P347 Inferring of population structure and migration routes of Island Southeast Asian goats by mtDNA, SRY and 50K SNP array analyses. Ryo Masuko*[1], Fuki Kawaguchi[1], Shinji Sasazaki[1], Muhammad I. A. Dagong[2], Sri R. A. Bugiwati[2], Joseph S. Masangkay[3], Jiaqu Wu[4], Takahiro Yonezawa[4], and Hideyuki Mannen[1], [1]*Laboratory of Animal Breeding and Genetics, Graduates School of Agricultural Science,Kobe University, Kobe, Japan,* [2]*Faculty of Animal Science, Hasanuddin University, Makassar, South Sulawesi, Indonesia,* [3]*College of Veterinary Medicine, University of the Philippines, Los Baños, Philippines,* [4]*Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan.*

[Introduction] This study aimed to estimate the population structure and migration routes for Island Southeast Asian (ISEA) goats using mtDNA D-loop region and SRY gene sequences, and SNP array. [Materials and Methods] The mtDNA D-loop region (481bp) and SRY gene 3′UTR (543bp) sequences were determined for 176 Philippine goats (123 males and 53 females) and 72 Indonesian goats (56 males and 16 females). We analyzed the mtDNA and SRY data with previously published data from the Old World populations in public database (5,939 mtDNA and 1,822 SRY sequences). We genotyped 77 Philippines and 60 Indonesian goats using the 50k Illumina BeadChip. Genetic structure and TreeMix analyses were performed by combining our data with 4,480 the Old World goats published in previous studies. [Results and Discussion] The mtDNA sequences of ISEA goats revealed 51 haplotypes, which were categorized into 2 haplogroups A (Philippines: 46/176) and B (Philippines: 130/176, Indonesia: 72/72). In ISEA male goats, 4 haplotypes (Y1AA, Y1B, Y2A, Y2B) were identified. Comparative analysis of mtDNA and SRY data in the Old World populations showed haplotype Y2A, which is predominantly in Southern Europe and Africa, was observed in ISEA, indicating a possible gene flow between ISEA and Europe and Eastern/Southern Africa. Using 50k genotype data, the genetic structure ($K = 6$) showed genetic influences from Europe and African populations to ISEA goats, but absent in Mainland Southeast Asian populations (Vietnam, Laos, and Cambodia). Europe and Eastern/Southern African goats had a Southeast Asian component. In addition, TreeMix analysis showed the gene flow between ISEA and Southern African region ($m \geq 28$) or Europe ($m \geq 38$), suggesting mutual gene flow events occurred in these regions. The gene flow events between geographically distant regions can be linked to human migrations. Considering geographical and historical backgrounds related to ISEA, Europe and Southern Africa, it suggested the gene flow between these regions by European activities during the Age of Discovery.

Key Words: Mitochondrial DNA, SRY, SNP, goat, diversity

P348 Genetic Distance among Criollo Sheep Populations. J. S. Cappello Villada[1], M. A. Revidatti*[1], S. A. De la Rosa[1], V. N. Morales[1], E. R. Tejerina[1], REZGEN-IBA-BIOVIS Consortium[2], and A. Martínez Martínez[3], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional del Nordeste, Corrientes, Corrientes, Argentina,* [2]*https://biovis.jimdofree.com/, Córdoba, Córdoba, España,* [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, Córdoba, España.*

This study is part of a broader project within RZGEN-IBA CYTED and Red CONBIAND, aimed at assessing genetic diversity and relationships among Criollo sheep populations across Iberoamerica. Genetic differentiation was estimated using Nei's DA (1983) genetic distances. A total of 39 STR markers were analyzed in 870 Criollo sheep from Argentina (5), Bolivia (1), Brazil (2), Chile (1), Colombia (1), Cuba (1), Ecuador (2), El Salvador (1), Mexico (6), Peru (1), Uruguay (1), and the USA (3). Three European breeds—Churra, Spanish Merino, and Fleischschaf—served as outgroups. Genetic distances were calculated using POPULATIONS v.1.2.28, and a Neighbor-Joining tree was constructed in SplitsTree4 v4.15.1. The analysis revealed population structure patterns, with distinct phylogenetic relationships. The GULF (USA) population consistently appeared as an outgroup, reflecting greater divergence. A well-defined cluster included Hair Sheep from Ecuador, Mexico, and Cuba, along with the Colombian Criollo, indicating close genetic ties. Four Argentine Criollo breeds grouped with Chocholteca Mexican Criollos, while Pantaneiro and Bolivian Criollos clustered with another Argentine population and 2 additional Mexican breeds, suggesting connectivity. Another cluster comprised Peruvian and Chilean Criollos. The Uruguayan Criollo, Navajo Churro, and Brazilian Criollo formed a distinct group, while the Ecuadorian Criollo clustered with El Salvador. The Mexican Katahdin was associated with the Florida Cracker, whereas European breeds separated from American genotypes. These results highlight shared genetic histories in some populations, such as Hair Sheep and Colombian Criollo, while others, like GULF, exhibit divergent trajectories. Differentiation among Argentine, Mexican, and Bolivian Criollos may reflect local adaptation and breeding practices. Additionally, the clustering of Peruvian and Chilean Criollos, along with the association of Uruguayan Criollo, Navajo Churro, and Brazilian Criollo, underscores regional genetic affinities. These findings contribute to conservation strategies and research on adaptation to diverse environments, improving genetic management efforts across Iberoamerica.

Key Words: microsatellite, sheep, biodiversity

P349 Influence of genetic map usage on genomic inbreeding estimation in Holstein cattle. M. Shihabi*[1], T. Druet[2], M. Ferencakovic[1], V. Cubric Curik[1], M. Špehar[3], N. Raguz[4], B. Lukic[4], and I. Curik[1,5], [1]*University of Zagreb Faculty of Agriculture, Zagreb, Croatia,* [2]*Unit of Animal Genomics, GIGA-R and Faculty of Veterinary Medicine, University of Liège, Liège, Belgium,* [3]*Croatian Agency for Agriculture and Food, Zagreb, Croatia,* [4]*Faculty of Agrobiotechnical Sciences Osijek, Osijek, Croatia,* [5]*Hungarian University of Agriculture and Life Sciences (MATE), Kaposvár, Hungary.*

Among genomic inbreeding coefficients, the Runs Of Homozygosity (F_{ROH}) method uniquely reflects identity-by-descent (IBD) segments, making it the most accurate measure of individual inbreeding. However, most studies assume a uniform recombination rate (1 cM = 1 Mb), although recombination varies greatly and is mainly influenced by chromosome size and selection, with the X chromosome exhibiting distinct patterns due to male hemizygosity. Consequently, inbreeding may be overestimated in regions with low recombination and vice versa, leading to inaccurate genome-wide estimates. This study aimed to evaluate the impact of using SNP-specific genetic maps compared with the standard model on overall and genome-wide inbreeding estimates in Croatian Holstein cattle. The data set included 417 cows genotyped with Illumina BovineSNP50 BeadChip, with 20,963 autosomal and 214 X-linked SNPs retained after quality control and genetic map integration. F_{ROH} was estimated using an empirical threshold-based approach (SVS) and a statistical HMM-based approach (RZooROH). Using SVS, mean F_{ROH} values under standard model were 0.123 for autosomes and 0.04 for X chromosome, while under genetic map model they were 0.111 and 0.068, respectively. RZooROH estimates were 0.104 (autosomes) and 0.055 (X chromosome) under standard model and 0.107 and 0.06 under genetic map model. Correlation between F_{ROH} estimates of the 2 models was high for autosomes (SVS: 0.872, RZooROH: 0.996), but markedly lower for SVS on X chromosome (0.037) compared with RZooROH (0.977). At the SNP level, correlations between models were 0.366 for SVS and 0.972 for RZooROH, indicating greater model sensitivity for SVS. In addition, F_{ROH} differences between models correlated with autosomal size (SVS: 0.405, RZooROH: 0.323), suggesting that standard model underestimates inbreeding on smaller autosomes. Results show that while RZooROH provides consistent F_{ROH} estimates across models, SVS shows discrepancies, particularly on the X chromosome. Given the influence of SNP density on inbreeding estimates, higher genotyping density and larger sample size are needed to refine model comparisons.

Key Words: Inbreeding, Cattle and related species, Population Genomics

P351 Why should we care about Portuguese native dog breeds?—A genome-wide perspective. Ludmilla Blaschikoff*[1,2,3], Octávio Serra[4], Dayna Dreger[5], Gabriella J. Spatola[5], Fernanda Simões[4], Heidi G. Parker[5], Elaine A. Ostrander[5], Catarina Ginja[2,3,6],