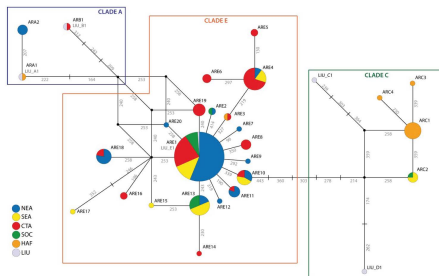




Badar Al-Qamashoui (Autor)
Towards Conservation of Omani Local Chicken
Management, Performance and Genetic Diversity

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CHAPTER 1

General introduction



1.1 Background

With an area of 309,500 km², Oman is the third largest country on the Arabian Peninsula. It is located in the southeastern part between latitudes 16°40' and 26°20' north and longitudes 51°50' and 59°40' east with a coastline extending for 3,165 km (DGMAN 2012). The Sultanate borders the Kingdom of Saudi Arabia in the West, the United Arab Emirates in the Northwest, the Republic of Yemen in the South, the Strait of Hormuz in the North and the Arabian Sea in the East.

Oman is generally an arid subtropical country with two distinct seasons: winter from November to April, and summer from May to October (Al-Mashakhi and El-Hag 2007). With the exception of some higher altitudes in the Interior and remote South, the climate in summer is hot and dry with a full-day average temperature of 38°C, whereas in the winter temperatures are mild (15–23°C). The precipitation is generally low and irregular, especially in the Interior region, with an average of 117.4 mm/year for the whole country (DGMAN 2012).

The country has a varied topography, including mountain ranges, arid deserts and fertile plains. The wide variation in climatic and landscape features is the reason for the country's abundant and unique faunal and floral biodiversity in the different agro-ecological zones (AEZ) (Al-Zidjali 1996; Al-Saadi 2013). Oman is separated into several agro-ecological zones (Table 2.1) based on topography and climate, parameters which influence crop water requirements and efficient use of water, land and water resources and cropping patterns (Al-Zidjali 1996).

Agriculture is an important economic sector and plays a crucial role for the food security objective of the Sultanate of Oman. The size of the cultivated area is 73,670 hectares (DGALR 2011) and around 40% of the population is still engaged in the agricultural sector (MoNE 1995). According to the target set for the agriculture sector in the 'Vision 2020', its contribution to GDP is expected to rise to 3.1% by 2020 with an annual growth of not less than 4.5% (CBO 2011). Date palm, banana, mango, coconut, vegetables and fodder and field crops are the major agricultural products and considered as the main plant genetic resources. In addition, the country possess indigenous grasses, medicinal plants, pastures, trees and shrubs, and forest resources (DGALR 2011).

Livestock production is a central farming activity in Oman. The total number of livestock in the country is around 2.5 million, composed of goats (1,685,420), sheep (380,990), cattle (326,240) and camels (127,010) (DGALR 2011). The majority of cattle and camels are in the most southern region of Dhofar whereas the majority of goats and sheep are kept in the Batinah plain. Non-official information from the 2013 Agricultural Census estimated the total number of local chickens in Oman as 2.4 million (personal communication; Dr. Khalid Alzadjali, Ministry of Agriculture and Fisheries).

Livestock farming has been practiced in Oman for thousands of years although its history remains debated. Ancient cave drawings (Figure S1.1) (AbdulNayeem 2000) and excavated bone remains from animals in Oman (Bokonyi 1992) and the Arabian Peninsula (Groucutt and



Petraglia 2012) support the presence of domesticated animals in the Late Stone Age period (Bokonyi 1992; Wilkens 2005). Other scholars, however, defend that maritime-oriented fishing cultures have appeared along the coast of Oman as early as the 7th millennium BP (Biagi 1994), giving rise to preliminary farming settlements. Discoveries of a first domestication event of dromedary camel in the south of Oman (Grigson et al. 1989; Zeder et al. 2006) and of horses in Saudi Arabia (SCTA 2013) around 5000 BP, have given further evidence for very early domestication activities. Being at a very important and strategic geographical location, Boivin et al. (2010) suggested that the ancient Arabian Peninsula played an important role in channeling plants, crops and animals between their centers of origin and their areas of dispersion. Besides the strong oceanic trade routes via the Arabian Sea and the Indian Ocean (Fuller et al. 2011), evidences for earliest inland trade routes from South to North of the Peninsula using camels have also been documented (Pickering 2007).

Many conservation and improvement programs for local livestock breeds, ranging from short- to long-term experiments, have been conducted by the Ministry of Agriculture and Fisheries of Oman (DGALR 2011). The main species targeted are cattle, sheep, goat and chickens. However, these programs lack studies analyzing the molecular genetic makeup of these species. Recently, the Ministry, in the framework of a national conservation strategy, has decided to update its programs by adopting the procedures recommended by the Food and Agriculture Organization of the United Nations, i.e. by using advanced genetic tools in conservation approaches (DGALR 2011).

1.2 Genetic diversity in livestock and role of conservation

Genetic diversity is defined as the variety of alleles and genotypes present in a population that is reflected in morphological, physiological and behavioral differences between individuals and populations (Frankham et al. 2002; Delany 2003). Local farm animals are an important reservoir of genetic diversity as it is essential to meet their current production needs in various environments and to facilitate rapid adaptation to changing breeding objectives (Notter 1999). However, the loss of genetic diversity within these farm animals has become a major concern in the last decades. Many indigenous breeds that have unique characteristics such as disease resistance and adaptation to their environment are being replaced by industrial breeds (Perera 2010; FAO 2012). Around 22% of the world's livestock breeds are classified as being at risk of extinction, due to loss of genetic diversity and decrease in population sizes by crossbreeding with commercial exotic breeds (FAO 2012). These specialized exotic breeds in many livestock species now suffer from the consequences of inbreeding, and as a result, many productive breeds are becoming more dependent on intensive management (Wollny 2003; Gibson et al. 2005). There is a need, therefore, to slow down the degradation of farm animal genetic resources and establish programs for their conservation and sustainable use (Gibson et al. 2005; Perera 2010).

Conserving programs aim to preserve valuable genetic resource in order to face any future environmental changes or disasters (Allendorf and Luikart 2007). They also aim to reserve these



populations as a source of rare alleles and contribute to the search for genes associated with health and quality traits (Gandini and Oldenbroek 1999; Mendelsohn 2003). In many cases conservation programs are structured to avoid inbreeding and conserve the observed phenotypic differences and genetic variation within the different lines (Marle-Koster and Nel 2003).

Several conservation options and strategies have been established (Gibson et al. 2005). Among these, the strategy which takes into account both within- and between- subpopulation components of coancestry is recommended (Caballero and Toro 2002; Ollivier and Foulley 2005; Fernandez et al. 2008). This approach has been used to determine the optimal contribution of each subpopulation in a synthetic population or gene pool of maximum gene or allelic diversity (Perez-Figueroa et al. 2009). Estimating these optimal contributions can be applied to prioritize subpopulations for conservation (Caballero and Toro 2002; Perez-Figueroa et al. 2009). Caballero and Toro (2002) stated that the procedure of contributions of minimum coancestry has been shown to maximize the genetic diversity of the population in terms of expected heterozygosity and effective population size. This approach has also been shown to be very effective in preserving the original distribution of allelic frequencies in conservation programs (Saura et al. 2008) and maintains to a certain extent the allelic richness of the population (Fernandez et al. 2008). Efficient conservation programs require a good knowledge of the genetic structure of these local populations, as well as an assessment of their diversity at the molecular level to provide recommendations regarding their future management (Boettcher et al. 2010).

1.3 Local chicken breeds: production system and genetic diversity assessment

Local “indigenous” chickens play a crucial role for the livelihood of most rural families in the developing world. Besides providing food, local chickens are important for income generation. Most rural families in developing countries are involved in local chicken husbandry due to its low capital investments (Jens et al. 2004; Gibson et al. 2005). Local chicken husbandry is frequently under the responsibility of women involved in most poultry management operations (Mwalusanya et al. 2002). The majority of households in these communities lacks the required husbandry skills, training and market opportunities to effectively improve animal production (Barua and Yoshimur 1997; Mwalusanya et al. 2002; IAEA 2004; Pica-Ciamarra and Dhawan 2010).

Free-range scavenging system is the main production system in the tropics and subtropics (Aini 1990; Barua and Yoshimur 1997; Dessie and Ogle 2001). Under this production system, local chicken flocks are managed extensively, which enables them to obtain most of their feed through scavenging. Local chicken types are characterized by considerable phenotypic variation (Mcainsh et al. 2004). They are considered as an important genetic reservoir that developed under harmful environmental conditions, diseases and predators. Their long adaptation to this harsh environments enables them to resist extreme temperatures, poor nutrition and absence of veterinary care, and in turn survive and reproduce (Hall 1986). It is assumed that by raising



chickens under these harsh environmental conditions, diverse allele and allele combinations will be produced through natural selection that gave these breeds adaptation and a reasonable ability to produce (Horst et al. 1996).

Local poultry breeds in many countries have provided an interesting alternative to commercial strains, providing typical products with particular meat qualities that are of great interest to the regional local markets (Zanetti 2009). Commercial chicken purebreds were selected for performance traits and managed as closed populations with well documented pedigrees and breeding history. Commercial poultry breeds have been selected to be reared in an optimum feeding system and therefore, scavenging conditions may not satisfy their nutritional needs (Leroy et al. 2012). Consequently, efforts for conserving local chicken are of greatest importance as they allow breeders to take advantage of unique adaptive traits present in this diversity that enables them to respond to changes in the environment (Besbes et al. 2007).

Molecular genetic markers have been widely used as tools to study the genetic diversity and to design conservation and breeding programs for local populations. A marker is an identified genome site that exhibits polymorphism (Beuzen et al. 2000). Among different molecular markers, microsatellites have been extensively used to describe the genetic diversity in many livestock species. Microsatellites are short DNA stretches consisting of a repeat motif of usually a two- or four-nucleotide sequence, also known as simple tandem repeats. They are characterized by their wide distribution in the genome, easy to use and highly polymorphic (Cheng and Muir 2005). Microsatellites can be amplified for identification by the polymerase chain reaction (PCR) process, using the unique sequences of flanking regions as primers (Beuzen et al. 2000; Cheng and Muir 2005). This process results in the production of enough DNA to be visible on agarose or polyacrylamide gels.

Many genetic diversity variables and approaches can be achieved by using microsatellites. These include allele frequencies, private alleles, proportions of polymorphic loci, observed and expected heterozygosity, phylogenetic relationships, genetic admixtures and population structures (Chikhi and Bruford 2005). Genetic differentiation among populations has been assessed using genetic distance measures such as Nei's (Nei and Li 1979), and Reynolds (Reynolds et al. 1983) genetic distances. Microsatellites have also been used in identifying genetically important populations for conservation (Bennewitz and Meuwissen 2005).

In chickens, microsatellite DNA typing has been extensively used for genotyping chicken (Romanov and Weigend 2001; Hillel et al. 2003; Granevitze et al. 2007). A set of 30 microsatellite markers in chickens has been recommended by the Food and Agriculture Organization, including ADL0268, ADL0278, ADL0112, LEI0192, LEI0234, LEI0094, LEI0166, MCW0206, MCW0295, MCW0081, MCW0014, MCW0183, MCW0067, MCW0104, MCW0123, MCW0330, MCW0165, MCW0069, MCW0248, MCW0111, MCW0020, MCW0034, MCW0103, MCW0222, MCW0016, MCW0037, MCW0098, MCW0284, MCW0078 and MCW0216 (FAO 2004).