Even within a single NOR array individual sequences may differ (Kim *et al.*, 2018). This work was aimed at studying the individual sequences that make up different NORs in Coturnix japonica. Methods: Using primers to the conserved region of the 18S ribosomal RNA gene, we amplified rDNA the range of fragments from the quail genome karyotype. The rDNA fragments were cloned, sequenced, analyzed bioinformatically and mapped by FISH. Results: Ribosomal gene derivatives were found to localize on the short heterochromatic arms of all acrocentric chromosomes in the complement. In addition to functional NOR sequences, we have found chimeric sequences containing fragments of transposable elements, fragments of MHC genes and some others. As it was shown earlier active transcription makes NOR a target for transposons and causes mutual amplification of the chimeric sequences of transposons and ribosomal genes (Buzdin *et al.*, 2007). Conclusions: In the genome of Japanese quail transposition of NOR sequences apparently led to the dispersal and amplification of NORs, three of which retained their functionality.

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S-2. Role of Epstein-Barr Virus Zebra protein in induction of t(8;14) translocation

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Burkitt lymphoma (BL) is an aggressive Non-Hodgkin Lymphoma characterized by a chromosomal translocation involving the MYC oncogene located on the chromosome 8 and one of the immunoglobulin gene loci located on the chromosomes 2, 14 or 22. The African endemic form of BL is associated with the Epstein Barr Virus (EBV). EBV life cycle includes two phases: lytic and latent. The switch from latency to lytic cycle (EBV reactivation) is initiated by the EBV Zebra protein. We study the role of EBV reactivation in the formation of one BL characteristic translocation t(8;14). Our hypothesis is that the Zebra-

triggered EBV reactivation provokes nuclear architecture remodeling in B-cells and induces spatial proximity (colocalization) of MYC and IGH loci. In theory, the closer the two loci are, the higher the probability of translocation between them is. Methods: 3D FISH was used to study MYC and IGH loci proximity in B-cell lines, in naïve B-cells from healthy donors and in B-cells from EBV-infected African children. These children were divided into three groups according to their infection status (no infection, latency and reactivation). We used an EBV-positive B-cell line inducibly expressing Cas9 and gRNAs targeting MYC and IGH loci to study the consequence of prolonged MYC-IGH proximity on the occurrence of BL characteristic translocation t(8;14). After induction of DSBs in the targeted loci, the translocation (8;14) occurs with a frequency of 2x10-3 and is detectable by qPCR. Results: We demonstrated that EBV reactivation by various methods in our model significantly increases MYC-IGH colocalization rate. The same effect was not observed in B-cells from healthy donors treated with Zebra suggesting involvement of EBV in this process. Also, in children, no difference was observed between the latency and reactivation groups, probably due to the very low percentage of EBV-infected B-cells *in vivo* (less than 1 %). Then, exploiting our model, we found that EBV reactivation increased both MYC-IGH proximity and translocation rate when DSBs were induced on MYC and IGH. Conclusion: Our work provides the first experimental proof that spatial proximity loci increases the probability of translocations between these loci and explains the link between EBV and specific chromosomal translocations leading to BL.

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S-3. The topological relationship between ribogenesis, mRNA transcription/splicing and the tension of actin cytoskeleton

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To study the topological relationship between the nucleolar fibrillar centres, perinucleolar heterochromatin, nuclear speckles (splicesomes) and the lamin- associated heterochromatin after RNA transcription inhibition. Methods: MCF7 breast cancer cells were treated in 3D preserving conditions by increasing concentration/time of Actinomycin D (AcD). Immunofluorescent staining, confocal microscopy, and image analysis were performed. Results: In control cells with active rRNA and mRNA synthesis, the perinucleolar repressive heterochromatin labelled by H3K9Me3/cen forms extended structures bent around nucleoli, speckles located more externally are also extended, lamin B1 ideally outlines the nuclear envelope (NE), while actin filaments form fibrils both circular around NE and perpendicular or at angles to it, attached to the cellular membrane. When the nucleolar synthesis is initially suppressed by low AcD, the remnant Pol I cofactor RPA194 forms a few large granules at the nucleolar margin, H3K9Me3 heterochromatin condenses in round clumps between them, while speckles also condense as regular circular structures