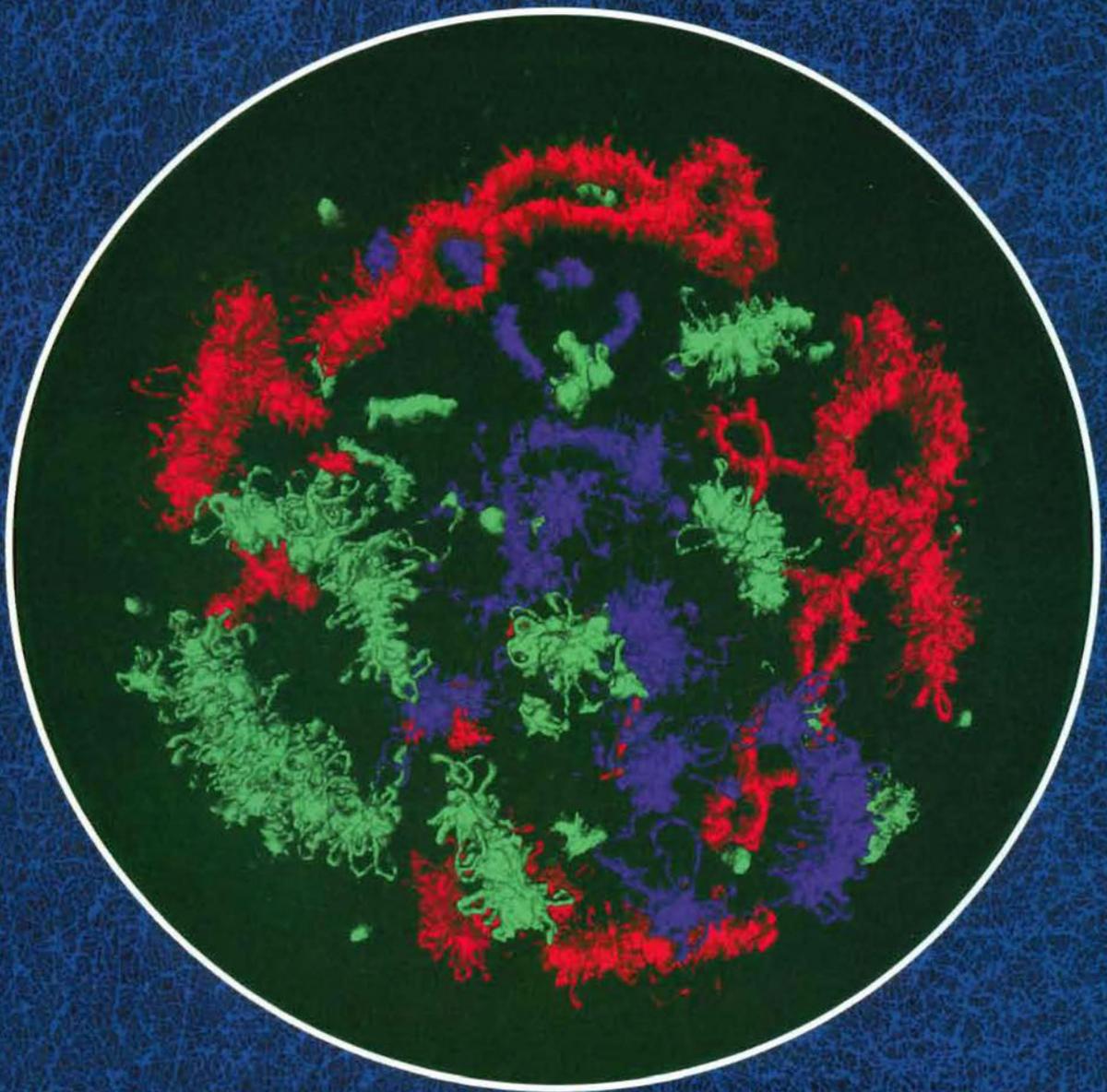


CHROMOSOME RESEARCH

The Biology of Chromatin and Chromosomes



Chromosome Research

Volume 20 · Number 6 · August 2012

A Tribute to Simon W.L. Chan, PhD (1974–2012) 657

Visualization of the spatial positioning of the *SNRPN*, *UBE3A*, and *GABRB3* genes in the normal human nucleus by three-color 3D fluorescence in situ hybridization

R. Kawamura · H. Tanabe · T. Wada · S. Saitoh · Y. Fukushima · K. Wakui 659

Praomys tullbergi* (Muridae, Rodentia) genome architecture decoded by comparative chromosome painting with *Mus* and *Rattus

R. Chaves · S. Louzada · S. Melcs · J. Wienberg · F. Adegá 673

Predicting nucleosome binding motif set and analyzing their distributions around functional sites of human genes

T. Bao · H. Li · X. Zhao · G. Liu 685

Homoeology of *Thinopyrum junceum* and *Elymus rectisetus* chromosomes to wheat and disease resistance conferred by the *Thinopyrum* and *Elymus* chromosomes in wheat

R.I. McArthur · X. Zhu · R.E. Oliver · D.L. Klindworth · S.S. Xu · R.W. Stack · R.R.-C. Wang · X. Cai 699

Germ line-limited and somatic chromosomes of *Acricotopus lucidus* differ in distribution and timing of alterations of histone modifications in male gonial mitosis and meiosis

W. Staiber 717

The radial nuclear positioning of genes correlates with features of megabase-sized chromatin domains

A.C. Kölbl · D. Weigl · M. Mulaw · T. Thormeyer · S.K. Bohlander · T. Cremer · S. Dietzel 735

An integrated cytogenetic and physical map reveals unevenly distributed recombination spots along the papaya sex chromosomes

C.M. Wai · P.H. Moore · R.E. Paull · R. Ming · Q. Yu 753

Study of methylation of histone H3 lysine 9 and H3 lysine 27 during X chromosome inactivation in three types of cells

Y. Li · T. Tan · L. Zong · D. He · W. Tao · Q. Liang 769

ABSTRACTS

20th International colloquium on animal cytogenetics and gene mapping 779

Chromosome Res (2012) 20:779–814

DOI 10.1007/s10577-012-9313-0

ABSTRACTS

**20th International colloquium on animal cytogenetics
and gene mapping**

Published online: 14 September 2012

²Molecular Animal Breeding and Biotechnology, Gene Center, LMU, Munich, Germany

³Molecular Animal Breeding and Biotechnology, LMU, Oberschleissheim, Germany.

Three-dimensional (3D) super-resolution fluorescence microscopy and 4D (space-time) live cell microscopy support key concepts of chromosomal organization and dynamics in cycling mammalian cells (Cremer and Cremer, 2010; Strickfaden et al., 2010, 2012; Markaki et al. 2010, 2012). Each individual interphase chromosome occupies a spatially distinct chromosome territory (CT). CTs are built up from networks of chromatin domains (CDs) with a size of approx. 1 Mb and are pervaded by channels of the interchromatin compartment (IC). Transcription and DNA-replication occurs at the surfaces of CDs lining the IC, whereas splicing speckles and nuclear bodies are harbored in the interior of IC lacunas. Individual CDs recruit the replication machinery transiently during different time windows of S-phase. The resulting replication foci form spatial patterns typical for early, mid and late S-phase. Locally constrained Brownian motions of CTs and CDs result in some interdigitation of CDs between neighboring CTs, but not in extensive intermingling of chromatin fibers. We report on results of studies extending current investigations of nuclear architecture in cultured cell types to nuclei of bovine preimplantation embryos.

O5

Genomic analysis of cattle *rob(1;29)*

De Lorenzi L.¹, Genuardo V.², Gimelli S.³, Rossi E.⁴, Perucatti A.², Zannotti M.¹, Malagutti L.¹, Molteni L.¹, Iannuzzi L.², Parma P.¹

¹Department of Animal Science, Milan University, Via Celoria 2, 20133 Milan, Italy

²National Research Council (CNR), ISPAAM, Laboratory of Animal Cytogenetics and Gene Mapping, Naples, Italy

³Department of Genetic and Laboratory Medicine, Geneva University Hospital, 1211 Geneva 14, Switzerland

⁴Medical Genetics, University of Pavia, 27100 Pavia, Italy

Robertsonian translocation (*rob*) involving chromosome 1 and 29 represents the most frequent chromosome abnormality observed in cattle breed intended for meat production. The negative effects of this anomaly

on fertility are widely demonstrated and in many Countries screening programs, in the aim to eliminate carrier subjects from reproduction, are currently performed. Despite of *rob(1;29)* was first observed in 1964, the genomic structure of this anomaly is still partially unclear. In this work we demonstrated that, during the fusion process, around 5.4 Mb of pericentromeric region of BTA29 move to proximal q-arms of *rob(1;29)*. Moreover, we clearly showed, by dual color FISH technique, that this fragment is inverted. Finally we showed no deletion/duplication occurs during the fusion process originating the *rob(1;29)*.

Acknowledgements. This study was partially supported by the Rural Development Plan under the Project PSR, Misura 214, e2 of Campania, “Razze Autoctone a Rischio di Estinzione della Regione Campania—RARECa”

O6

Nuclear architecture of the imprinted locus *IGF2* in pig

Lahbib-Mansais Y.^{1,3}, Barasc H.^{2,3}, Hamont L.^{1,3}, Mompert F.^{1,3}, Iannuccelli E.^{1,3}, Gellin J.¹, Riquet J.^{1,3}, Yerle-Bouissou M.^{1,3}

¹INRA, UMR 444, Génétique Cellulaire, F-31326 Castanet-Tolosan, France

²INRA, UMR 444, Génétique Cellulaire, F-31076 Toulouse, France

³Université de Toulouse, INP, ENVT, UMR 444, Génétique Cellulaire, F-31076 Toulouse, France

To better understand how genome organisation within the nuclear space might influence gene expression, we focused on the imprinted region including *IGF2*, located on porcine chromosome 2. The particularity of this model is that an imprinted locus which is monoallelically expressed allows us, in a same nuclear context, to compare the nuclear position of the two alleles and consequently to search for a potential correlation between nuclear position and expression status. For this purpose, we developed experiments combining 3D RNA/DNA FISH to analyse by confocal microscopy the position of each allele (tagged with nascent RNA or not) with respect to its chromosome territory. In foetal liver, we demonstrated that the transcriptionally active allele is always located at the border or outside its chromosome territory. To extend the study to the whole imprinted region, we used BACs covering the region (1 Mb) to compare the two parental chromosomal