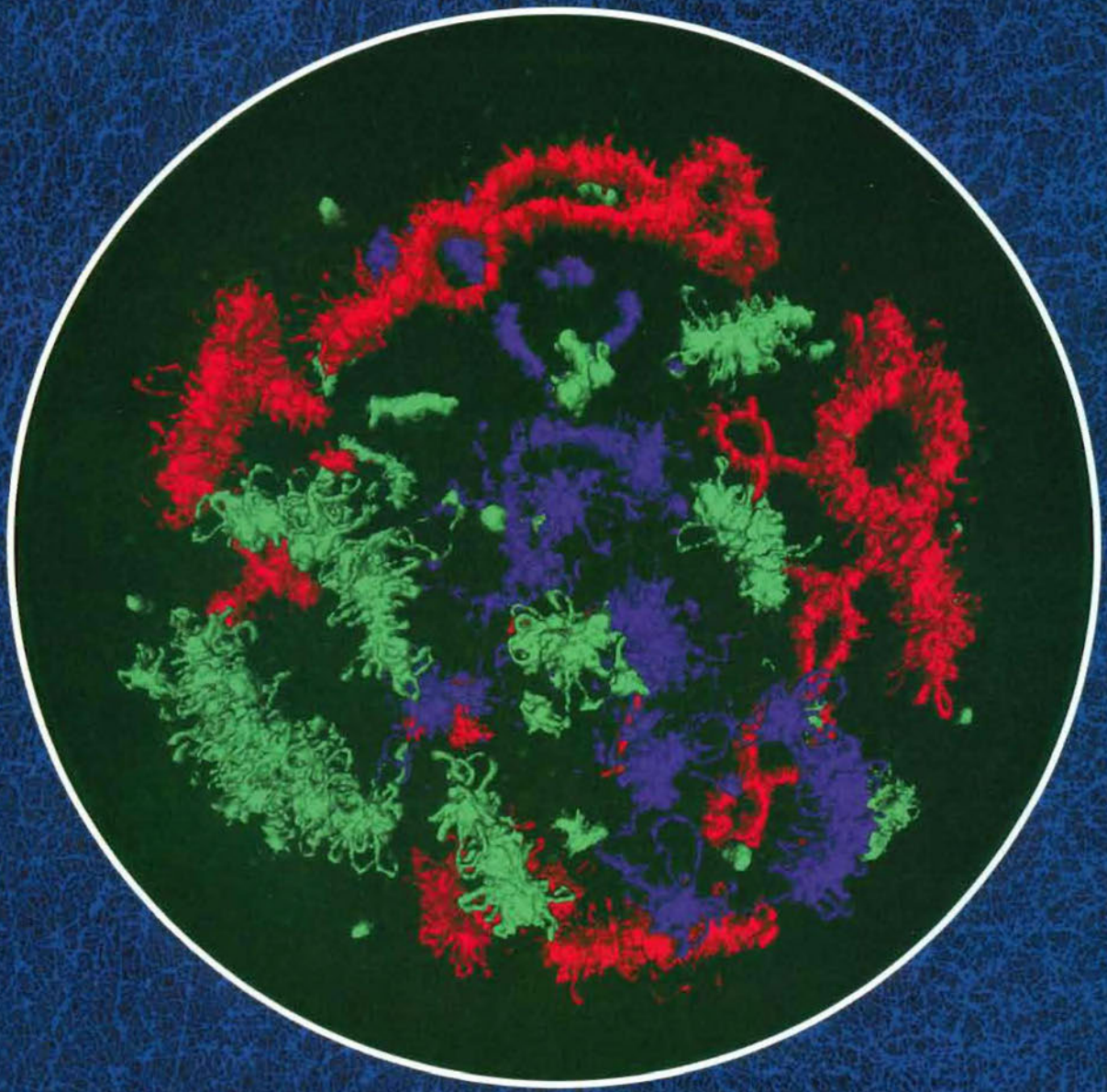
Volume 20 Number 6 2012 ISSN 0967-3849

CHROMOSOME RESEARCH

The Biology of Chromatin and Chromosomes



Springer

Chromosome Research

Volume 20 · Number 6 · August 2012

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

[2]Molecular Animal Breeding and Biotechnology, Gene Center, LMU, Munich, Germany
[3]Molecular Animal Breeding and Biotechnology, LMU, Oberschleissheim, Germany.

Three-dimensiomal (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], Genualdo 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]
[1]Department of Animal Science, Milan University, Via Celoria 2, 20133 Milan, Italy
[2]National Research Council (CNR), ISPAAM, Laboratory of Animal Cytogenetics and Gene Mapping, Naples, Italy
[3]Department of Genetic and Laboratory Medicine, Geneva University Hospital, 1211 Geneva 14, Switzerland
[4]Medical 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 intend 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], Mompart F.[1,3], Iannuccelli E.[1,3], Gellin J.[1], Riquet J.[1,3], Yerle-Bouissou M.[1,3]
[1]INRA, UMR 444, Génétique Cellulaire, F-31326 Castanet-Tolosan, France
[2]INRA, UMR 444, Génétique Cellulaire, F-31076 Toulouse, France
[3]Université 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