Deutscher Tropentag 1999 in Berlin
Session: Biodiversity and Development of Animal Genetic Resources

Genetic Distance Estimation between Chicken Populations of Tropical and Subtropical Countries based on Microsatellites

Klaus Wimmers[1], Siriluck Ponsuksili[2], Torsten Hardge[3], Anne Valle-Zarate[4] and Peter Horst[5]

[1, 2] Institut für Tierzuchtwissenschaft, Rheinische Friedrich-Wilhelms-Universität Bonn, Endenicher Allee 15, 53115 Bonn, Germany
[1] kwim@itz.uni-bonn.de; [2] spon@itz.uni-bonn.de
[3, 5] Institut für Nutztierwissenschaft, Humboldt Universität zu Berlin, Invalidenstr. 42, 10115 Berlin, Germany
[3] torsten.hardge@rz.hu-berlin.de; [5] phorst@rz.hu-berlin.de
[4] Institut für Tierproduktion in den Tropen und Subtropen, Universität Hohenheim, Garbenstr. 17, 70593 Hohenheim, Germany
[4] valle@uni-hohenheim.de

Abstract
The identification of important genetic resources and the prevention of further loss of genetic variation is an important task. In developing countries selection pressure for production traits is low and traditional chicken breeds are used in rural animal production systems. Therefore the evaluation of exotic local chicken populations as genetic resources is of interest in efforts to maintain genetic variation. Using 22 microsatellites, 22 local chicken populations (n=405) derived from Bolivia, India, Cameroon, Nigeria and Tanzania were evaluated for their genetic variability and were compared with an experimental chicken line, Dahlem Reds, derived from commercial Rhode Island Reds. Between 2 and 11 alleles per locus were detected. All populations showed high heterozygosity with the lowest value of 45% (Aseel from India) and highest value of 67% (Arusha from Tanzania). A dendrogram was constructed based on CHORD distance by UPGMA analysis. Within this tree the populations were assorted according to their geographical origin. Bootstrapping values were between 37 % and 99%. The contribution of the determination of genetic variability with genetic markers to the decision on conservation and/or further use of the populations in crossbreeding programs designed to create genetic stocks with improved adaptability and productivity in tropical countries is discussed.

Keywords: chicken, genetic resources, biodiversity

Introduction
Poultry production is an important livestock sector in the tropics contributing to a high proportion of human supply with animal protein through meat and eggs. It is especially favourable to the smallholder systems of the developing countries of the tropics due to low capital investments, high cost efficiency and low production risk. Though the importance of local chicken populations in human supply, information on their genetic make up with respect to performance, adaptability, resistance, genetic variability and genetic relationships is scarce. In chicken breeding high selection pressure and the use of only a few breeds potentially leads to the loss of genetic variation. This is mostly recognised as the loss of rare breeds especially in developed countries. This led to the sense that the identification of important genetic resources and the prevention of further loss of genetic variation is an important task. In developing countries selection pressure for production traits is low and traditional breeds are

used in rural animal production systems. Therefore the evaluation of exotic local breeds as genetic resources is of interest in efforts to maintain genetic variation. An important contribution to the identification of genetic resources is the estimation of genetic variation within and between populations. Here we report on the estimation of genetic variability of local chicken populations of several tropical and subtropical countries based on microsatellite analysis. The study was done in the framework of an EC STD3 project "Evaluation of local poultry resources for creating genetic stock with improved adaptability, productivity and disease resistance in tropical environments" (project co-ordinator: Prof. Dr. P. Horst).

Material and Methods

Twenty-two local chicken populations (n=405) derived from Bolivia, India, Cameroon, Nigeria and Tanzania were evaluated for their genetic variability by genotyping at 22 microsatellite loci. The samples of Bolivian, Nigerian and Tanzanian populations were collected in different ecological zones of these countries. The Cameroon population was originally sampled in the North-West-Province and then kept as small flock at the research station of the Institute of Animal Science, Humboldt University of Berlin. The Indian chickens were kept at the Central Avian Research Institute, Izatnagar, India. In addition, 20 individuals of an experimental chicken line derived from commercial Rhode Island Reds, Dahlem Reds, were used for comparison. These experimental line was also used for crossbreeding with the exotic chicken in the project mentioned above.
Genotyping were done by routine PCR protocols as described elsewhere and microsatellite alleles were detected and counted using an automated DNA-sequencer and the corresponding software (A.L.F., Pharmacia-Biotech).
Heterozygosity was calculated according to Nei (1987). For estimation of genetic variation between the populations the CHORD genetic distance (Cavalli-Sforzy and Edwards, 1967) was calculated with the PHYLIP software (Copyright 1986-1993 by J. Felsenstein and University of Washington).

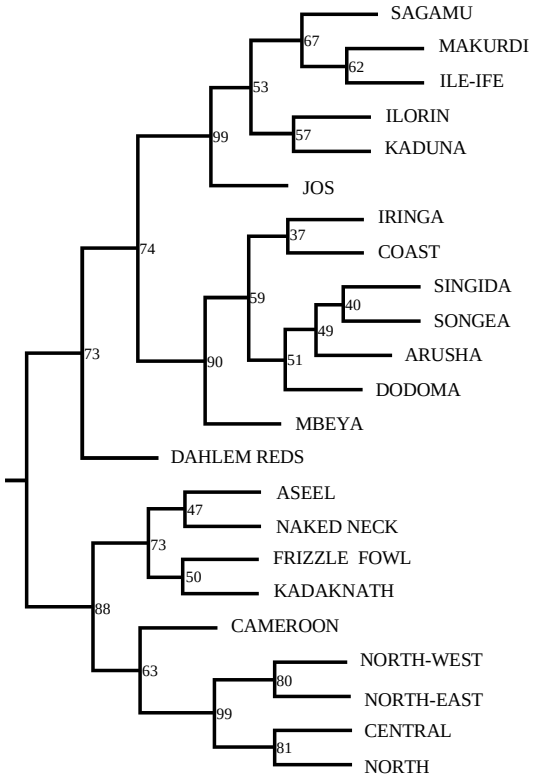
Result and Discussion

Between 2 and 11 alleles per locus were detected. All populations showed fairly high heterozygosity with the lowest value of 45% (Aseel from India) and highest value of 67% (Arusha from Tanzania). A dendrogram constructed based on CHORD distance by UPGMA analysis revealed that within this tree the populations were assorted according to their geographical origin (Figure 1). Bootstrapping values were between 37 % and 99%. Heterozygosity estimates were based on a set of markers showing substantial heterogeneity in the number of alleles and polymorphic information content. The use of a mixture of highly variable and less variable markers should reduce the danger of overestimating genetic variability which might occur if only highly variable microsatellites are used. For all populations (except Aseel from India) heterozygosity values were observed exceeding the values estimated for commercial breeds but similar to those found for populations of Wild Jungle Fowl (Siegel et al., 1992).
The bootstrapping values and the fact that the populations were assorted according to their geographical origin support the reliability of the results. The African populations, especially the Nigerian ones, were much more closely related to the Dahlem Reds than the Bolivian and Indian populations. This may be due to efforts made during this century to improve the local chicken populations in Africa by crossing with exotic commercial chicken.
Though the genetic distance estimate reflect only a quite small part of the potential of a line to be of future use, i.e. to represent an important genetic resource, the calculation of mean genetic distance to all other populations may serve as a valuable parameter to draw a first

decision on the conservation or the merging of some populations. North from Bolivia, Aseel from India, Jos from Nigeria and Mbeja from Tanzania showed the highest mean genetic distance to all other populations under study. These populations might be regarded as the most interesting for any conservation efforts or direct use in appropriate breeding programs aiming at the generation of genetic stocks with improved productive adaptability in tropical environment.

However, the estimates of genetic distance given here are based on allele frequencies of loci of non-coding genomic regions. Though the use of microsatellite loci is regarded as the best available method to assess genetic variability, it is still unclear to what extend variation found in microsatellites is related to genetic variation in traits of interest. As long as this information is not available (- methods with a high potential to deliver this kind information are currently under development -) one should take genetic distance estimates together with information on breeding history and phenotypic characteristics in order to judge on the possible future usefulness of a population. Once this knowledge about the structure, variability and function of different genomic regions exists it should be possible to preserve just these genomic regions instead of animals.

Nigeria



Tanzania

India

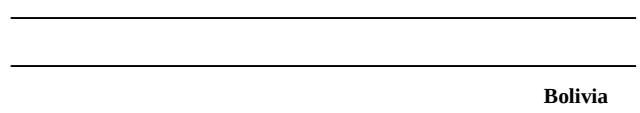


Figure 1.: Dendrogram of local chicken populations from subtropical and tropical countries and Dahlem Reds based on CHORD genetic distance values. Numbers at the branches are bootstrapping values (% of 1000 replicates).

Acknowledgments

The authors would like to thank Dr. D.P. Singh, Central Avian Research Institute, Izatnagar, India, Prof. Dr. E.B. Sonaiya, Department of Animal Science, Obafemi Awolowo University, Ile-Ife, Nigeria, Ing.Agr. F. Choque, Facultad Ciencias Agricolas y Pecuarias, Universidad Tecnica de Oruro, Oruro, Bolivia, Dr. M.J. Mafeni, I.R.Z.V. Mankon, Bamenda, Cameroon and Dr. A. M. Katule, Department of Animal Science and Production, University of Agriculture Morogoro, Tanzania for providing blood or DNA samples.

References

Cavalli-Sforza, L.L., Edwards, A.W.F., (1967). Phylogenetic analysis: models and estimation procedures. Evol 32, pp.550-570.

Nei, M. (1987). Molecular evolutionary genetics. Columbia University Press, New York.

Siegel, P.B., Haberfeld, A., Mukherjee, T.K., Stallard, L.C., Marks, H.L., Anthony, N.B., Dunnington, E.A., (1992). Jungle fowl domestic fowl relationships - a use of DNA fingerprinting. J. World Poul. Sci. 48, pp.147-55.