

Morphological Approach to Genetic Variability of the Asiatic Wild Ass (*Equus hemionus*) Using Non-metric Skull Characters*

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Abstract

Key words:

Asiatic wild ass, epigenetic variability, *Equus hemionus*, fluctuating asymmetry, non-metric skull characters, population genetics, Southern Mongolia,

Article information:

Received: 07 May 2015

Accepted: 19 Nov. 2015

Published: 26 Nov. 2015

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Cite this paper as:

The Asiatic wild ass (*Equus hemionus*) is a globally endangered large mammal threatened by competition with livestock, poaching as well as habitat fragmentation and loss. Because of these environmental stresses it can be assumed that the species suffers from lower developmental stability and that barrier effects could cause genetic isolation. To gain more insight into the population genetics of the Asiatic wild ass, a series of 440 skulls found in two Gobi regions of Mongolia were examined. The epigenetic variability and epigenetic distance between the samples as well as their fluctuating asymmetry were studied by using 62 non-metric skull characters to test and evaluate possible genetic depletion, genetic isolation and the general influences during ontogenesis. The high epigenetic variability, $I_{ev} = 0.39$ did not differ between the two regions indicating no evidence of genetic depression. The very low, but significant epigenetic divergence of $MMD = 0.05$ between the Dzungarian Gobi and the Southern Gobi suggests restricted connectivity. The moderate degree of fluctuating asymmetry ($FA = 0.11 - 0.15$) found gives no signs of reduced developmental stability. Thus, our results suggest that Asiatic wild ass from Mongolia are from genetically viable populations.

Lkhagvasuren, D., Batsaikhan, N., Samiya, R., Schafberg, R., Stubbe, A., Stubbe, M. & Ansorge, H. 2015. Morphological approach to genetic variability of the Asiatic wild ass (*Equus hemionus*) using non-metric skull characters. *Mong. J. Biol. Sci.*, 13(1-2): 3-12.

Introduction

The Asiatic wild ass (*Equus hemionus hemionus* Pallas, 1775) is one of the most endangered large mammal species not only in Mongolia, but also in the world (Clark *et al.*, 2006; Moehlman *et*

al., 2008). It was once widespread throughout steppe and semi-desert habitats. Today it occurs only in the Dzungarian Gobi, Trans-Altai Gobi, Northern Gobi and Alashan Gobi in Mongolia

*Results of the Mongolian-German Biological Expeditions since 1962, contribution No. 324