Genetic Comparison of Two Different Arabian Oryx Populations in UAE Based on Microsatellite Analysis

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Abstract—This is a genetic comparison study of Arabian Oryx (Oryx leucoryx) population at two different locations (A &B) based on nuclear microsatellite DNA markers. Arabian Oryx is listed as vulnerable and endanger by the World Conservation Union (IUCN). Thirty microsatellite markers from bovine family were applied to investigate the genetic diversity of the Arabian Oryx and to set up a molecular inventory. Among 30 microsatellite markers used, 13 markers were moderately polymorphic. Arabian Oryx at location A has shown better gene diversity over location B. However, mean number of alleles were less than location B. Data of within population inbreeding coefficient indicates inbreeding at both locations (A&B). Based on the analysis of polymorphic microsatellite markers, the study revealed that Arabian Oryx need a genetically designed breeding program.

Keywords—Arabian oryx, Microsatellites

I. INTRODUCTION

THIS report is the first study on the genetic structure of the Arabian oryx (*Oryx leucoryx*) populations present in two different locations at the Management of Nature Conservation Center (MNC), UAE. The antelope Arabian oryx was extirpated from the wild as a result of massive hunting during early 1970[s] [1]. Fortunately, the efforts of captive breeding programs succeeded to preserve the Arabian oryx, which was later reintroduced in certain protected areas [2]-[3]-[4]. Recently, [5] have recommended maintaining a global perspective for the captive genetic management of Oryx.

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II. METHOD

DNA was extracted from blood, using QIAamp DNA midi kit (QIAGEN). Thirteen markers were used in this study [6]. All PCR amplification reactions were conducted in ABI 9700 Thermocycler. The amplicon was genotyped using GeneMapper 4.0 version (ABI 3100 Genetic Analyzer; Applied Biosystems).

III. DATA ANALYSIS

Mean number of alleles and Hardy -Weinberg equilibrium values were calculated using ARLEQUIN version 3.1 software [7] and within population inbreeding coefficient values were calculated for each locus using F-STAT version 2.9.3 [8].

IV. RESULTS AND DISCUSSION

Data analysis revealed that 8 markers out of 13 were deviating from Hardy -Weinberg equilibrium (HW) test at location B see Table1. We plotted the statistical data to show the deviation from HW equilibrium and gene diversity for both populations see Fig. 1 & 2. Intriguingly, population B (4.077) has shown lower diversity despite higher number of alleles over population A (3.846). The variation in means number of alleles and Fis at location A&B might be explained by the sample sizes.

To understand the genetic distribution of the two Arabian oryx populations we have calculated log likelihood values (Population Assignment) using GenAlEx6 program [9]-[10]. Log likelihood values at location B showed high degree of similarity between them see Figure 3. Thus, we suggest introducing males from location A for future breeding programs.

Since there is a substantial shortfall of heterozygosity at both locations, we suggest proper genetic management to be implemented. One approach is to use migrant male for future breeding programs.

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TABLE I
STANDARD DIVERSITY INDICES OF ARABIAN ORYX POPULATIONS AT LOCATION 'A' & 'B'

Marker	Location 'A'				Location 'B'			
Locus	Na	Fis	P- Value	Signif	Na	Fis	P- Value	Signif
ETH225	3	0.228	0.50632	ns	4	0.099	0.01622	*
ILSTS87	6	-0.038	0.40095	ns	5	0.005	0.10591	ns
BM6444	5	0.426	0.01038	*	7	0.215	0.00091	*
BMS2072	5	0.127	0.14445	ns	6	0.07	0.00173	*
INRABERN172	4	-0.118	0.81599	ns	4	0.013	0.83655	ns
ETH152	4	0.086	0.67113	ns	3	0.033	0.57934	ns
BM4505	3	-0.029	0.36055	ns	3	0.005	0.28376	ns
BM2113	3	-0.08	0.26504	ns	3	0.148	0.02639	*
MM12	2	0.333	0.25479	ns	2	-0.005	1	ns
OarHH64	5	0.185	0.47461	ns	6	0.126	0.00831	*
OarFCB48	3	0.24	0.54765	ns	4	0.185	0.00859	*
MAF50	3	0.299	0.00198	*	3	0.067	0.00084	*
ILSTS30	4	-0.097	0.19167	ns	3	0.471	0	*
Mean	3.846	0.112			4.077	0.109		

Na - Number of alleles present in the Arabian Tahr population.
Fis - Within population inbreeding coefficient
P - Hardy -Weinberg equilibrium
ns - Not significant (Well distributed among the individuals)
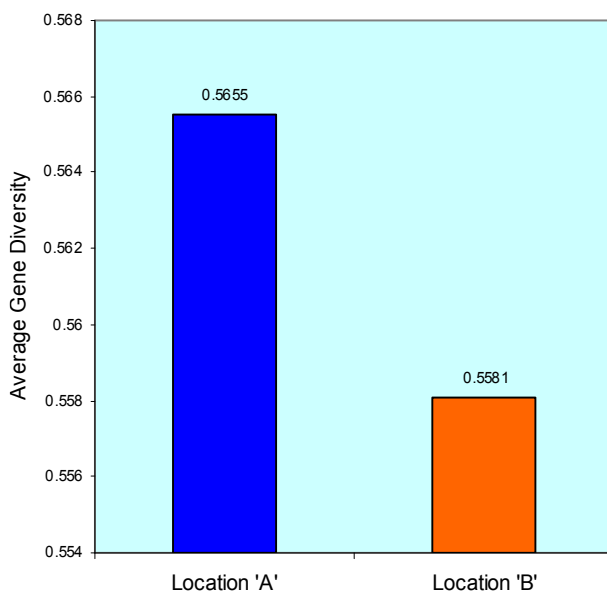***** - Significant deviation from Hardy -Weinberg equilibrium (P < 0.05)
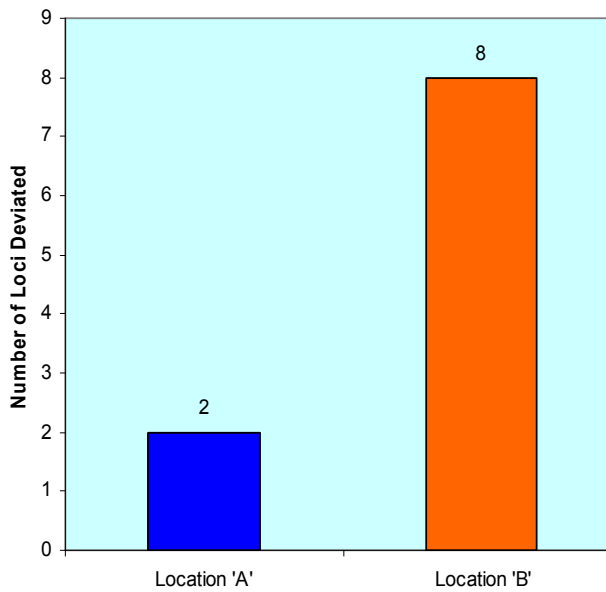

Fig. 1 Genetic diversity of A. Oryx population

Fig. 2 Deviation from Hardy -Weinberg equilibrium

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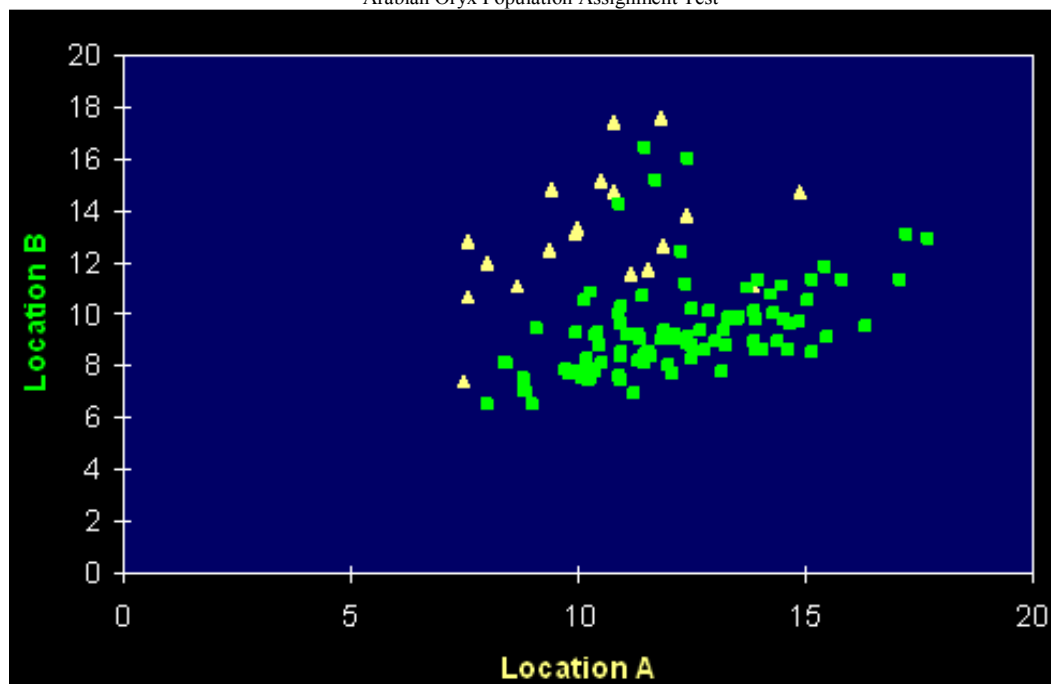International Journal of Bioengineering and Life Sciences
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Fig. 3 Illustrates the distribution of Arabian oryx population based on Log likelihood values
▲ Location A   ■ Location B

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