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# The effect of inbreeding level and genetic factors on longevity in Arabian oryx (*Oryx leucoryx*)

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Pedigree information was analysed of 2106 individuals recorded from 184 zoological gardens. Two single-trait animal models (including inbreeding coefficients as linear or quadratic covariables) were employed. Three data subsets were formed relative to the length of life. Heritability estimates were obtained using the DFREML algorithm. Moreover, phenotypic, genetic and environmental trends were estimated. Mean inbreeding level was 3.8% for all individuals, and 11.2% for the inbred animals. The inbreeding effects (evaluated as partial linear regression) ranged from -93 days (for individuals living longer than 500 days) to 25 days (for all individuals included). Heritability estimates appeared low. Generally, the time trends were non-negative, indicating the high efficiency of the realized breeding strategy.

#### KEY WORDS: Arabian oryx / inbreeding / restricted maximum likelihood / heritability / longevity

Arabian oryx (Oryx leucoryx) is a small antelope, formerly inhabitating deserts and semideserts of the north-eastern Africa and the Arabian Peninsula. Population had begun to disappear due to over-hunting from the mid XIX century which led to the species extinction in the natural environment in the 1970's [Henderson 1974]. In 1962 the protection programme was started [Spalton *et al.* 1999] using three specimens captured in Oman. Over the next years, several animals (from Arabian countries) were included in the captive breeding. In spite of relatively small initial population size, reproductive abilities of the species led to creation of several subpopulations. First reintroduction of oryx was performed in a stony desert plateau in central Oman. Over the next years the species was gradually reintroduced to Saudi Arabia, Jordan and other countries of the Middle East.

With a small and more or less closed population the risk of inbreeding is obvious, but very little is known about the current inbreeding level within the species. However, some studies on inbreeding within the population considered have been reported [Marshall and Spalton 2000]. An increase of the inbreeding rate leads to reduction of genetic variation, and in consequence has a negative effect on the adaptation ability [Falconer 1989, Lacy 1994]. A number of authors reported inbreeding depression manifesting itself in weakening of fitness and performance traits, especially in populations of livestock [Brückner 1980, Hagger *et al.* 1989, Boujenane and Chami 1997, Rodriganez *et al.* 1998, Thompson *et al.* 2000].

Length of life is one of the most important characters in wild animals. According to current knowledge, the trait is affected both by environmental and genetic factors. Furthermore, longevity is determined by many *loci*. On the other hand, early mortality in particular can be strongly influenced by chromosomal and gene point mutations [Keightley 1998, Higgins and Lynch 2001]. It is known that the probability of lethal or semilethal genotype expression increases when relatives are mated. Hence, the inbreeding effects can vary in relation to the animals' age.

The objective of this study was to estimate the inbreeding level, its trend over time and its effects on length of life in the captive-bred Arabian oryx population. Moreover, genetic and phenotypic trends of longevity were also estimated.

# Material and methods

The data were extracted from International Species Information System [ISIS 2001] resources from the Minnesota Zoological Garden, edition of January 2001. Pedigree information was analysed of 2106 individuals from 184 zoological gardens (from 30 countries). The animals included were born in the years 1900-2000. A single record structure was as follows:

- animal code;
- sire code;
- dam code;
- sex of animal;
- date of birth;
- date of death;
- inbreeding coefficient.

The data were divided into three-year periods of birth groups, except from the first period (Tab. 1). As the breeding programme for the oryx population was introduced in the 1970s, the number of individuals recorded before that time was relatively small. The highest mortality of individuals falls within the first month of life while sexual maturation appears at the age of about 500 days. Therefore, the following three datasets have been studied: DATA 1 (all individuals), DATA 2 (individuals that survived)

more than 31 days), DATA 3 (individuals that survived more than 500 days).To estimate the inbreeding effects two following linear models were employed.Model I (including the inbreeding coefficient as a linear covariable):

where:

 $y_{ijk} = m + s_i + p_j + bx_{ijk} + a_{ijk} + e_{ijk}$ 

 $y_{iik}$  - length of life (days) of *ijk*-th individual;

m – overall mean;

 $s_i$  - fixed effects of *i*-th sex;

 $p_i$  – fixed effects of *j*-th birth period;

b – linear regression coefficient;

 $x_{iik}$  - inbreeding coefficient of *ijk*-th individual included as covariable;

 $a_{iik}$  - random additive genetic effect of *ijk*-th individual;

 $e_{iik}$  - random error associated with *ijk*-th observation.

Model II (including inbreeding coefficient as a quadratic covariable):

$$y_{ijk} = m + s_i + p_j + b_i x_{ijk} + b_2 x_{ijk}^2 + a_{ijk} + e_{ijk}^2$$

where:

 $b_1$  and  $b_2$  – quadratic linear coefficients;

other symbols – as for model I.

The fixed and random effects as well as regression coefficients and variance components were evaluated by the use of the derivative-free restricted maximum likelihood algorithm (DFREML) – Meyer [1989]. The DFREML package programme was applied [Meyer 2000]. The mean inbreeding depression was estimated using partial regression coefficients (for average inbreeding level 3.8%). The use of animal model enabled (due to the incorporation of the additive relationship matrix) the inclusion of deep pedigree information, especially for animals born in the last years. Estimates of residual variances were taken as criteria of model adequacy for describing relationships between the inbreeding level and longevity.

Moreover, the phenotypic and genetic trends were estimated. The genetic trends were obtained as averaged additive genetic effects per period of birth.

### **Results and discussion**

Changes in the numbers of inbred and non-inbred individuals over time are shown in Table 1. Mean inbreeding coefficient of the studied population was 3.8%. It might be underestimated due to incompleteness of pedigree information particularly in the beginning of captive breeding. Generally, the proportion of inbred animals in the three data sets was very similar (about 37% - Tab. 1). The ratio of inbred and non-

										(/W/ L4		F: (%)
Year class n	u	$F_{a}(\%)$	$\mathbf{n}_{\mathrm{F}}$	$F_{i}(%)$	u	$F_{a}(\%)$	$\mathbf{n}_{\mathrm{F}}$	$F_{i}(%)$	u	Fa (%)	$\mathbf{n}_{\mathrm{F}}$	(0)1+
1974 7	78	1.12	5	17.5	72	1.22	S	17.5	67	1.12	4	18.75
974-1976 5	57	2.19	17	7.35	53	2.24	21	7.42	50	2.25	15	7.50
977-1979 12	127	6.34	56	14.39	113	6.30	51	13.96	105	6.07	47	13.55
980-1982 14	140	3.79	56	9.47	114	3.78	45	9.58	96	3.51	36	9.36
983-1985 20	203	4.15	74	11.35	186	4.15	99	11.69	175	3.94	59	11.68
986-1988 25	297	5.31	153	10.30	282	5.17	143	10.19	259	5.27	134	10.19
989-1991 423	23	3.55	199	7.55	381	3.35	170	07.51	322	3.52	142	7.97
992-1994 336	36	3.21	100	10.77	304	3.01	83	11.02	234	3.41	73	10.89
995-1997 27	273	4.51	72	17.09	251	4.24	63	16.88	189	5.11	52	18.59
998-2000 172	72	5.28	60	18.55	159	6.33	54	18.64	104	6.01	36	17.38
Fotal 2106	90	3.84	792	11.22	1915	3.69	969	11.26	1601	4.28	598	11.26

Table 1. Number of individuals and their inbreeding coefficients within DATA sets

inbred animals decreased, while the inbreeding level (especially for inbred individuals) strongly increased. When all the animals were considered the highest inbreeding level (4.2%) was recorded for DATA 3. Lowest inbreeding was observed for DATA 2. The trends in inbreeding level were similar within subclasses. Generally, it corresponds to changes of inbreeding level in milu deer (*Elaphurus davidianus*) and Przewalski's horse (*Equus caballus przewalskii*) – (Szablewski, unpublished data).

From the stock breeder's perspective inbreeding can be used for developing lines for subsequent crossing to make use of the heterosis phenomena. In case of wild species, however, inbreeding depresses fitness traits. The reduction of fitness after close inbreeding can be caused by a number of genetic factors [Crnokrak and Roff 1999], e.g. by an increase of homozygosity and in consequence by unmasking of recessive unfavourable alleles.

Mean length of life was 1175 days (with standard deviation of 1626). Considering genetic and environmental effects on longevity it is worth to pay attention to heritability which reflects the relative impact of both. As shown in Table 2, the heritability estimates ( $h^2$ ) of longevity obtained in this study were relatively low, ranging from 0.045 (for DATA 3, model II) to 0.074 (for DATA 2, model II). Similar  $h^2$  were found in various wild and domestic species. Vollema [1998] reported very low  $h^2$  estimates (less than 0.1) of longevity in dairy cattle. Similar results were found in red deer [Kruuk *et al.* 2000] as well as in *Drosophila melanogaster* [Baret *et al.* [1996] and Mitchell

Table 2. Ir es	Inbreeding effects, heritabi estimates for length of life.	ects, heritability esti ength of life.	mates and their st	andard deviations	Table 2. Inbreeding effects, heritability estimates and their standard deviations (in parentheses) as well as error variance estimates for length of life.	l as error variance
Data set		Mean level of inbreeding (%)	Regression coefficients	Estimate of error variance	Mean inbreeding depression (in days)	Heritability estimates
DATA 1	DATA 1 Model I Model II	3.8	-3.3x -6.5x + 43.2x <sup>2</sup>	1453890 1454292	-13 22	$0.067 (\pm 0.030) \\ 0.067 (\pm 0.030)$
DATA 2	DATA 2 Model I Model II	3.6	3.9x 5.2x -5.2x <sup>2</sup>	1311462 1311655	14 -49	$0.073 (\pm 0.034) \\ 0.074 (\pm 0.038)$
DATA 3	Model I Model II	4.3	-3.9x 7.5x - 7.8x <sup>2</sup>	1253461 1258673	-17 -84	$\begin{array}{c} 0.049 \ (\pm 0.025) \\ 0.045 \ (\pm 0.026) \end{array}$

*et al.* [2001] showed that the estimated  $h^2$  in humans exceeded 0.2. It seems that heritability might be underestimated as the assumption of normality of the distribution was not fulfilled, which may lead to overestimation of error variance [Besbes *et al.* 1993]. Boujenane and Chami [1997] reported that inbreeding depression is deeper for traits of low than of high heritability.

Inbreeding level was relatively low in the three data sets studied. The partial linear regression coefficients of the inbreeding level on longevity appeared negative. In general, negative interrelations were also obtained by the use of partial quadratic regression model (positive  $b_1$  and negative  $b_2$ , coefficients). As shown in Table 2, inbreeding in the oryx resulted in negligible depression of the length of life for all individuals (DATA 1) and individuals that survived for more than 500 days (DATA 3). Conversely, the linear regression coefficient for DATA 2 (individuals that survived more than 31 days) was positive. Generally, similar tendencies occurred when quadratic regression equations were employed. Mean square error was applied as a criterion for choosing the best model (including linear or quadratic regression). Error variance estimates for models with linear regression were smaller than those with the quadratic one. Hence, the simpler animal model (including linear partial regression) is preferred for evaluation of inbreeding effects in the studied population. Differences in estimated inbreeding depression among the oryx data sets might have been caused by higher mortality in the first and last period of time. As noted above, longevity is strongly affected by environmental factors (low heritabilities were estimated).

Inbreeding is an important problem in small populations of wild animals. Therefore, special mating systems to reduce the inbreeding rate are still being developed. Over the last three decades, the protection strategy has been realized in the oryx population [Marshall and Spalton 2000]. As previously noticed it resulted in the decreasing ratio of inbred to non-inbred animals (Tab. 1).

The genetic and phenotypic trends are shown in Figures 1 and 2, respectively. In general, the mean genetic value increased, especially over the last two decades when the genetic improvement programme was implemented. It should be stressed

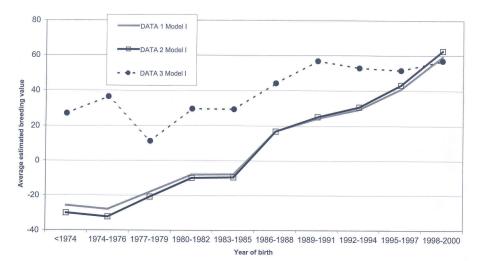


Fig. 1. Genetic trends for longevity in Arabian oryx population.

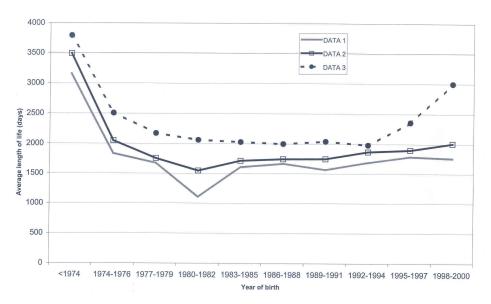


Fig. 2. Phenotypic trends for longevity in Arabian oryx population.

that over the period in question, the mean genetic value increased by 120 days for all individuals (DATA 1) – Figure 1. Smaller differences were observed in two data sets (90 days for DATA 2 and 31 days for DATA 3). This corresponds to the unpublished results got by Szablewski on milu deer and Przewalski's horse where positive genetic trends in longevity were also obtained. Examined were also dependencies between genetic trends and inbreeding level. Within DATA 1 and DATA 2 these relations were positive whereas occurred non-positive for oldest individuals (DATA 3).

The phenotypic trends for longevity (in all three data sets) as illustrated in Figure 2 show two distinct periods. First, from year 1970 to 1980, was marked by a decreasing longevity. The second – from 1980 to 2000 – shows a tendency to stabilize, with an increasing number of individuals. It could be associated with the implementation of the breeding strategy. However, the dependencies between mean phenotypic values and the inbreeding level were positive for inbred animals, but negative when all individuals were considered. Since the residual variances were very high, average environmental effects for all data sets varied over time. As noted earlier, the effects of inbreeding were only slightly affected by the age of individuals.

Analysis of heritability and genetic trend of longevity leads to the conclusion that major role is played by environmental effect. However, consistent increase in breeding value suggests genetic adaptation to captive breeding. It should be kept in mind that from the perspective of conservation of genetic diversity lack of genetic trend would be most favourable. Changes in genetic potential reflect variation in gene frequencies and may be related to loss of some alleles. In general, due to the breeding strategy employed, inbreeding rate in Arabian oryx seems to be on a safe level, especially over the last decades.

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# Wpływy inbredu i czynników genetycznych na długość życia oryksa arabskiego (*Oryx leucoryx*)

#### Streszczenie

Zbadano zależności między poziomem inbredu a długością życia oryksa arabskiego. Wykorzystano informację o 2106 osobnikach ze 184 ogrodów zoologicznych. Wykorzystano dwa jednocechowe modele zwierzęcia (uwzględniając liniowy i kwadratowy wpływ inbredu). Analizowano trzy podgrupy zwierząt utworzone w zależności od długości życia. Do szacowania odziedziczalności wykorzystano algorytm DFREML. Ponadto oszacowano trendy genetyczne, fenotypowe i środowiskowe długości życia. Średni poziom inbredu dla wszystkich osobników wyniósł 3.8%, natomiast 11.2% dla osobników zinbredowanych. Efekty inbredu (oszacowane na podstawie współczynników regresji cząstkowej) zawierały się w przedziale od -93 dni (dla osobników żyjących powyżej 500 dni) do 25 dni (dla wszystkich osobników). Oszacowany współczynnik odziedziczalności był niski. Ogólnie trendy były nieujemne, co wskazuje na skuteczność realizowanej strategii hodowlanej.