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ABSTRACTS

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P286 Withdrawn

P287 Withdrawn

P288 Historical biogeography of Philippine native pigs and the perplexing mitochondrial DNA variation in Philippine wild pigs. J. Layos*[1,2], C. Godinez[1,3], L. Liao[4], Y. Yamamoto[1], and M. Nishibori[1], [1]*Laboratory of Animal Genetics, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan,* [2]*College of Agriculture and Forestry, Capiz State University, Capiz, Philippines,* [3]*Department of Animal Science, Visayas State University, Leyte, Philippines,* [4]*Laboratory of Aquatic Ecology, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan.*

The Philippines is an archipelago of 7,641 islands situated in Island Southeast Asia at the crossroads of past human migrations in the Asia-Pacific region. It was believed to have never been connected to the Asian continent, even during the severe Quaternary sea-level drops. As a result, the history of pig dispersal in the Philippines remains controversial due to the limited molecular studies and the absence of archeological assemblages that exhibit signs of pig domestication. This study provides the first comprehensive screening of the mitochondrial DNA of Philippine native pigs (n = 175) and Philippine wild pigs (n = 9) to resolve their earlier dispersal history by conducting phylogenomic analysis altogether with domestic pigs and wild boars corresponding roughly to their geographic origin. Results revealed a demographic signal of pig ancestry exhibiting a close genetic affiliation from mainland Southeast Asia and Northeast Asia Regions which corroborates a gene flow that might have arisen through human migration and trade. Here, we proposed 2 possible dispersal routes. One is through Northeast Asia paralleled with the Neolithic expansion in Island Southeast Asia and Oceania, and the other is through mainland Southeast Asia, which may have traversed through the Sundaic Region to Palawan and the Sulu Archipelago. Despite geographical barriers to migration, numerous genetic lineages have persisted on various Philippine islands and even warrants the recognition of a Philippine Lanyu-type. The prehistoric population size dynamics predate a demographic expansion during the Late Pleistocene ages as the Southern regions to be the probable origin, eventually expanded toward the Central regions. The intriguing signal of disparity detected among the molecular result, morphology, and distribution range of the numerous Philippine endemic wild pigs opens a new challenging approach in shedding the complexities between these animals.

Key Words: genetic diversity, historical biogeography, mitochondrial DNA, Philippine native pigs, phylogenomics

P289 Reassessing phylogeny and Bayesian divergence dating provide new insights on the evolutionary history of chickens in Southeast Asia. C. J. P. Godinez*[1,2], J. K. N. Layos[1,3], Y. Yamamoto[1], L. M. Liao[4], M. Duangjinda[5], and M. Nishibori[1,2], [1]*Laboratory of Animal Genetics, Hiroshima University, Higashi-Hiroshima, Japan,* [2]*Visayas State University, Leyte, Philippines,* [3]*Capiz State University, Capiz, Philippines,* [4]*Laboratory of Aquatic Ecology, Hiroshima University, Higashi-Hiroshima, Japan,* [5]*Khon Kaen University, Khon Kaen, Thailand.*

The domestication of chickens has contributed various benefits to the sustenance and cultural development of mankind. The profound timings of their domestication have attracted wide interest in molecular phylogeny and phylogeography studies as it remains debatable up to today. Previous studies indicated that island Southeast Asia (SEA) sits as the region where specific haplogroup D mitochondrial lineage diversified, while most of the chicken populations in the mainland SEA observed to have diverse maternal lineages. However, population history and lineage-specific divergence time estimates of these populations in the aforesaid regions are not well studied. Here, we analyzed 332 complete mitochondrial DNA control-region sequences sampled in the mainland SEA and 144 sequences represented island SEA and Oceania. One hundred 27 haplotypes were newly identified and were distributed across major divergent haplogroups except haplogroup C. Phylogenetic analyses based on neighbor-joining method, maximum likelihood, and Bayesian inference revealed newfound divergent sub-haplogroup V2 sampled from the domestic chickens in Cambodia and Laos and red junglefowl from Thailand at the basal position. Significant posterior probability supported the Philippine-Pacific sub-clade, suggesting a Philippine origin of Pacific chickens. Bayesian divergence time estimates revealed split time of Pacific chickens congruent to the increase of effective population size of Philippine chickens and corroborated the prehistoric human expansion events in the region. The newly identified sub-haplogroup V2 diverged later from the previously identified haplogroup V classified by most red junglefowl species sampled from Thailand and Cambodia. Our results suggest a high level of genetic variability of these chicken populations in the region which demonstrates conservation significance.

Key Words: divergence time estimate, evolutionary genomics, mitochondrial DNA, phylogeny, poultry and related species

P290 Genetic diversity and runs of homozygosity in Rendena cattle. E. Somenzi*[1], N. Franceschi[1], M. Barbato[1], L. Colli[1], E. Partel[2], M. Komjanch[2], A. Achilli[3], H. C. Hauffe[2], and P. Ajmone Marsan[1], [1]*Università Cattolica del Sacro Cuore, Piacenza, Italy,* [2]*Edmund Mach Foundation, San Michelle all'Adige, Trento, Italy,* [3]*Pavia University, Pavia, Italy.*

Rendena cattle are an autochthonous cattle breed from Val Rendena in the northern Italian region of Trentino Alto Adige. The breed is considered a dual-purpose breed (milk and meat) but recent selection has emphasized milk production and quality. The breed is characterized by a small-medium size, good fertility and high longevity, and is well adapted to the harsh Alpine environment. In this study 140 Rendena cows sampled in 31 different farms were genotyped with the GGP Bovine 100K SNP-chip (Neogen). In addition, their mitochondrial DNA was fully sequenced. Genotype data were used to estimate within-breed diversity and inbreeding, and were compared with SNP data from 56 Eurasian cattle breeds to evaluate population structure and relationships. Principal Component Analysis (PCA) and Neighbor-net analyses performed on the Eurasian data set indicated the Rendena cattle shared ancestry with cattle breeds of the Original Brown Swiss group. The analysis also revealed an original genetic makeup, thus confirming previous evidence from mitochondrial control-region data and lower density SNP profiles. Within-breed PCA highlighted the absence of substructure and excluded the presence of crossbred individuals or outlier animals. Some inbreeding was detected using a genome-wide analysis of runs of homozygosity (ROH) ($F_{ROH} = 0.08 \pm 0.03$). The ROHs distribution across chromosomes appeared homogeneous and related to chromosome size. Most ROHs were private or common to very few animals. Exceptions were found in 3 genomic regions - on BTA6, BTA10 and BTA16 - where ROHs were shared by > 25% of the animals tested. Noticeably, the ROH on BTA6 consisted in 33 consecutive homozygous SNPs shared by >50% of the animals. This region was found to harbor genes relevant for meat (NCAPG, LCORL) and milk production (LAP3). The mitochondrial DNAs mostly belonged to the T3 haplogroup, widespread in Central Europe. Exceptions were 10 animals with T2 haplogroups and single occurrences of the T5 and Q haplogroups.

Key Words: diversity, alps, mtDNA, ROH

P291 Genetic relationships among Canarian, African, and European goats using SNPs. M. Macri*[1,2], A. Martínez[2], M. G. Luigi[3], J.