

FUTURE OPPORTUNITIES FOR GENETIC IMPROVEMENT OF THE EGYPTIAN CAMELS

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SUMMARY

Evaluation of genetic makeup is an emerging approach for identifying individuals with high potentials for production in a highly successful manner. More recently, the Arabian camel has joined the club of mammals that have undergone full genome sequence, which opens the door for a whole-genome scan using high-density markers in the context of specific traits. These are the new key features of genomic selection and predictions in livestock. Nowadays, the scientific community worldwide gives more attention to study dromedaries because of their unique morphological characteristics and physiological functions. Camels are widely used for transportation and as a source of meat, milk, hair, entertainment, and celebration. Moreover, its high potential for disease resistance is an interesting matter. The FAO estimates showed a significant increase in the camel population in Egypt from 111,000 in 2010 to about 149,500 in 2017. There are four camel breeds in Egypt; Sudany, Maghraby, Falahy and Mowallad, and all belong to *Camelus dromedarius*. So far, these breeds have been characterized phenotypically and geographically but little is known about their genetic makeup. The current article summarizes the features of the Egyptian camel breeds, different prospects of utilizing camels in the country, and future opportunities for genetic improvement of the Egyptian camels. Such opportunities could be quantifying the breeding values with higher reliability earlier in life when combining DNA genotypes for millions of loci with pedigree and phenotype databases for thousands of animals. Furthermore, this information is necessary for understanding the unique biology of camel, and may be an adjunct tool towards conservation and planning genetic improvement strategies for camels in Egypt and worldwide.

Keywords: Dromedaries, genetics, breeds, and conservation

INTRODUCTION

Camel was the first domesticated animal in the Arabian Peninsula around 3000 to 4000 years ago and then was spread to whole Africa (Mikesell, 1955; Gifford-Gonzalez and Hanotte 2011, Almathen *et al.*, 2016). It is believed to be one of the last major livestock to be domesticated and is considered as one of the most important domestic animal genetic resources (AnGR) in arid and semi-arid regions (Cherifi *et al.*, 2017). There is an increasing interest of camel breeding in Egypt and worldwide (FAOSTAT, 2017) because of their ability to live in harsh conditions with poor food supplies and hot environment as well as high potential for disease resistance.

Camel is a multipurpose animal that is mainly used as a source of meat, milk, transportation, agricultural work, wrestling, racing and tourism (Ramadan and Inoue-Murayama, 2017). Camels have potentials for production of cheap and health meat and milk under harsh conditions compared to other domestic animals. Additionally, camel racing is a popular sport for entertainment associated with the Bedouin festivals in the Middle East region (Al Abri and Faye *et al.*, 2019). Nowadays, camel racing became an important business with regular social

events being linked to extensive training and scientific breeding programs.

Camels are distributed all over the Egyptian country; Nile Delta, oases, farming communities and across desert regions. According to FAOSTAT (2017), the total number of camels was estimated in Egypt to be 159,000 heads and this number represents 1.1%, 0.9% and 0.7% of the total camel's number reared in Arabian countries, Africa and all over the world, respectively (Table 1). There is a remarkable yearling growth rate in camel populations worldwide and this rate was described to be moderate in Egypt (Faye, 2015). However, camels are not representative in Ancient pharos drawings as other types of animals such as donkeys, horses...etc., but the proposed time for camel entry to Egypt is about 1400 B.C. (Epstein, 1971). Camels in Egypt are following *Camelus dromedaries* family, which is often referred to as the Arabian camel (Al-Swailem *et al.*, 2010). Phenotypically, there are four different camel breeds in Egypt, which are Sudani (common for riding and racing), Falahi or Baladi (used for transportation and agricultural operations), Maghrabi (dual-purpose, for meat and milk), Mowallad, (hybrid between Maghrabi and Falahi) (Wardeh *et al.*, 1990). Additionally, there is a tourism attraction for riding camels on beach, dunes or around the pyramids in Egypt, and also for entertainment. In view of

encounter the significantly increasing of demand on animal products, awareness has arisen for the breeding of camels to offset the huge deficiency in the animal production specially milk and meat. On the other hand, studying genetic diversity of Egyptian camels as one of the most important AnGR in desert areas has a remarkable influence in planning genetic improvement strategies and conservation of species (Sallam *et al.*, 2012).

Numerous studies have implemented molecular genetic techniques in order to understand the genetic architecture of Egyptian camel breeds (Mahrous *et al.*, 2011; Othman *et al.*, 2016; Othman *et al.*, 2017 and Cherifi *et al.*, 2017, Al-Soudy *et al.*, 2018). However, further efforts are required to unravel the camel genome and rely this to the production traits to be used in selection and genetic improvement strategies for camel. This review deals with the current situation of camel breeding in Egypt, diversity and performance of Egyptian camel breeds

and the implemented molecular genetic studies using different perspectives.

Camel breeds in Egypt:

There is only one type of camels, which is one humped camel and four different camel breeds are distinguished in Egypt (Figure 1). The geographical distribution of different breeds of the Egyptian livestock species is well determined; conversely, the Egyptian camel breeds are not well geographically defined (i.e. there is no specific breed for specific zone). One explanation for that might be due to the large population number that transferred from the African horn and Upper Egypt to the north of Egypt. The total number of camel population was substantially increased over the last four years from 2011 to 2014 and remained about constant thereafter (Table 1).

Table 1. Total number of camel population and meat production from 2010 to 2017.

	Year							
	2010	2011	2012	2013	2014	2015	2016	2017
Live animals (1000)	111	137	142	153	158	152	156	149.5
Meat production*	45	37	35	38	40	38	39	39.5

* Total meat production in tones (FAOSTAT, 2017)



Maghrabi



Falahi



Sudani



Mowallad

Figure 1. Camel breeds in Egypt

The Camel in ancient Egypt:

The proposed time of camel domestication is before 2000 B.C. (Bulliet, 1978 and Ripinsky, 1985). However, the word camel has not been found on any of the ancient Egyptians archeological findings, the evidence that camel has been used in wars during different eras (Saber, 1998). Moreover, Moller (1906) found a limestone with the shape of a sitting camel at Abusir-el-Melek, about 20 miles south of Cairo; he mentioned that these findings go back to 3000 B.C. Few studies suggested that according to the findings, the proposed time that camels entered to Egypt either from north or south was during the first and the medium of the millennium B.C. (Walz, 1956 and Rowley-Gonway 1988).

Modes of camel utilization in Egypt:**Meat production:**

Compared to other livestock species, camel meat is healthier and had benefits as it has low fat content and is highly nutritious (Kadim *et al.*, 2008). The camel is a good source of meat in areas where the arid climate adversely affects other animals. The male dromedary carcass can weigh about 400 kg (Knoess, 1977). According to FAO statistics, there is an obvious slight increase in the total camel meat production during 2011 to 2017 to be 37 and 39.5 tones of meat, respectively (Table 1). Egypt is one of the top 10 countries producing meat camels (FAOSTAT, 2017). Egypt also records a unique slaughtering rate of camels of 121%, slaughtering the equivalent of more than its own camel population, which indicates that Egypt import more live animal than it owns.

Milk production:

During the last decade, demand for camel milk has increased both locally (in arid regions) and internationally along with various camel dairy products (Al Abri and Faye, 2019). This emphasized establishing large camel dairy farms worldwide. Camel milk is mainly produced from dromedaries (Zhang *et al.* 2005) and it is rich in insulin and insulin-like proteins. The unique camel insulin, unlike the insulin contained within other animal milks, is incorporated within micelles and is thus protected from digestion and proteolysis in the upper gastrointestinal tract (Agrawal *et al.*, 2011; Malik *et al.*, 2012). Moreover, camel milk is rich in lactoferrin and immunoglobulin with potent antimicrobial and anti-inflammatory properties, including bacterial inhibition, antiviral effects (HCV, HIV), antifungal, anti-oxidant, anti-inflammatory and anti-cancer actions (Alhaider *et al.*, 2013; Habib *et al.* 2013; Ismael *et al.* 2013; Kanwar *et al.* 2015). It also contains lower β -casein and no β -lactoglobulin resulting in its hypo-allergic property (Konuspayeva *et al.*, 2009).

Unfortunately, milk does not play a significant role in the economic importance of the Egyptian camels. Until now, the record for total milk

production by camels in Egypt is not available and still underestimation. Daily milk production (DM) and the total milk yield (MY) of Egyptian camels were estimated with adequate feed supply to be in average 13 kg and 3500 kg, respectively. Conversely, it was 4 kg and 1500 kg for DM and MY, respectively, in shortage of feed supply (El-Bahay 1962; Shalash, 1979 and Abdalla *et al.*, 2015). The wide range in milk yield reflects the high potential of milk production by Egyptian camels.

Riding and tourism

There is a tourism attraction for riding camels around the pyramids in Egypt, and also for entertainment. Camel riding was recorded to be one of the top 10 things that tourists would love to do in front of pyramids, sphinx and ancient tombs of kings in Luxor and Aswan, during their stay in Egypt (unofficial source).

Molecular genetic studies applied to Egyptian camels:

Planning genetic improvement strategies for any given species is mainly dependent on selecting animal with superior genetic merit. As a consequence, identifying genetic variations among and between individuals is substantial for prediction of genetic merit of each member. Recently, molecular genetic techniques are widely used as a useful tool to screen the polymorphisms and variation in a group of animals and rely that on specific phenotype of interest, which is known as genetic association studies. Few reports have been conducted on Egyptian camel breeds either for diversity and conservation or identifying marker associated with a specific phenotype (Table 2).

Mahrous *et al.* (2011) studied the genetic variations among and between the Egyptian camel breeds using RAPD and microsatellite markers. Genetic distance matrix separated the studied breeds into two branches; (Baladi, Maghrabi and Mowallad) and Somali and Sudani in the second branch. Using different genetic approach, similar results were reported by Othman *et al.* (2017), who studied the cytochrome b conservation in Egyptian camel breeds. The 208-bp fragments from camel mtDNA cyto b were amplified using PCR for 54 camels. The alignment of camel cyto b sequences showed the presence of two polymorphic sites resulting in four haplotypes. They concluded that cyto b sequence is highly conserved among all camel breeds. In context of genetic diversity and population structure, Cherifi *et al.* (2017) used 20 microsatellite markers in six populations representing Algerian and Egyptian camels. Interestingly, a weak genetic structure among the studied camel population was observed.

Othman *et al.* (2016) amplified 488-bp of κ -casein gene in 50 Maghrabi breed samples reared in Egypt and digested them with *AluI* endonuclease. Three genotypes were observed, CC (12%), TT (48%) CT (40%).

Table 2. Utilization of molecular genetic techniques in Egyptian camels

Year	Breeds	Locations	Method	Investigation	Reference
2011	Four Egyptian breeds	Egypt	RAPD ¹ and microsatellites	Two distinguished groups; (Sudani) and (Maghraby, baladi and Mowallad)	Mahrous <i>et al.</i> (2011)
2015		Tunisia, Egypt, and Algeria		3 variant sites in the first intron (486G/C, 798G/A, 799C/T) of nucleotide sequence of MSTN gene	Muzzachi <i>et al.</i> (2015)
2015	Four Egyptian breeds	Egypt	PCR-RFLP ²	Identified SNP at GH gene	Abd El-Aziem <i>et al.</i> (2015)
2015	Maghraby	Egypt	Sequencing of GH ³ gene	Identified single SNP at intron 1 of GH gene	Shawki <i>et al.</i> (2015)
2016				two SNPs were detected in 5 UTR region of the GH gene	El-Kholy <i>et al.</i> (2016)
2016	Maghraby	Egypt	Sequencing of Casein gene	of a single SNP was identified	Othman <i>et al.</i> (2016)
2017	Four Egyptian breeds	Egypt	mtDNA ⁴ cytochrome b	Cytochrome b is highly conserved among the breeds	Othman <i>et al.</i> (2017)
2017	Algerian breeds and Four Egyptian breeds	Egypt and Algeria	microsatellites	Weak genetic structure and unique evolutionary history	Cherifi <i>et al.</i> (2017)
2018	Four Egyptian breeds	Egypt	Microsatellites and start codon targeted markers	Two distinguished groups; (Balady, Sudani and Somali), and Maghrabi	Al-soudy <i>et al.</i> (2018)

¹ Random Amplified polymorphic DNA,

² Restriction fragment length polymorphism

³ Growth hormone

⁴ Mitochondrial DNA

Shawki *et al.* (2015) found a SNP (419C>T) in the GH intron1 by genotyping 23 Maghrabi camels reared in Egypt. Abdel-Aziem *et al.* (2015) amplified a 613-bp fragment of camel GH in five camel breeds reared in Egypt (Sudani, Somali, Mowallad, Maghrabi and Falahy). The results showed that the Maghrabi breed had higher frequency for allele C (0.75) than those in the other tested four breeds. Moreover, two SNPs (111G>C and 380G>A) were detected in 630 bp of 5 UTR region of the GH gene in 11 male dromedary camels and showed significance with many meat characters including dressing percentage with hump, dressing percentage with liver and number of fibers hump (El-Kholy *et al.* 2016). Interestingly, only 3 variant sites in the first intron (486G/C, 798G/A, 799C/T) were detected in the 3.6 kb of nucleotide sequence of MSTN gene spanning the three exons and part of the three introns, 5UTR and 3 UTR regions by Muzzachi *et al.* (2015) in 22 dromedary camels from three different African populations (Tunisia, Egypt, and Algeria).

Future opportunities and challenges:

It is a challenge to our society to combine knowledge and skills to help make the camel a popular animal to breed; an animal, which is such an obvious solution to improving human nutrition in the

arid zones of the world. In camel's holding countries, the integration of animal breeding association and decoction-makers is rapidly needed. Consequently, planning short-term and long-term genetic improvement strategies for camels are required. This is the sufficient guarantee to conserve AnGR of camels and maintain unique genetic merit from generation to generation. Genetic improvement of livestock is one of the major goals of animal production scientists and the main goal for animal breeders and geneticists worldwide. Selection is an effective tool for genetic improvement, which was for long time based only on morphological characteristics as an indicator for the entire genetic contribution of the individual. Exploring the full genome sequence of most of the economically important livestock such as bovine, sheep and pigs made the processes of genetic selection and, therefore, the genetic improvement much more feasible, rapid, powerful and highly accurate.

Relatively high genetic variability within camel breeds was reported (Al Abri and Faye, 2019). This is probably due to the lack of selection and the nature of camels movement between countries (Almathen *et al.*, 2016). Thus, genetic improvement of camel in context of specific traits is feasible through selection and breeding programs. Al Abri and Faye (2019)

proposed three possible strategies for genetic improvement of camels. The first one is to screen the single genes in camels that are easier to select for. These genes are so far well known in other livestock but to our knowledge are not mapped yet in dromedaries, except for coat color genes (Almathen *et al.*, 2018). The second is the traditional genetic selection using Best Linear Unbiased Prediction (BLUP) to calculate the estimated breeding values (EBVs) using phenotypic and pedigree information (Henderson, 1984). Using genomic relationships in BLUP instead of pedigree information is the third strategy. This is commonly known as genomic breeding value (GBV) and also is a necessary step for the genomic selection (GS) (Meuwissen *et al.*, 2001). The later one is the most appropriate to be implemented in camel because it is not traditionally pedigreed. However, GBV and GS require estimation of the effect of a large number of genetic markers, usually SNPs that are spread out in the entire genome of reference population with the availability of phenotypic information (Hayes, 2009).

Due to lack of genomic tools and genetic information about camels, compared to other livestock species, there are a lot of limitations and challenges for the genetic improvement processes. The first and the major responsibility for genetic improvement of Arabian camels are hanging on the camels-holding countries which have more than 70% of the total number of camel population all over the world. Recently the genomes of the two-humped Asian camel and the single-humped Arabian camel have been sequenced (Wu *et al.*, 2014 and Wu *et al.*, 2015). The Arabian camel genome is the first mammalian genome to be sequenced in the Middle East. The recent publications of whole genome drafts of the dromedary (*Camelus dromedaries*), domestic Bactrian camel (*C. bactrianus*) and wild Bactrian (*C. ferus*) open the door for extensive genomics studies in Old World camelids. Until now, no genome-wide screening tool is today available and no population genomics study has so far been published for these species.

Recently, the availability of high-throughput SNPs genotyping in affordable manner for livestock (Van Tassell *et al.*, 2008) makes the genomic studies are the best of choice for many researchers to conduct the association studies (Kijas *et al.* 2013). Association studies such as genome-wide association studies (GWAS) and candidate gene association studies (CGA) approaches have multiple applications such as quantitative trait loci (QTL) detection and genomic selection (Eggen, 2012; Snelling *et al.*, 2012) and can be used to identify chromosomal regions that are associated with a specific phenotype without any pedigree information (Neibergs *et al.*, 2010). The ultimate goal of association studies is to identify genetic factors potentially associated with specific phenotype; consequently, these factors could be used to make predictions about who is unique and to identify the biological pathways of the desired trait (Bush and Moore, 2012).

The successful genome-based study is mainly dependent on the availability of DNA-platforms with reasonable number of SNP markers for the corresponding species and well-defined phenotype in a large population size with pedigree information. Unfortunately, in camels, the previous elements are absent to conduct a successful genome-based study. To overcome the availability of DNA-platforms genotyping, one possible solution is the genotyping by sequencing (GBS), which was developed by Elshire *et al.* (2011). The GBS is an ideal method for association studies in case of no commercial SNP chips available for the studied animal. It uses high throughput, short-read sequencing to provide low cost genotyping with high information content (De Donato *et al.*, 2013). To reduce problems in camel caused by no commercial SNP kits available and the high sizes of gaps in the camel genome draft, reduced representation libraries are produced using a restriction enzyme that targets genomic regions while multiplexing with barcodes reduces the cost for individual samples. Using this technology, DNA samples can be genotyped at over 2 million sites. Genotypes obtained using GBS can be used to examine relationships among lines, perform linkage and genome wide association studies, and perform genomic selection.

Concerning genomic studies, phenotype definition is a critical issue, unlike in Egypt; most of the camel herds in developing countries lack breed societies. Therefore, phenotypic recording is seldom practiced in camel populations. The last challenge facing the genetic improvement in camels is difficulty in disseminating superior genetics due to the difficulty of performing Artificial Insemination (AI). This is primarily due to the difficulty in semen collection and handling. However, multiple attempts by several research groups tried to unravel the physiology of reproduction (El Bahrawy *et al.*, 2018).

CONCLUSION

This review illustrated different Egyptian camel breeds, their mode of utilization and presented several molecular studies that tried to unravel the genetic architecture of camels in Egypt. The identification of key genes involved in the adaptation to the desert environment may have applications in breeding programs and may provide some perspective for disease-resistance research in different animal species. Future studies on camel genome and transcriptome may contribute to a detailed understanding of these important physiological mechanisms with relevance to human medical conditions.

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