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BIOCEV

LABORATORY OF

GERM CELL DEVELOPMENT

meiosis, genetic recombination, epigenomics, fertility, gametogenesis

In the picture:
1. Ondřej Mihola | **2.** Srdjan Gašić | **3.** Lenka Šebestová | **4.** Tatyana Kobets | **5. Zdeněk Trachtulec** | **6.** Eliška Linhartová

Not in the picture:
Karel Třešňák

Genetic recombination is the quintessence of gametogenesis; it ensures not just the reshuffling of parental alleles and thus higher variability among the offspring, but first of all the proper segregation of chromosomes during the meiotic cell divisions and thereby fertility. The sites of meiotic double-strand DNA breaks and thus the sites of recombination are determined in many mammals by the PRDM9 (PR/SET-domain carrying 9) protein, an epigenetic factor that carries histone-3-lysine-4-methyltransferase and DNA-binding activities. This protein is essential for fertility in the laboratory mouse but not in the dog. Some, yet not all mice heterozygous for certain Prdm9 mutations display sex-specific sterility, but it is unknown whether the difference in fertility is caused by the variation in Prdm9 mutations or in the genetic background. Sterile human patients with heterozygous PRDM9 mutations have been identified, but these mutations have not been confirmed as causative. In contrast, a fertile woman carrying both copies of PRDM9 inactivated was found. We participated in production of Prdm9 mutants harbouring deletions in one of the exons encoding the catalytic PR/SET domain of both the mouse and the rat, and thus obtained a unique opportunity to analyse the precise genomic distribution of recombination sites along with the fertility of heterozygous and homozygous animals on precisely defined genetic backgrounds.

Selected recent papers:

Balcova M, Faltusova B, Gergelits V, Bhattacharyya T, Mihola O, Trachtulec Z, Knopf C, Fotopulosova V, Chvatalova I, Gregorova S, Forejt J: Hybrid Sterility Locus on Chromosome X Controls Meiotic Recombination Rate in Mouse. **PLoS Genet 2016** 12(4): e1005906. [pubmed] [doi].

Baker CL, Petkova P, Walker M, Flachs P, Mihola O, Trachtulec Z, Petkov PM, Paigen K: Multimer Formation Explains Allelic Suppression of PRDM9 Recombination Hotspots. **PLoS Genet 2015** 11(9): e1005512. [pubmed] [doi].


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