

Tropentag, September 19-21, 2012, Göttingen -Kassel/Witzenhausen

"Resilience of agricultural systems against crises"

Assessment of Genetic Diversity and Population Structure of Omani Local Chicken Using 29 Microsatellites

BADAR A. AL-QAMASHOUI¹, STEFFEN WEIGEND², HENNER SIMIANER¹, OSMAN MAHGOUB³

¹Georg-August-Universität Göttingen, Dept. of Animal Sciences, Germany

²Institute of Farm Animal Genetics of the Friedrich-Loeffler-Institute, Breeding and Genetic Resources, Germany

³Sultan Qaboos University, College of Agricultural & Marine Sciences, Dept. of Animal and Veterinary Sciences, Oman

Abstract

This study attempted to assess genetic variation and population structure of indigenous chickens in Oman. Twenty nine microsatellite markers were investigated in 158 birds from six agroecological zones: Batinah (BT), Dhofar (DF), North Hajar (NH), East Hajar (EH), Musandam (MU), and East Coast (EC). Among all loci, a total of 217 alleles was observed across all populations. The average number of alleles per locus was 6.9 \pm 3.3 and ranged from 2 (MCW 98 and MCW 103) to 20 (LEI094). The average number of alleles per population ranged from 5.0 ± 1.9 (DF) to 5.5 ± 2.9 (NH). Across populations the observed heterozygosity was 0.54 ± 0.02 , while the expected heterozygosity was 0.62 ± 0.03 . For the six populations, observed and expected heterozygosity ranged from 0.51 (EC) to 0.58 (NH) and from 0.57 (BT) to 0.66 (DF), respectively. Mean deficit of heterozygotes within populations (FIS) was 0.130 ± 0.024 , and mean fixation index between populations (FST) was 0.034 ± 0.005 indicating low population differentiation. The mean global deficit of heterozygotes across populations (FIT) was 0.159 ± 0.023 . The mean polymorphic information content (PIC) was 0.561, ranging from 0.521 to 0.585. Genetic distance calculated based on Nei's standard distance identified DF as distant population from all populations while the smallest distance was between BT and NH populations. Model based clustering using algorithm implemented in STRUCTURE software package was used to detect population substructures and presence of admixture. The results showed that individuals of the six populations were clustered into 3 groups: (NH and BT) and (EC, EH and MU) with a high degree of admixture within the groups. In contrast, individuals of DF population made up a separate cluster. The results suggest considerable diversity and population substructure of the Oman indigenous chickens studied. The Dhofar (DF) population was identified as most distant and most inbred (FIS=0.193) of these populations. Further studies are needed to evaluate these populations as an important reservoir of genetic diversity.

Keywords: Genetic variation, microsatellites, Omani local chickens

Contact Address: Badar A. Al-Qamashoui, Georg-August-Universität Göttingen, Dept. of Animal Sciences, Albrecht Thaer Weg 3, Göttingen, Germany, e-mail: B.Alqamashoui@agr.uni-goettingen.de