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105. Link between organization and transcription of Ribosomal RNA genes in mouse growing oocytes and at the very beginning of embryonic development.

Maimouna Coura Koné1,2, Martine Chebrout1,2, Habib Jan3, Renaud Fleurot1,2, Niels Galjart4, Pierre Adenot1,2, Nathalie Beaujean1,2, Pascale Debey1,2, Amélie Bonnet-Garnier1,2

1INRA, UMR1198 Biologie du Développement et Reproduction, F-78350 Jouy-en-Josas, France., 2ENVA, F-94700 Maisons Alfort, France., 3Plant Breeding Department Justus-Liebig University Giessen, Germany., 4Department of Cell Biology and Genetics, Erasmus

During the final stages of mouse oogenesis, large-scale modifications occur in the nucleus of fully-grown oocytes and are correlated with transcriptional silencing. Indeed, while oocytes with uncondensed chromatin (NSN) are able to synthesize rRNA, more advanced oocytes with dense chromatin around the nucleolus (SN) are transcriptionally silent. Conversely, transcription of ribosomal genes (rDNA) is switched off in 1-cell stage embryos and then rRNA synthesis starts at the end of the 2-cell stage. In this context, we have investigated the organization of rDNA with 3D-FISH (Fluorescent In Situ Hybridization on 3D-preserved nuclei) approaches. We have also examined the relative position of these genes with regards to pericentromeric heterochromatin domains. We observed that in SN oocytes, in 1-cell and early 2-cell stages embryos (when rDNAs are not transcribed), the ribosomal sequences are clustered in highly condensed foci and juxtaposed to major satellite sequences which formed a discontinuous ring around nucleolus-like structures. On the other hand, in NSN oocytes, at the late 2-cell stage and further stages of embryonic development (when rRNA are transcribed), ribosomal sequences form necklace structures and are less in contact with pericentromeric regions. These results suggest a close link between the spatial organization (relaxed or clustered) of ribosomal genes sequences and their transcriptional states (active or silent).