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Conference Report

Abstracts of the 25th International Colloquium on Animal Cytogenetics and Genomics (25th ICACG), 26–29 June 2024, Naples, Italy

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1. Introduction

The 25th International Colloquium on Animal Cytogenetics and Genomics is dedicated to the memory of Dr. James (Jim) Womack, a pioneer in gene mapping, especially in cattle. The meeting opened with an obituary presented by Prof. Penny Riggs, a former student at Texas A&M University (TAMU) and now a professor in the same department.

The meeting was organized into 10 sessions, beginning with General Opening Session 1, which featured three main lectures highlighting the fields of animal cytogenetics and genomics. As expected, among the 83 accepted abstracts for publication, those related to animal genomics were more prevalent than those focused solely on cytogenetics. However, several abstracts combined the two disciplines (Cytogenomics) to provide a deeper understanding of animal genomes and to better identify latent chromosome abnormalities related to fertility. Various genomic approaches were reported in several abstracts, aimed at improving the selection of animals for productive traits, disease resistance, and animal biodiversity.

Given the numerous abstracts on water buffalo (river type), a specific session was dedicated to this species, which is particularly important in Eastern, South American, and Mediterranean countries. Nonetheless, research on a wide range of animal species, including domestic and non-domestic animals, non-mammalian vertebrates, and invertebrates, was also presented. Special attention was given to the posters, which were displayed throughout the meeting. Additionally, 15 of the posters, selected by the chairpersons of the poster session, are presented and discussed on the final day. Five posters received awards. All abstracts underwent peer review, and only a few required corrections or modifications. In conclusion, the colloquium featured 13 lectures (L), 27 oral communications (O), and 43 posters (P). Each presentation was numbered according to the congress program. Special thanks to the editorial staff of the "Biology and Life Science Forum" journal for their assistance with the abstract's review and editing.

2. Dr. James (Jim) Womack Obituary

O1—Gene Mapping Is Good for You!—Remembering Dr. James E. Womack

Penny K Riggs and Womack Lab Former Students
Texas A&M University, College Station, TX, USA; riggs@tamu.edu (P.K.R.)

A true pioneer in the field of comparative animal genomics, Prof. Jim Womack (30 March 1941–13 August 2023) is remembered for his remarkable career, scientific achievements, and mentorship of 50 doctoral students and countless additional graduate students, post-doctoral scientists, and visiting scholars. Jim completed a Bachelor of Science degree at

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and fixated in Carnoy. Giemsa staining, Ag-NOR, and C-banding were performed following routine techniques, and telomere FISH was performed according to Dako instructions. Cytogenetic data were plotted against the most recent phylogeny to infer the hypothetic direction of rearrangements. Most species exhibited 2n = 36, except *O. guibei* (2n = 44), *Naja kaouthia* (2n = 38), and *C. flavolineatus* (2n = 34)—an undescribed diploid number was found in the latter species. The Henophidia representative, *Boa constrictor* exhibited homomorphic XX/XY, contrasting with the ZZ/ZW found in caenophidians. Ag-NOR in *P. olfersii* and *P. patagoniensis* corroborated translocations in NOR-carrying micro and macrochromosomes. FISH and C-banding revealed centromeric heterochromatin in *Boa constrictor* XX/XY, unlike heterochromatic and repetitive content accumulation on the W chromosome in some Caenophidia, including a large heterochromatic block and repetitive telomeric sequences in *N. kaouthia*. FISH also unveiled different interstitial signs by comparing the island *B. insularis* to the continental *B. jararaca*. These results highlight important variations in diploid number, morphology, and chromosome architecture, including sex chromosome evolution complexity and evincing rearrangements throughout snake karyotypic evolution and diversification.

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10.6. P40—Identification of Species-Specific Indels in Bubalus bubalis, Bos taurus, Capra hircus, and Ovis aries

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InDels are the second most common type of variation across eukaryote genomes. Several studies have shown that InDels are the major cause of evolutionary changes, contributing significantly to intra-interspecific divergence. The aim of this study was to identify specie-specific short-InDels for *Bubalus bubalis*, *Bos taurus*, *Capra hircus*, and *Ovis aries*. For this purpose, genomic sequences of all *Artiodactyla* and *Perissodactyla* species available in GeneBank were aligned for candidate genes associated with milk and meat qualitative and quantitative traits. The in silico investigation has evidenced that *Ovis aries* and *Bubalus bubalis* are characterized by a 14 bp deletion at the 5′UTR of the αs2-casein encoding gene (*CSN1S2*, KT283354.1:g.643-644delAGAAATCAAATCTT) and by a deletion of an heptamer at exon 10 (3′UTR) of the *PRLR* gene encoding for the Prolactin Receptor (MF461277.1:g.12162-12163delCACTACC), respectively. Likewise, the 5′UTR of the αs1-casein encoding gene (*CSN1S1*) of *Capra hircus* is characterized by a 28 bp sequence (KC951931.1:g.1989-2016insTGTACAATGCCATTAATATATTGTACAA). In particular, the first 20 nucleotides are absent in *Bubalus bubalis* and *Bos taurus* sequences, while the last 7 bp are constitutively deleted in *Ovis aries*. Finally, it was evidenced that *Bos taurus* is characterized by the deletion of 16 bp (AB076403.1:g.1207-1208delGAGTAGGTTATGGCTT) at intron 1 of the myostatin gene (*MSTN*). To verify the specificity of these genetic markers, four allele-specific PCR protocols were developed. The genotyping of a preliminary panel of 400 samples (100 each species, belonging to different breeds) seems to confirm the in silico analyses. These markers may become a new tool to carry out phylogenetic studies or to set up PCR methods to verify the animal origin of the components of a product.

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