

33rd Conference of the **International Society for Animal Genetics**

July 15–20, 2012, Cairns, Australia

Programme and Abstract Book

P3032 Phylogenetic re-analyzing of Iran's Jebeer based on cytochrome b sequence. M. R. Nassiri^{1,2}, M. Mahdavi¹, and A. Javadmanesh*³, ¹Department of Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad, PO Box 91775-1163, Mashhad, Khorasan, Iran, ²Department of Agricultural and Animal Biotechnology, Institute of Biotechnology, Ferdowsi University of Mashhad, PO Box 91775-1163, Mashhad, Khorasan, Iran, ³JS Davies Epigenetics and Genetics group, School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy Campus, Roseworthy SA 5371, Adelaide, South Australia, Australia.

There are 3 species of Gazelle genus living in Iran: Gazella gazella, Gazella subgutturosa and Jebeer. Among them taxonomic position of the Jebeer is ambiguous. Jebeer lives mainly in central and southern desert areas of Iran. Some reports considered Jebeer to be conspecific with Gazella gazella. Also, others found it to be closer to Gazella dorcas and Gazella bennetti. The goal of this study was to analysis genetic and phylogenetic of cytochrome b region in Jebeer of Iran. In this regard 5 biological samples from Shirahmad's Wildlife Refuge of Sabzevar (Khorasan, Iran) were collected (36°5'6"N and 57°53'4"E). After DNA extraction, Cytochrome b region of mitochondrial DNA has been amplified and sequenced with ABI 3130 automated device. Sequenced fragments were compared with 190 sequences from Gazella genus that have been classified based on species with regard to homology and evolutionary divergence using MEGA v5, CLC Main Workbench v5.5 and BioEdit v7.1 software packages. Our results showed that among all Gazelle sp., Jebeer had the shortest distance (0.003) with G. bennetti and longest distances with G. dorca and his sister taxon G. saudiya that are equal to 0.073 and 0.074, respectively. These findings might underscore the necessity of establishing Jebeer as a Gazella bennetti species.

Key Words: mitochondrial DNA, Jebeer, Iran

P3033 The use of DNA to reveal a potentially deadly package! Two wildlife forensic case studies from the Australian Museum. R. N. Johnson^{*1}, A. G. King¹, C. Vockler¹, and G. M. Cooke^{1,2}, ¹Australian Museum, Sydney, NSW, Australia, ²University of NSW, Kensington, NSW, Australia.

Australian enforcement agencies are increasingly embracing the use of DNA to assist in the investigation of wildlife cases. In certain instances, DNA can provide important information including species identification or pedigree information, which cannot otherwise be determined. Wildlife crime is not only a risk to the wellbeing of individual animals targeted. It puts local and global biodiversity at risk as well as local industry through potential pest threats to agriculture. It can also pose significant disease risk to both human and animal health. This presentation will outline two very different cases that demonstrate the utility of DNA identification in wildlife forensic cases. The first is a NSW police case involving a threatening package, where the contents were identified using transfer DNA. The other is a quarantine investigation, where we were asked to distinguish between a number of cryptic snail species and develop a diagnostic test to discriminate the invasive species from its non-invasive congeners. Through sharing our insights and experience with the techniques used in these successful yet diverse cases, we hope to encourage further uptake of the use of DNA by authorities where the quite unique skills involved in wildlife forensic work are required.

Key Words: wildlife forensics, DNA-diagnostics, law enforcement

P3034 Sequence-based genotyping of the SLA class I and II loci in Asian wild boars. Woo-Young Jung^{*1}, Dong-Won Seo¹, Hyun-Tae Lim², Chak-Sum Ho³, and Jun-Heon Lee¹, ¹Department of Animal Science and Biotechnology, Chungnam National University, Daejeon, Korea, ²Department of Animal Science, College of Agriculture, Gyeongsang National University, Jinju, Korea, ³Gift of Life Michigan, Histocompatibility Laboratory, 3861 Research Park Drive, Ann Arbor, MI, USA.

The porcine MHC (major histocompatibility complex), called SLA (swine leukocyte antigen), has been known to play very significant roles in controlling immune responses to foreign infectious agents such as bacteria and virus. It has also been known to affect vaccine responsiveness. Knowledge of SLA diversity in domestic pigs is rapidly growing while it remains largely unknown in wild pigs. In this research, we investigated the 2 highly polymorphic SLA class I (SLA-1 and SLA-2) and 3 class II (DRB1, DQB1 and DQA) loci using the cDNA SBT (sequence-based typing) method in 4 Asian wild boars. We identified a total of 12 novel SLA alleles consisting of 7 class I (arbitrarily designated SLA-1*wy06, SLA-1*wy07, SLA-1*wy08, SLA-1*wy09, SLA-1*wy10, SLA-2*wy11 and SLA-2*wy12) and 5 class II (arbitrarily designated SLA-DRB1*wy01, DQB1*wy02, DQB1*wy03, DQA*wy04 and DQA*wy05) sequences. On the other hand, we also detected 4 class II alleles (DRB1*0102, DRB1*0401, DQB1*0601 and DQA*0301) which are frequently observed in the domestic pigs. This sharing of SLA alleles may indicate a very recent divergence between the domestic and wild pig populations in Asia. These results will provide valuable information for understanding the SLA allelic architecture in swine.

Key Words: MHC, SLA, Asian wild boar