

Editorial

Joint Conference Of The 24th International Colloquium In Animal Cytogenetics And Genomics (Icacg) And The 23rd International Chromosome Conference (Icc).

Daruen K. Griffin.

School of Biosciences, University of Kent, Canterbury CT2 7NJ, UK.

We were all impacted by the global coronavirus outbreak, and cytogenetic conferences were no different. Both the 24th International Colloquium in Animal Cytogenetics and Genomics (ICACG) in Canterbury and the 23rd International Chromosome Conference (ICC) were scheduled for 2021 in Canberra. A joint gathering appeared to be the most practical choice given the need to switch to an online format and the clear overlap in the topics covered by the two conferences. Therefore, ICC2021 and ICACG2021 convened scientists in the fields of cytogenetics, genetics, genomics, genome organization, and related applied sciences in the biomedical, plant, and animal domains from July 13–17, 2021. Several hundred people attended the gathering, which was a huge success despite its remote location.

Following a brief introduction by the organizers, Professor Jenny Graves began the event with an engrossing discussion on chromosomal and epigenetic sex determination on July 13 at 12 p.m. in Canterbury and 9 p.m. in Canberra. The 24th International Colloquium on Animal Cytogenetics and Genomics, which generally adheres to Canterbury time On July 14 and 15, we focused on (ICACG2021), which covered the following subjects: • Animal cytogenetics; • Emerging technologies; • Accessory chromosomes; • Genome evolution; • Chromosome dynamics in germ cells: structure, regulation, and evolution; • Complex, elusive, and functionally significant elements of the genome and more.

After that, it was time for the 23rd International Chromosome Conference (ICC2021), which was held in Canberra. The

plenary session took place on July 16 and 17. Jaroslav Doležal used three different methods to reveal the 3D topology of plant mitotic chromosomes; Ana Pombo discussed the specialization of brain cell types encoded in chromatin topologies; and Ting Wu “doubled down” on pairing, moving from ultra-conservation to super-resolution imaging; Rob Neely discussing the application of expansion microscopy in chromosomal research. The following subjects were then covered in specialized sessions:

- Preimplantation testing and reproduction in mammals;
- Genome instability;
- Nucleus-based genome function;
- Chromosome dynamics and telomeres;
- Chromosome evolution, structure, and holocentricity

We begin with an endangered species' karyotype organization. The species of interest in this instance is the yellow cardinal (*Gubernatrix cristata*), and Sandra Bülau and associates initially reported using traditional Giemsa staining before moving on to 18S rDNA probes. These authors revealed 18S rDNA clusters in four microchromosomes, displaying an avian-typical $2n = 78$ with 12 macrochromosome and 27 microchromosome pairs [1]. Mitsuaki Ogata and associates focused on the evolution of the W chromosome by recurrent recycling in a specific frog species (*Glandirana rugosa*).

The existence of two heteromorphic sex chromosome systems (XY and ZW) divided into geographic groups was an intriguing example of intermittent W chromosome evolution. populations. Analysis of mitochondrial cytochrome b

***Corresponding Author:** Daruen K. Griffin, School of Biosciences, University of Kent, Canterbury CT2 7NJ, UK.

Received: 22-Feb-2025, ; **Editor Assigned:** 24-Feb-2025 ; **Reviewed:** 12-Mar-2025, ; **Published:** 20-Mar-2025.

Citation: Daruen K. Griffin. Joint Conference of the 24th International Colloquium in Animal Cytogenetics and Genomics (ICACG) and the 23rd International Chromosome Conference (ICC). Journal of DNA Research. 2025 March; 1(1).

Copyright © 2025 Daruen K. Griffin. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

sequences revealed three clades in this work, which sought to understand the evolutionary dynamics of the heterogeneous W chromosomes. Genomic DNA analysis revealed that autosomal alleles of the XY populations were deeply introgressed into the third ZW sub-group. During evolution, a new mechanism for recycling X chromosomes into W chromosomes at least four times was discovered [2].

Miroslav Plohl and Eva Šatovič-Vukšić examined classification issues with repetitive DNA sequences in bivalve mollusks.

They summarize how specificities in repetitive DNA organizational patterns might make it difficult to categorize (and investigate) a sizable portion of repetitive sequences, and they propose that the primary causes of these difficulties are The presence of numerous complicated loci, the peculiar, widely dispersed arrangement of short satellite DNA arrays, and the preponderance of transposable elements in satDNA arrays [3].

Sarbast Mustafa and colleagues examined the chromosomal makeup and nature of endogenous retroviruses (ERVs) in sheep as we turned our focus to domestic animals.

Despite the fact that ERVs have been described in humans and a few model organisms, domestic species have not yet received this information. Next-generation sequencing is used to Using molecular cytogenetics, genomic databases, and bioinformatic methods, the scientists examined two domestic breeds of Iraqi sheep and Jaagsiekte sheep. Centromeric areas were shown to be somewhat preferred by three ERV types [4]. The economic effects of reciprocal translocations (RTs) in domestic pigs were examined by Nicole Lewis and associates. These typically don't have any additional phenotype, although they can cause hypoprolificacy (a decrease in litter size). These scientists reexamined the occurrence of RT in a number of European pig herds and calculated their economic impact, recommending Despite the fact that ERVs have been described in humans and a few model organisms, domestic species have not yet received this information. Next-generation sequencing is used. As we wrap off, Suziane Barcellos and her colleagues provide a cutting-edge and straightforward technique for preparing chromosomes for avian embryos. Members of the families Icteridae, Columbidae, Furnariidae, Estrildidae, Thraupidae, Troglodytidae, and Ardeidae were among the species under study. Remarkable outcomes consistently display high-quality chromosomes and outstanding mitotic indices.

from every species in just three hours [6]. Lastly, Mohammed Yusuf and associates demonstrate a fascinating 3D ultrastructural imaging method that uses serial block-face scanning electron microscopy (SBFSEM) to visualize chromosomes. There are details on how DNA is arranged during the cell cycle, packed, and compressed from chromatin into chromosomes [7]. We sincerely hope you find these fascinating new studies enjoyable.

REFERENCES

1. Bülau, S.; Kretschmer, R.; Furo, I.; de Oliveira, E.; de Freitas, T. Karyotype Organization of the Endangered Species Yellow Cardinal (*Gubernatrix cristata*). *DNA* 2021.
2. Ogata, M.; Shams, F.; Yoshimura, Y.; Ezaz, T.; Miura, I. W Chromosome Evolution by Repeated Recycling in the Frog *Glandirana rugosa*. *DNA* 2022.
3. Šatovič-Vukšić, E.; Plohl, M. Classification Problems of Repetitive DNA Sequences. *DNA* 2021.
4. Mustafa, S.; Schwarzacher, T.; Heslop-Harrison, J. The Nature and Chromosomal Landscape of Endogenous Retroviruses (ERVs) Integrated in the Sheep Nuclear Genome. *DNA* 2022.
5. Lewis, N.; Rathje, C.; Canedo-Ribeiro, C.; Bosman, L.; Kiazim, L.; Jennings, R.; O'Connor, R.; Silvestri, G.; Griffin, D. Incidence, Reproductive Outcome, and Economic Impact of Reciprocal Translocations in the Domestic Pig. *DNA* 2021.
6. Barcellos, S.; de Souza, M.; Tura, V.; Pereira, L.; Kretschmer, R.; Gunski, R.; Garnero, A. Direct Chromosome Preparation Method in Avian Embryos for Cytogenetic Studies: Quick, Easy and Cheap. *DNA* 2022.
7. Yusuf, M.; Sajid, A.; Robinson, I.; Lalani, E. 3D Ultrastructural Imaging of Chromosomes Using Serial Block-Face Scanning Electron Microscopy (SBFSEM). *DNA* 2022.