-Boichard, H. Jianlin; unpublished data S. Weigend). A global analysis of all available data should be aimed for. However, difficulties in merging microsatellite data sets generated in different laboratories are generally known. A first attempt at merging data sets was undertaken by Berthouly *et al.* (2008), who successfully calibrated 14 of 22 markers (marked in grey in Fig. 1) and thus could include data previously generated in a different laboratory in their analyses.

Insight into the extent of diversity of a wide range of chicken breeds originating from various continents and regions (see Figure 1) has been gained using microsatellites in numerous studies (Wimmers *et al.*, 2000; Berthouly *et al.*, 2008; Chen *et al.*, 2008) including the European research project AVIANDIV and follow-up studies (Rosenberg *et al.*, 2001; Hillel *et al.*, 2003; Granevitze *et al.*, 2007). Overall, results suggested that Jungle Fowl populations and traditional unselected breeds are widely heterogeneous populations that may include a large portion of the total genetic diversity. Within commercial chickens, broiler lines were slightly more polymorphic than layers. Among the layers, the white layers were less polymorphic than the brown layers. In recent years, there has been concern about reduced genetic variability in commercial white egg layers that originated from a sole breed, the Single Comb White Leghorn. Although findings of the AVIANDIV project support this concern to some extent, commercial lines still exhibit a considerable amount of variation at microsatellite loci.



Reference	origin of breeds	# of breeds	ADL0268	MCW0078	MCW0081	MCW0248	MCW0295	MCW0222	MCW0067	MCW0069	MCW0183	MCW0330	MCW0037	ADL0278	LEI0094	MCW0034	MCW0216	LEI0166	MCW0014	MCW0111	MCW0098	MCW0123	MCW0165	ADL0112	LEI0234	MCW0206	MCW0103	MCW0104	MCW0016	MCW0020	MCW080*	MCW0284	LEI0192
Berthouly 2008	French, Asian	20																															
Granevitze 2007	Asian, European	65																															
Muchadeyi 2007	Zimbabwean	13																															
Mwacharo 2007	East African	19																															
Rosenberg 2001	European	20																															
Tadano 2007	Japanese	11																															
Tadano 2008	Japanese	8																															
Zanetti 2007	Italian	5																															
<b>Total # breeds genotyped per marker</b>			135	135	135	135	135	135	130	130	130	130	128	128	125	120	120	118	118	118	118	113	113	113	115	115	98	98	98	85	39	39	

\* not FAO recommended  
in unterster spalte sind doppelte breeds rausgerechnet!

Reference	Origin of breeds	# of breeds	ADL0268	MCW0078	MCW0081	MCW0248	MCW0295	MCW0222	MCW0067	MCW0069	MCW0183	MCW0330	MCW0037	ADL0278	LEI0094	MCW0034	MCW0216	LEI0166	MCW0014	MCW0111	MCW0098	ADL0112	LEI0234	MCW0206	MCW0123	MCW0165	MCW0103	MCW0104	MCW0016	MCW0020	MCW0284	LEI0192	# of additional markers
Berthouly 2008	French, Asian	20																													0		
Granevitze 2007	Asian, European	65																													1		
Muchadeyi 2007	Zimbabwean	13																													1		
Mwacharo 2007	East African	19																													0		
Tadano 2007	Japanese	11																													26		
Tadano 2008	Japanese	8																													26		
Zanetti 2007	Italian	5																													0		
<b>Total # breeds genotyped per marker</b>			135	135	135	135	135	135	130	130	130	130	128	128	125	120	118	118	118	118	118	113	113	113	115	115	98	98	98	19	19		

Figure 1: Seven biodiversity studies in which a subset or all 30 FAO recommended microsatellites were employed. Markers included in the respective study are marked in black. The reference, origin of breeds, number of breeds per study and number of additional non-FAO-recommended markers, as well as the total number of breeds to date evaluated per marker are given. Breeds included in multiple studies were counted only once in the total number of breeds evaluated per marker. The grey-shaded markers were successfully calibrated for a global analysis (Berthouly et al. 2008). It should be noted that there are additional studies available, which were not included in this list, due to either focusing exclusively on commercial or inbred lines (Crooijmans et al. 1996; Zhou and Lamont 1999) or employing non-FAO recommended markers (Wimmers et al. 2000) and using pooled DNA (Crooijmans et al. 1996; Hillel et al. 2003).



Hillel *et al.* (2007) undertook a large-scale analysis of 2,000 individuals from 65 populations representing different chicken types from various geographical regions. Individuals were genotyped at 29 microsatellite loci and a model-based Bayesian population structure analysis (as implemented in STRUCTURE) was carried out. Results indicated that the 65 populations split into groups corresponding to their geographic origin and cultivation history, i.e. Asia, Europe and Africa. Using the same set of chicken populations, Granevitze *et al.* (2007) showed that the degree of polymorphism varies between clusters. The relatively low genetic diversity observed in the native European breeds, mainly standardized fancy breeds, was presumably due to positive assortative mating and small effective flock size. In contrast, native populations from Africa and Asia had high genetic diversity and did not show a typical population structure. Differentiation between these populations (also called ecotypes) may be seen only between populations of distant areas and countries (Muchadeyi *et al.*, 2007; Mwacharo *et al.*, 2007; Chen *et al.*, 2008; Berthouly, 2008).

It should be noted that microsatellites are predominantly located in non-coding regions of the genome, and may collectively be considered as neutral to selection. Hence, differences in allele frequencies among populations are probably the result of genetic drift and founder effects, on the one hand, and crossbreeding, in many cases unrecorded, on the other hand. One of the challenges in the near future will be to build the link between modern genomic tools and variation in genes encoding functional variance. The chicken genome sequence draft and its ongoing improvement, and the huge number of available single nucleotide polymorphisms (SNPs) may provide an excellent source of information for this purpose. Depending on their localization and function in the genome (coding/non-coding genome region; synonymous/non-synonymous to amino acid sequence), the use of SNPs in biodiversity studies can lead to different phylogenetic outcomes (Soller *et al.*, 2006).

In the AVIANDIV project, 1 SNP per 50 bp was found on average in a subset of 10 highly diverse chicken populations (10 individuals per population; Schmid *et al.*, 2005). This SNP frequency is much higher than reported by the International Chicken Polymorphism Map Consortium (Wong *et al.*, 2004), who found about 5 SNP per 1,000 bp by comparing sequences of different domestic breeds. The high frequency found in the AVIANDIV project presumably reflects the wide genetic spectrum of chicken breeds collected, suggesting a much greater actual number of SNP in the chicken genome than previously assumed.

As in other farm animal species, initiatives are underway to develop genomic 60K SNP arrays for chickens. SNP arrays with a lower number of loci have already been used to assess genetic diversity in the chicken. Genotyping ~3000 SNPs in commercial chicken lines and other resource populations indicated that individual commercial breeding lines have lost 70% or more genetic diversity. Only 25% of this loss can be recovered by combining all stocks of commercial poultry (Muir *et al.*, 2007). However, it appears that modern breeding was not the primary source of this loss of alleles. The majority of the alleles were lost prior to the formation of the current industry. Andreescu *et al.* (2007) assessed the extent of linkage disequilibrium (LD) in nine commercial broiler breeding populations using genotype data for 959 and 398 SNPs on chromosomes 1 and 4, respectively. Results showed



that in these lines LD did not extend much beyond  $\sim 0.5$  cM, which is shorter than previously reported for other livestock species. However, it seems to be much larger in White Leghorn based breeds. At short distances (within 1 cM), LD tended to be consistent across related populations. Calculating the correlation of LD between neighboring SNPs within and between populations closely matched the line relationships based on marker allele frequencies. Thus, there are clues that this approach is equivalent to estimating kinship coefficients, and it might be of interest in future biodiversity studies not only in the chicken.

Saturated SNP data will allow a new level of characterization of the chicken gene pool that will aid in elucidating the biological function of genes, and hence the assessment of genetic diversity in functional traits at the molecular level. We should, however, keep in mind that the new, high-throughput SNP assays are still expensive, although costs will reduce over time. The link between modern genomics and biodiversity will facilitate a sustainable management of genetic diversity in poultry as in other farm animal species and ensure its exploitation for human benefits.

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# The breed of the month - Establishing a conservation flock in "Vorwerkhuhn" chicken breed - a case study of *in-situ* conservation of local chicken breeds in Germany

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The "Vorwerkhuhn" is an old German chicken breed created by Oskar Vorwerk at the beginning of the 20th century. Besides the fact that this breed is pretty to look at, we used this breed to establish the first German chicken conservation flock, according to a well defined concept recommended by FAO (FAO, 1998). At the time of the establishment of the conservation flock of the "Vorwerkhuhn" in 1999, the breed was at risk of extinction.



## Principle

The project started by collecting individuals from nine fancy breeders and currently 14 breeders are involved. The genetic management of the population is based on sire rotation, i.e. each sire is replaced by one of his sons in every generation, to avoid mating of closely related birds, and hence to reduce the rate of inbreeding. All birds have pedigree information from the father's side. Sire families are usually established in January of each year, and hatching eggs are collected for three hatches. The first hatching eggs rotate, i.e. they are given to the next breeder in the chain. From these, hatched males are the potential sires for the next generation. The second and third hatch of the breeding season are used to obtain the potential breeding hens. The generation interval is one year.

## Record keeping

Pedigree information and phenotypic records (including body weight) are recorded electronically. Information are available starting with the founder population. All potential breeding cocks and dams are phenotypically evaluated (in fall) according to the breed standard. The weight of hatching eggs (should be above 54g) is recorded, as well as body weight at 2, 8, 16, and 20 wks of age. A few breeders record laying performance during the whole year (optional).



## Veterinary control

Blood samples of two males and two females per flock are taken and checked for *Salmonella pullorum* and *Mycoplasma gallisepticum* infections. Excrements (one sample per flock collected from four different sites in each stable) are checked for endoparasites, bacteria in general, and salmonella. In some cases (depending on the region) blood samples are tested for H5- and H7- antibodies.

## Cross breeding and niche market

Since laying performance of the "Vorwerkhuhn" is rather low (about 180 eggs) and eggs are small (50-55g) as well, it is difficult to place the breed into a niche market. To improve the economic situation for breeders we started a crossing experiment to obtain hybrids for egg and partly meat production as well. Thereby, the conservation flock remains untouched (no crossing into it). We used a commercial line from Lohmann Tierzucht GmbH (Lohmann Tierzucht GmbH is supporting the project) to cross females with Vorwerkhuhn cocks. Chicks can be color sexed. This hybrid is called "Kollbecksmoor Huhn". Our first results show that this hybrid has acceptable laying performance (250 eggs, 60g) and the bird can be sold at a reasonable price to small producers.

## Additional information

More information on the "Vorwerkhuhn" conservation flock can be found at: <[www.erhaltungszucht-vorwerkhuhn.de/index.html](http://www.erhaltungszucht-vorwerkhuhn.de/index.html)>. To learn more about the „Kollbecksmoor Huhn“ see: <[www.kollbecksmoorhuhn.de](http://www.kollbecksmoorhuhn.de)>.

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## Events calendar

- World Biodiversity Congress  
Chiang Mai, Thailand, 20-22 November 2008
- 10th World Conference on Animal Production  
Cape Town International Convention Centre, Cape Town, South Africa, 23-28 November 2008
- Horizons in livestock sciences conference 2008. Christchurch Convention Centre - New Zealand. 28-30 October 2008.  
[www.csiro.au/events/Horizons2008.html](http://www.csiro.au/events/Horizons2008.html)
- 64th British Cattle Conference, 2009. Telford, England. 19-21



January 2009. [www.cattlebreeders.org.uk/conference/index.php5](http://www.cattlebreeders.org.uk/conference/index.php5)

- ANA World Conference "Animal nutrition: preparedness for the challenge". New Delhi, India. 14-17 February 2009. [www.anft.org](http://www.anft.org) or else [www.anaworldcon2009.in](http://www.anaworldcon2009.in)
- Joint International Agricultural Conference 2009. Wageningen, NL. 6-8 July 2009. [www.jiac2009.nl](http://www.jiac2009.nl)

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