Iranian Journal of Applied Animal Science

A Review of Microsatellite Marker Usage in the Assessment of Genetic Diversity of *Camelus*

Review Article

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Received on: 7 Jan 2014
Revised on: 3 Apr 2014
Accepted on: 30 Apr 2014
Online Published on: Mar 2015

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Online version is available on: www.ijas.ir

ABSTRACT

Camels have been regarded as the desert ship and they play multi-utility role in the world. Estimation of genetic parameters is foremost step towards managing the genetic resources for their conservation and sustainable utilization. Microsatellite markers have been extensively used in cattle, sheep, goat and camels. However, genetic characterization studies on camels has been poorly recorded. There has been a rapid increase in amount of molecular data produced from indigenous camel populations, which clearly shows awareness among the scientific community. Based on the studies carried out in Australia, Kenya, Saudi Arabia, Canary Islands, India, Egypt and Tunisia the camels have shown very wide genetic diversity via the predefined microsatellite markers. It is highly recommended that to use following microsatellite markers to find the highly informative heterozygosity data: YWLL08, YWLL09, YWLL38, YWLL44, YWLL59, VOLP03, VOLP08, VOLP10, VOLP32, VOLP67, LCA66, CVRL01, CVRL05, CVRL06, CVRL07 and CMS50. These markers have shown a high level of allelic richness and polymorphic information content. Therefore, future genetic diversity analysis on camel can be based on these highly useful markers.

KEY WORDS biodiversity, camel, conservation, genetic diversity, microsatellite.

INTRODUCTION

Camel domestication was believed to begun in the Arabian Peninsula around 3000BC (Mikesell, 1955). Since then it has dispersed to the whole African via Horn of Africa (Gifford-Gonzalez and Hanotte, 2012). According to latest studies worldwide total camel population is 24.7 million head and the largest population has been found in Somalia (7 million). Ninety seven different breeds are currently listed on FAO DAD-IS database. Nevertheless, it is an incomplete data set and is mainly based on morphological features, which did not include breeds reported from the Kingdom of Saudi Arabia. Camels are indispensable companion of pastoral society not only in Arabian Peninsula and the African continent. They play a variety of roles such as transportation, provision of meat, milk and hair and are used for sport, draught potential and to demonstrate wealth (Gautam *et al*. 2004; Nolte *et al*. 2005; Mehta and Sahani, 2007; Spencer *et al*. 2010). Despite these numerous values for different societies, the lack of selection for economically valuable trait has resulted in a low level of variation within population (Vijh *et al*. 2007).

Genetic characterization

Endemic animals continued to be concern from conservationists all over the world (Duchev and Groeneveld, 2006) and genetic characterization is the primary step in conservation of genetic resources (Rout *et al*. 2008). Moreover, appropriate management and conservation strategies for animal genetic resources require assessment of genetic diversity both within and among populations (Bjørnstad and Røed, 2002). An improved knowledge of genetic diversity

and variability within and between populations is very vital for conservation and management of biodiversity, especially in identifying genetically unique structures (Zhuravlev *et al*. 2010).

Genetic characterization can be carried out by different methods such as biochemical / cytogenetic and molecular techniques, but the former lacks the power to show polymorphism (Meghen *et al*. 1994; Gizaw *et al*. 2011). Protein polymorphisms known as allozymes are the first biomarkers widely used in livestock characterization studies. Several livestock breeds have been characterized for variations in different proteins (Hanotte and Jianlin, 2005).

Molecular markers

Genetic characterization can be carried out in livestock researches using protein polymorphism, various molecular biology techniques such as restriction fragment length polymorphism (RFLP), protein polymorphism, randomly amplified polymorphic DNA (RAPD) (Yadav and Yadav, 2007; Mahrous *et al*. 2011; Al-Swailem *et al*. 2007), amplified fragment length polymorphism (AFLP), mitochondrial DNA (mtDNA), short tandem repeat (STR or microsatellites) and single nucleotide polymorphism (SNP). Microsatellites have shown clear advantage over the other markers (Vignal *et al*. 2002; Güven *et al*. 2010). In dromedary camels, protein polymorphism has shown very little genetic variation (Guerouli and Acharbane, 2005). Therefore, in camels microsatellites has been the primary option for characterizing genetic diversity studies carried out across the continents of: Saudi Arabia (Mahmoud *et al*. 2012; Mahmoud *et al*. 2013), South Africa (Nolte *et al*. 2005), India (Gautam *et al*. 2004; Mehta and Sahani, 2007; Vijh *et al*. 2007; Banerjee *et al*. 2012), Tunisia (Ould Ahmed *et al*. 2010), Canary Islands (Schulz *et al*. 2012), Kenya (Mburu *et al*. 2003), Egypt (Mahrous *et al*. 2011) and Australia (Spencer *et al*. 2010). A Camelid microsatellite set was produced using published data from South American Camelids, Alpacas and Ilamas. This set comprised of sixteen primers with highest polymorphism (Nolte *et al*. 2005), although global diversity assessing diversity in camel genetics are not limited to these markers and has used a range of different microsatellite markers (Table 1).

Microsatellite based studies in camels

Australian camel research was carried out using 484 samples with 28 markers and showed little genetic diversity since they descend from a small group of parent animals imported from Afghanistan (Spencer *et al*. 2010). Studies carried out by Mburu *et al*. (2003) with distinguished four Kenyan camel populations (268 samples), Pakistan (32 samples), United Arab Emirates (10 samples), Saudi Arabian (22 samples) and Chinese Bactrian (28 samples) camel samples using fourteen microsatellite markers found lower diversity than in non-Kenyan camel breeds.

Table 1 Microsatellite markers used in the various camel genetic diversity studies

Locus	Studies used
YWLL02	Nolte *et al*. 2005
YWLL08	Nolte *et al*. 2005; Mehta and Sahani, 2007; Mahrous *et al*. 2011; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Schulz *et al*. 2010; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
YWLL09	Gautam *et al*. 2004; Nolte *et al*. 2005; Mehta and Sahani, 2007; Vijh *et al*. 2007; Mburu *et al*. 2003
YWLL29	Mehta and Sahani, 2007
YWLL36	Mehta and Sahani, 2007
YWLL38	Nolte *et al*. 2005; Spencer *et al*. 2010; Mehta and Sahani, 2007; Vijh *et al*. 2007; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Schulz *et al*. 2010; Mburu *et al*. 2003; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
YWLL40	Mehta and Sahani, 2007
YWLL44	Gautam *et al*. 2004; Nolte *et al*. 2004; Spencer *et al*. 2010; Mehta and Sahani, 2007; Vijh *et al*. 2007; Mahrous *et al*. 2011; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Schulz *et al*. 2010; Mburu *et al*. 2003; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
YWLL58	Gautam *et al*. 2004; Mehta and Sahani, 2007
YWLL59	Gautam *et al*. 2004; Mehta and Sahani, 2007; Mahrous *et al*. 2011; Mburu *et al*. 2003
VOLP03	Nolte *et al*. 2004; Spencer *et al*. 2010; Mehta and Sahani, 2007; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Ould Ahmed *et al*. 2010; Schulz *et al*. 2010; Mburu *et al*. 2003; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
VOLP08	Gautam *et al*. 2004; Nolte *et al*. 2005; Mehta and Sahani, 2007; Vijh *et al*. 2007; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Schulz *et al*. 2010; Mburu *et al*. 2003; Mahmoud *et al*. 2013
VOLP10	Gautam *et al*. 2004; Nolte *et al*. 2005; Spencer *et al*. 2010; Mehta and Sahani, 2007; Vijh *et al*. 2007; Banerjee *et al*. 2012; Schulz *et al*. 2010; Spencer and Woolnough, 2010
VOLP32	Spencer *et al*. 2010; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Schulz *et al*. 2010; Mburu *et al*. 2003; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
VOLP67	Nolte *et al*. 2004; Spencer *et al*. 2010; Mehta and Sahani, 2007; Vijh *et al*. 2007; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
LCA18	Vijh *et al*. 2007
LCA33	Nolte *et al*. 2005
LCA37	Nolte *et al*. 2004; Spencer *et al*. 2010; Banerjee *et al*. 2012
LCA56	Nolte *et al*. 2004; Spencer *et al*. 2010; Banerjee *et al*. 2012
LCA59	Mehta and Sahani, 2007
LCA63	Nolte *et al*. 2005; Mehta and Sahani, 2007; Vijh *et al*. 2007; Banerjee *et al*. 2012; Spencer and Woolnough, 2010
LCA65	Spencer *et al*. 2010; Spencer and Woolnough, 2010
LCA66	Nolte *et al*. 2004; Spencer *et al*. 2010; Mehta and Sahani, 2007; Vijh *et al*. 2007; Mahmoud *et al*. 2012; Banerjee *et al*. 2012; Schulz *et al*. 2010; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
LCA70	Spencer *et al*. 2010; Spencer and Woolnough, 2010
LCA77	Nolte *et al*. 2004; Spencer *et al*. 2010; Banerjee *et al*. 2012; Spencer and Woolnough, 2010
LCA90	Vijh *et al*. 2007
CVRL01	Spencer *et al*. 2010; Vijh *et al*. 2007; Mahmoud *et al*. 2012; Ould Ahmed *et al*. 2010; Schulz *et al*. 2010; Mburu *et al*. 2003; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
CVRL02	Vijh *et al*. 2007; Ould Ahmed *et al*. 2010; Mburu *et al*. 2003
CVRL04	Vijh *et al*. 2007
CVRL05	Vijh *et al*. 2007; Ould Ahmed *et al*. 2010; Schulz *et al*. 2010; Mburu *et al*. 2003; Mahmoud *et al*. 2013
CVRL06	Vijh *et al*. 2007; Mahmoud *et al*. 2012; Ould Ahmed *et al*. 2010; Schulz *et al*. 2010; Mburu *et al*. 2003; Mahmoud *et al*. 2013
CVRL07	Spencer *et al*. 2010; Vijh *et al*. 2007; Ould Ahmed *et al*. 2010; Schulz *et al*. 2010; Mburu *et al*. 2003; Spencer and Woolnough, 2010
CVRL08	Vijh *et al*. 2007
CMS9	Mahmoud *et al*. 2012; Mahmoud *et al*. 2013
CMS13	Vijh *et al*. 2007; Mahmoud *et al*. 2012; Mahmoud *et al*. 2013
CMS16	Spencer *et al*. 2010; Vijh *et al*. 2007; Spencer and Woolnough, 2010
CMS17	Mahmoud *et al*. 2012; Mahmoud *et al*. 2013
CMS50	Spencer *et al*. 2010; Mahmoud *et al*. 2012; Spencer and Woolnough, 2010; Mahmoud *et al*. 2013
CMS58	Vijh *et al*. 2007
CMS121	Vijh *et al*. 2007; Mahmoud *et al*. 2012; Mahmoud *et al*. 2013

Saudi Arabian camel populations (four populations), using 160 hair samples that were inspected with sixteen markers, displayed considerable amount of genetic variation mainly due to a high level of crossbreeding among camel breed (Mahmoud *et al*. 2012). Nolte *et al*. (2005) camels from south Africa, Namibia and Botswana using 234 samples altogether with 12 loci. South African camels showed close relationship among them. Egyptian camels (four breeds) showed low genetic distances due to the fact that they originated from a common ancestor (Mahrous *et al*. 2011).

Indian camels (four populations) were assessed using 23 microsatellite markers and showed lower genetic diversity when compared with South African and Sudanese camels (Vijh *et al*. 2007). Another study by Gautam *et al*. (2004) on Jaiselmari camel showed lower than the study carried out by Vijh *et al*. (2007). Whereas, the study on Bikaneri camels did find a considerable amount of genetic heterozygosity for their improvement of production and management and for conservation purposes (Mehta *et al*. 2007).

Polymorphic information content (PIC) is a measure of the informativeness of the marker, ranging from 0 to 1 and a loci with PIC value of close to 1 has with many alleles that are desirable for genetic diversity studies. Generally the markers show PIC values lower than 0.5, which implies a locus moderately informative (0.5>PIC>0.25) and the rest of them were highly informative (PIC>0.5) (Botstein *et al*. 1980). The markers have been used in studies that showed genetic variability and indicate the usefulness of PIC markers in future studies.

CONCLUSION

There is a massive volume of indigenous camel breeds that are not genetically characterized such as Somalia and Somaliland, Iranian, Mauritanian and Ethiopian camels. Globally camel genetic characterization studies have mainly been completed using microsatellite markers. Therefore, the following microsatellite markers can be considered while genetically characterizing the genetically non-characterized camels of the world. Markers such as YWLL02, YWLL29, YWLL36, YWLL40, LCA18, LCA33 and CMS58, show a low amount of variability and PIC values throughout and not as useful for research. Whereas markers YWLL08, YWLL09, YWLL38, YWLL44, YWLL59, VOLP03, VOLP08, VOLP10, VOLP32, VOLP67, LCA66, CVRL01, CVRL05, CVRL06, CVRL07 and CMS50, show higher more alleles per locus and high PIC values. These markers are useful in describing heterozygosity levels and informative and it was concluded these markers are well suited for genetic characterization of camels in near future.

ACKNOWLEDGEMENT

I would thank Dr. Jernej Jakse of University of Ljubljana, Slovenia for his comments on manuscript and as well as Dr. Abdul Raziq of Society of Animal, Veterinary and Environmental Scientists (SAVES).

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