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A Global Assessment of Population Structure and Genetic Diversity in Chicken Populations from Africa, Asia, Europe, Red Jungle Fowls and Commercial Breeds

Lyimo, C.M[abc]., Weigend, A[a]., Janßen-Tapken, U[a]., Msoffe, P.L[c]., Simianer, H[b]. and Weigend, S[a].

[a] Institute of Farm Animal Genetics of the Friedrich-Loeffler-Institute, 31535 Neustadt - Mariensee, Germany
[b] Georg-August-Universität-Göttingen, Department of Animal Sciences, 37075 Göttingen, Germany
[c] Sokoine University of Agriculture (SUA), Morogoro, Tanzania

Introduction

Animal genetic diversity provides fundamental options for sustainable development of livestock production. The erosion of animal genetic resources has accelerated in recent years as a consequence of development of intensive livestock production systems. Genetic variation is the base for any future breeding strategy in all farm animal species and therefore genetic diversity within a species needs to be conserved. Analyses of genetic diversity regarding distinctiveness and demographic characterization of sub-populations are important when deciding conservation priorities (Groeneveld *et al.,* 2010). In this study, the genetic relationships and stratification of a wide range of chicken populations within and between global regions were investigated by using multilocus microsatellites genotypes. Regional patterns of genetic diversity for chicken populations from Africa, Asia and Europe were assessed by analysing the extents of genetic polymorphism at 29 microsatellite markers in 114 chicken populations from different selection and management regimes. In addition to local populations sampled in various regions, the set analysed also included three populations of Red Jungle Fowl, nine commercial pure breeds and one inbred line which were used as reference for comparison.

Material and Methods

A total of 3344 individuals from 114 chicken populations representing 22 countries of Africa, Asia and Europe were evaluated. The populations sampled included 22 ecotypes from Africa, 26 breeds from Asia and 53 breeds from Europe. These populations were previously genotyped in our laboratory at 29 microsatellite markers (Muchadeyi *et al*., 2007; Bodzar *et al.* 2009; Granevitze *et al.,* 2009; Cuc *et al.,* 2010; Mtileni *et al.,* 2011, Lyimo *et al.* unpublished). Twenty-eight of these microsatellite markers are from the set of microsatellites recommended by the FAO (2011). Mean number of alleles per locus and population as well as allele frequencies for each locus and population were computed using Microsatellite-Toolkit (Park 2001). Wright's fixation indices (F_{ST} and F_{IS}) were estimated using FSTAT 2.9.3.2 software. Population structure was analysed using a model-based clustering algorithm implemented in STRUCTURE software

version 2.3.3 to assign individuals to clusters. Based on STRUCTURE outputs for $2 \leq K \leq 9$ numbers of clusters a schematic tree was constructed according to the most frequent solutions among 100 runs with solution's similarity coefficients ≥ 0.95 (Rosenberg *et al.,* 2007).

Results and Discussion

Highest average heterozygosity and mean number of alleles were found in African and Asian chicken populations (Table 1). European and commercial breeds showed higher differentiation (F_{ST}) than Asian and African ecotypes. The inbred line studied displayed highest inbreeding coefficient (F_{IS}) and lowest diversity compared to all other populations under study. Muchadeyi *et al.* (2007); Goroga *et al.* (2011); Mtileni *et al.* (2011) and Lyimo *et al.* (unpublished) reported over 85% of the total genetic variation resulted from within chicken ecotypes of Zimbabwe, Malawi, Sudan, Ethiopia, South Africa and Tanzania. Though European populations showed low variability, they still possess higher genetic variation than an inbred line. The degree of heterozygosity found in the Red Jungle Fowl populations was comparable to that of African and Asian populations. Compared to all other categories of chicken populations, commercial lines displayed lowest F_{IS} estimates indicating that these populations have been managed to limit the increase of the degree of inbreeding.

Table 1: Genetic Diversity between various categories of chicken populations

Population	No. of population	H_E ± std	H_O± std	MNA±std	F_{ST}	F_{IS}
African chickens	22	0.614±0.027^{a}	0.584±0.02^{a}	5.32±2.43^{a}	0.088±0.013^{d}	0.049±0.01^{b}
Asian chickens	26	0.602±0.031^{a}	0.576±0.02^{a}	5.12±2.41^{a}	0.120±0.013^{cd}	0.044±0.01^{b}
European chickens	53	0.454±0.037^{b}	0.418±0.02^{b}	3.19±1.22^{b}	0.302±0.013^{b}	0.080±0.01^{b}
Commercial lines	9	0.453±0.036^{b}	0.441±0.02^{b}	3.28±1.33^{b}	0.322±0.013^{b}	0.028±0.01^{b}
Inbred sub-lines	4	0.025±0.014^{c}	0.018±0.01^{c}	1.14±0.37^{c}	0.684±0.013^{a}	0.315±0.15^{a}
Red Jungle Fowl	3	0.610±0.031^{a}	0.581±0.02^{a}	4.76±1.88^{a}	0.169±0.013^{c}	0.046±0.02^{b}

Different superscript letters in a column indicate significant differences (Tukey's HSD, $P<0.05$)

H_E = Expected heterozygosity, H_O = Observed heterozygosity, MNA = Mean number of alleles

F_{IS} = Average Inbreeding coefficient within subpopulation, F_{ST} = Differentiation between subpopulations

Regarding population differentiation, European populations had a very similar F_{ST} estimated as commercial lines which are kept as closed populations without admixture. This suggests that European breeds have been bred as isolated breeds with small effective population size as reported previously (Granevitze *et al.,* 2007). From the STRUCTURE analysis, most likely population clusters appeared at K = 3 (Figure 1) established by applying Evanno method, with 100% of runs being identical with similarity coefficient of ≥95%. At K=2, the pool of chicken populations separated into two main groups of Asian and European chicken populations. Both clusters included chicken populations from Africa. At K=3, African populations clustered between gene pools of Asian and North-western Europe populations, overlapping with breeds from Southern Europe, broilers and brown layers. Northwest European populations together with Mediterranean populations clustered together with egg white layers.

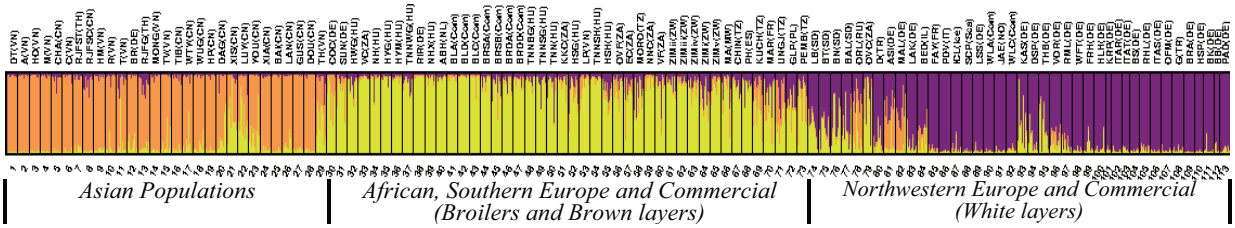

Figure 1: Population structure at K=3 of 113 chicken populations from various origin

Majority of Asian chicken population stayed together in one cluster until at K=7 (figure 2). At this level, East-Asian chickens split from Southeast Asian populations. Pham *et al.* (2013) observed two main gene pools that separated Vietnamese local populations and chickens of Chinese origin in Vietnam with some admixture in Tau Vang, H'mong and Ri. In the gene pool of European chicken populations, the highest degree of population stratification has been observed. At K≤9, populations sampled in Europe were found in each of the clusters.

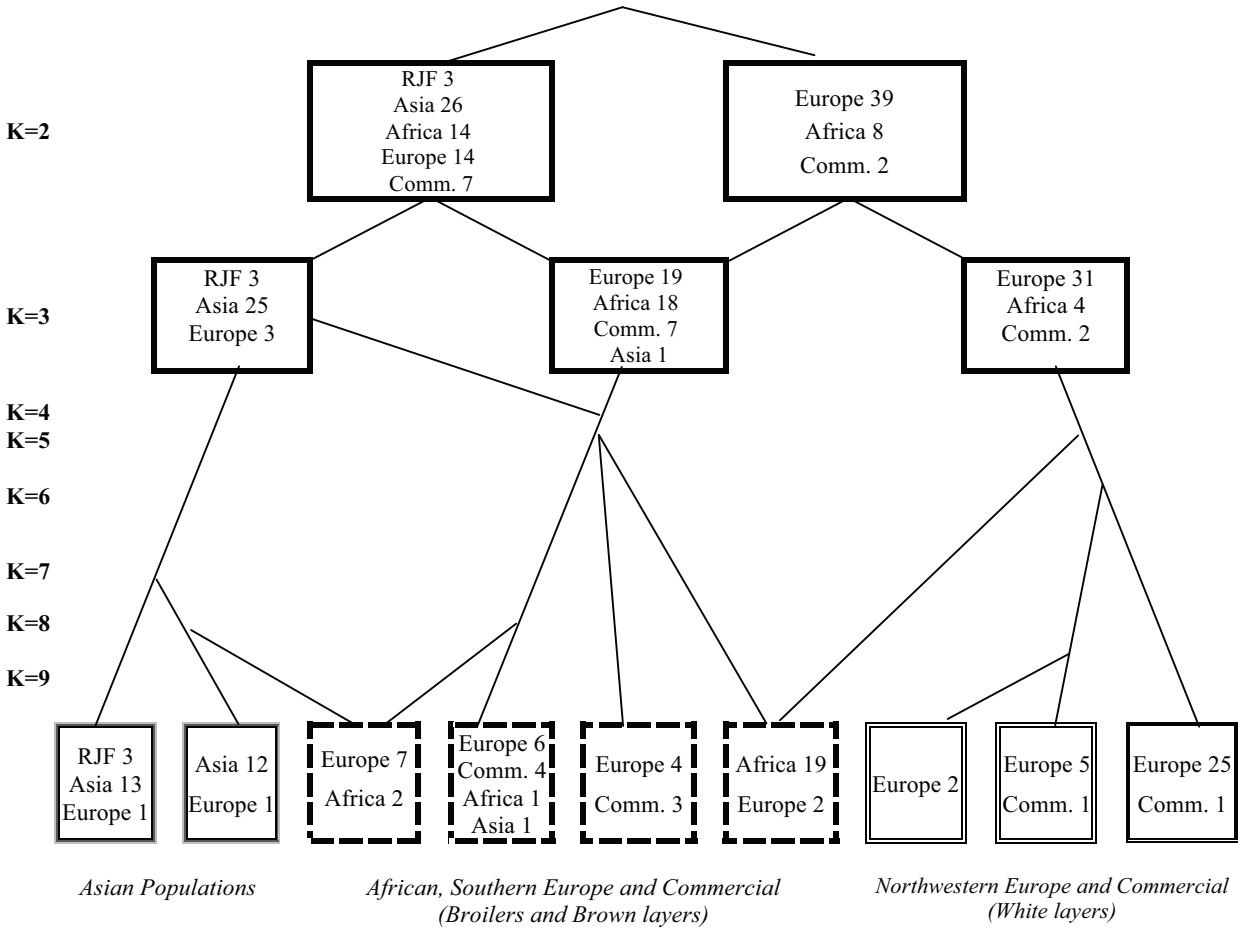

Figure 2: Schematic evolution of clusters (2 ≤K≤ 9) from 113 chicken populations analysed from multilocus genotypes using STUCTURE software

Although European breeds have lower heterozygosity than Asian and African breeds, nevertheless they have higher range of genetic diversity distributions. Thus, altogether they might have significantly contribution to a global genetic diversity as they are more differentiated (F_{ST}) from each other compared to Asian and African breeds. The existence of traditional farming system in Africa, prevailing extensive management of chicken flocks and a limitation of selection practices may have contributed to this higher genetic variation within the population. A similar observation was made in Asian chicken populations where most of the populations were not selected for a specific trait (Rajkumar *et al*., 2008).

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