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Editorial

The Joint Meeting of the 23rd International Chromosome Conference (ICC) and the 24th International Colloquium in Animal Cytogenetics and Genomics (ICACG)

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As the coronavirus struck the globe, we were all affected, and cytogenetic conferences were no exception. The 23rd International Chromosome Conference (ICC) was due to take place in Canberra in 2021, as was the 24th International Colloquium in Animal Cytogenetics and Genomics (ICACG) in Canterbury. With the necessity to move online and the obvious overlap in the subject matter of the two conferences, a joint meeting seemed the most sensible option. Thus, from the 13 to 17 July 2021, ICC2021 and ICACG2021 brought together researchers in cytogenetics, genetics, genomics, genome organization, as well as related applied sciences in biomedical, plant and animal fields. Despite its remote nature, the meeting was a great success, and several hundred participants attended.

On the 13 July, at 12 pm in Canterbury and 9 pm in Canberra, after a brief introduction by the organisers, Professor Jenny Graves kicked off proceedings with a fascinating talk on chromosomal and epigenetic sex determination. Keeping roughly in line with Canterbury time, the 24th International Colloquium on Animal Cytogenetics and Genomics (ICACG2021) held our attention from the 14 to 15 of July, covering the following topics:

- Emerging technologies;
- Animal cytogenetics;
- Accessory chromosomes;
- Genome evolution;
- Chromosome dynamics in germ cells: structure, regulation and evolution;
- Complex, elusive, and functionally important elements of the genome.

Then, switching to Canberra time, it was the turn of the 23rd International Chromosome Conference (ICC2021). On the 16 and 17 July, the plenary session was held, with Jaroslav Doležel uncovering the 3D topology of plant mitotic chromosomes using three different approaches; Ana Pombo talking about the specialization of brain cell types encoded in chromatin topologies; Ting Wu "doubling down" on pairing, from ultra-conservation to super-resolution imaging; and Rob Neely talking about expansion microscopy and its use in chromosome analysis. Specialised sessions were then held on the following topics:

- Mammalian reproduction and preimplantation testing;
- Genome instability;
- Genome function in the nucleus;
- Telomeres and chromosome dynamics;
- Evolution, structure holo- and mono-centric chromosomes.

You can re-live all of the talks by following https://www.griffin-lab.com/icc. However, the papers presented in this Special Issue are those that attracted considerable interest from the two conferences through their innovative contributions. The presented manuscripts are based on the conference presentations but contain at least 30% of new and unpublished material not included in the talks.

We start with the karyotype organization of an endangered species. In this case, the yellow cardinal (*Gubernatrix cristata*) is the species of interest, with Sandra Bülau and

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colleagues first reporting on conventional Giemsa staining and progressing to 18S rDNA probes. Showing an avian-typical 2n = 78, with 12 macrochromosome and 27 microchromosome pairs, these authors demonstrated 18S rDNA clusters in four microchromosomes [1]. Mitsuaki Ogata and colleagues turned their attention to W chromosome evolution by repeated recycling in a particular species of frog (*Glandirana rugosa*). An interesting case of intermittent W chromosome evolution was demonstrated, specifically the presence of two heteromorphic sex chromosome systems (XY and ZW) separated into geographic populations. In this study, to uncover the evolutionary mechanisms of the heterogeneous W chromosomes, analysis of mitochondrial cytochrome b sequences detected three clades, and genomic DNA analysis showed that autosomal alleles of the XY populations were deeply introgressed into the third ZW sub-group. A novel mechanism of X chromosomes being recycled into W chromosomes at least four times during evolution was uncovered [2]. Eva Šatović-Vukšić and Miroslav Plohl considered classification problems of repetitive DNA sequences in bivalve mollusks. Summarizing how specificities in repetitive DNA organizational patterns can lead to an inability to classify (and study) a significant fraction of repetitive sequences, they suggest that the main reasons for such challenges are the predominant association of satDNA arrays with transposable elements, the existence of many complex loci and the unusual, highly scattered organization of short satelltite DNA arrays [3].

Turning our attention to domestic animals, Sarbast Mustafa and colleagues considered the nature and chromosomal landscape of endogenous retroviruses (ERVs) in sheep. Although ERVs have been characterized in humans and some model organisms, this information is hitherto lacking in domestic species. Using next-generation sequencing, bioinformatic tools, the availability of genomic databases, and molecular cytogenetics, the authors studied Jaagsiekte sheep and two Iraqi domestic breeds. Three ERV classes were identified with some preference for centromeric regions [4]. Nicole Lewis and colleagues considered the economic impact of reciprocal translocations (RTs) in domestic pigs. These can lead to hypoprolificacy (litter size reduction) but do not usually have any other phenotype. These authors reappraised RT incidence across several European pig herds and modelled the economic impact of them, suggesting that the true incidence is nearly twice that previously reported. The potential economic impact of an undetected RT ranged from GBP 69,802 to GBP 51,215,378, providing a strong case for proactive screening by breeding companies [5].

We end with novel technological developments, with Suziane Barcellos (and colleagues) demonstrating a sophisticated and direct chromosome preparation method for bird embryos. The studied species included representatives from the families Icteridae, Columbidae, Furnariidae, Estrildidae, Thraupidae, Troglodytidae and Ardeidae. Impressive results show consistently excellent mitotic indexes with high-quality chromosomes from all species in a time frame of only 3 h [6]. Finally, Mohammed Yusuf and colleagues present an exciting 3D ultrastructural imaging technique to visualise chromosomes using serial block-face scanning electron microscopy (SBFSEM). Insights into how DNA is packaged, condensed from chromatin into chromosomes, and organized throughout the cell cycle are provided [7].

We very much hope that you enjoy these exciting new studies.

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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**, *1*, 77–83. [CrossRef]
2. Ogata, M.; Shams, F.; Yoshimura, Y.; Ezaz, T.; Miura, I. W Chromosome Evolution by Repeated Recycling in the Frog Glandirana rugosa. *DNA* **2022**, *2*, 172–184. [CrossRef]
3. Šatović-Vukšić, E.; Plohl, M. Classification Problems of Repetitive DNA Sequences. *DNA* **2021**, *1*, 84–90. [CrossRef]
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**, *2*, 86–103. [CrossRef]
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**, *1*, 68–76. [CrossRef]
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**, *2*, 22–29. [CrossRef]
7. Yusuf, M.; Sajid, A.; Robinson, I.; Lalani, E. 3D Ultrastructural Imaging of Chromosomes Using Serial Block-Face Scanning Electron Microscopy (SBFSEM). *DNA* **2022**, *2*, 30–43. [CrossRef]