Effect of smoking on human leukocyte epigenome

Students: Polina Pavlova, Maria Firuleva

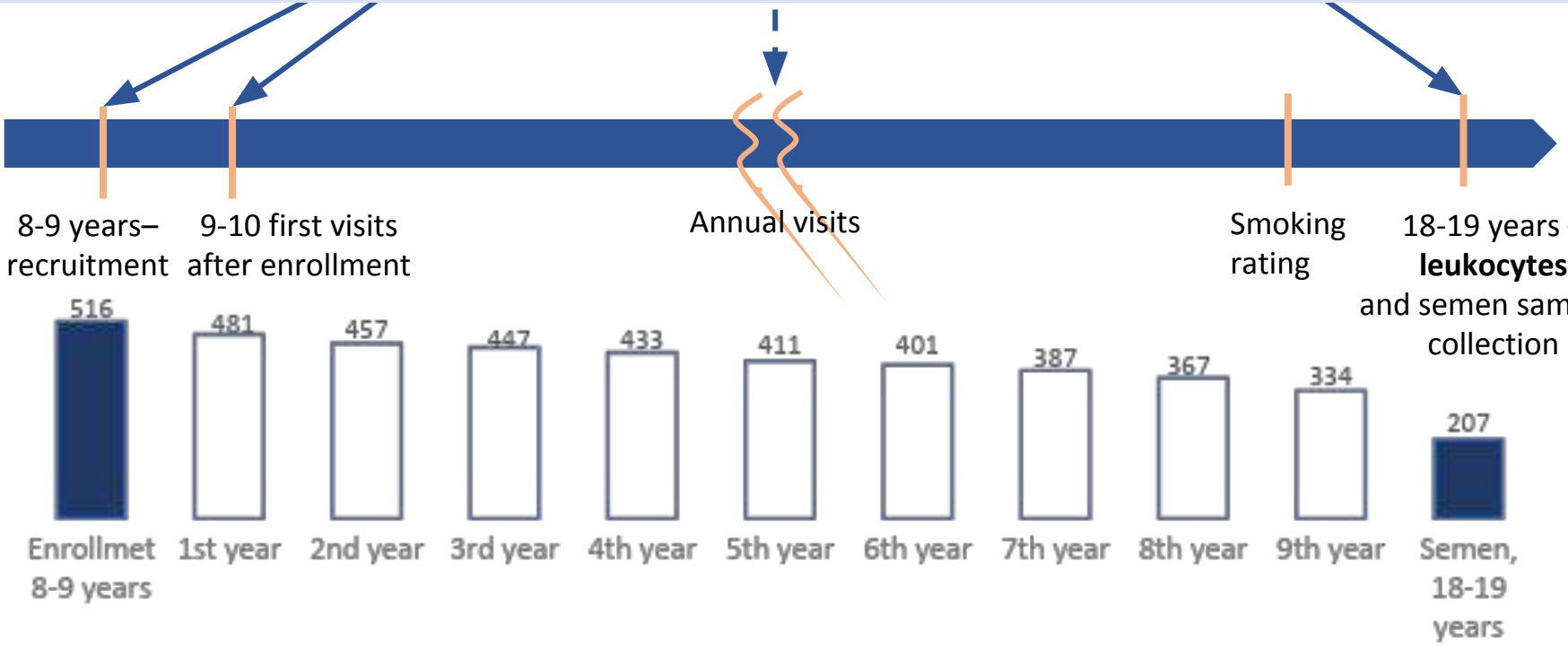
Supervisors: Oleg Sergeev, Yulia Medvedeva, Julia Kornienko;

A.N. Belozersky Research Institute of Physico-Chemical Biology, Moscow State University,

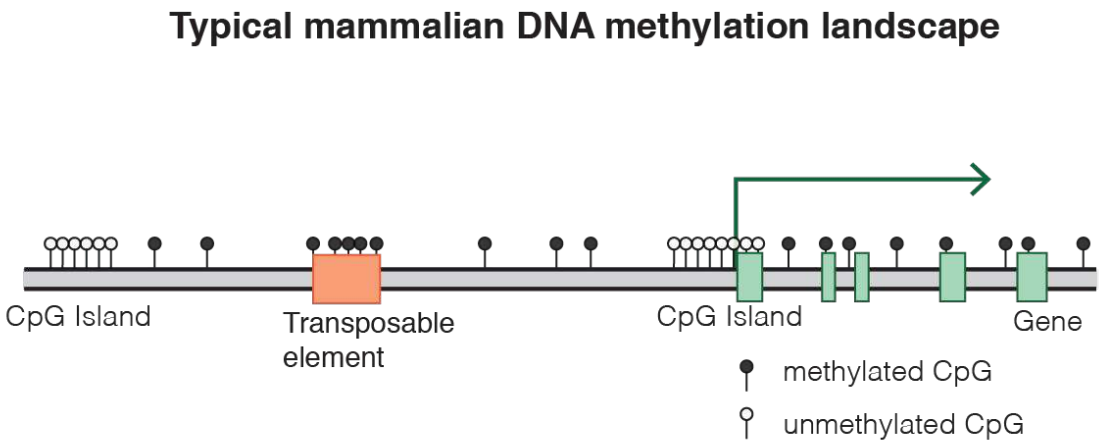
Institute of Bioengineering, Research Center of Biotechnology RAS

The Russian Children's Study (RCS)
Male Reproductive Health

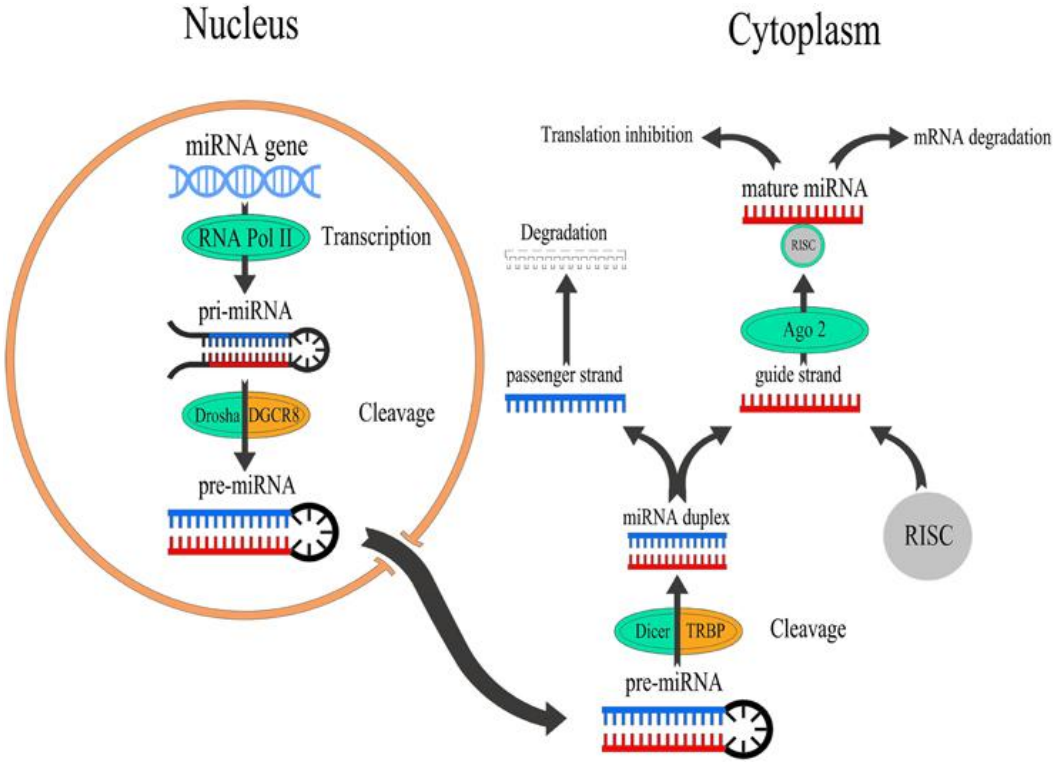
Biennially - blood sampling; annually - urine sampling, follow up of growth and puberty, interviewing
=> 20 000+ sample aliquots and 1000+ analyzing parameters in total



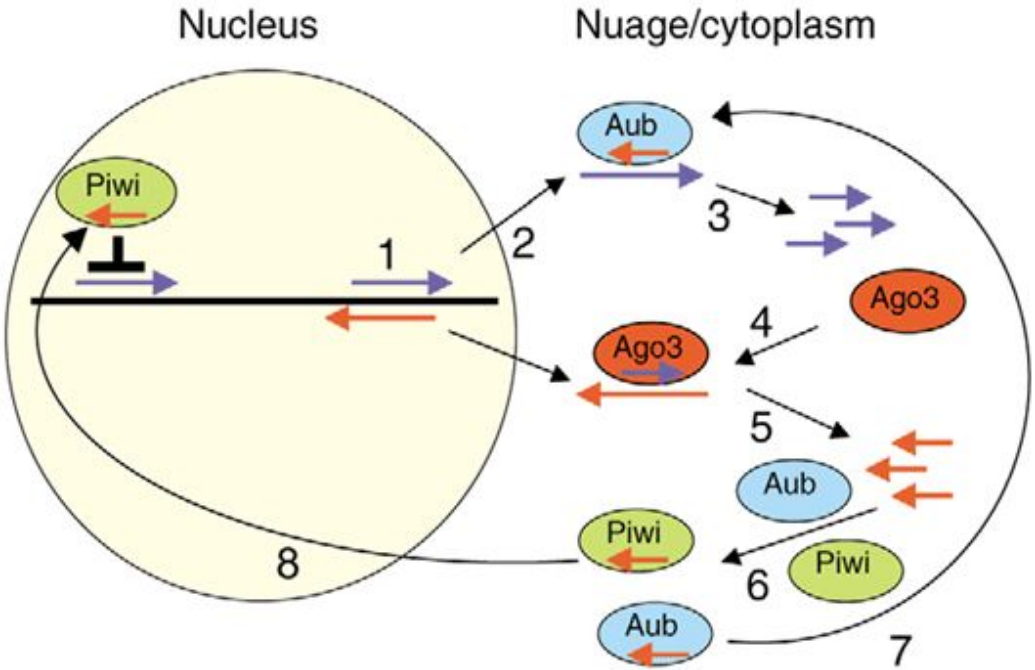
Introduction. DNA methylation



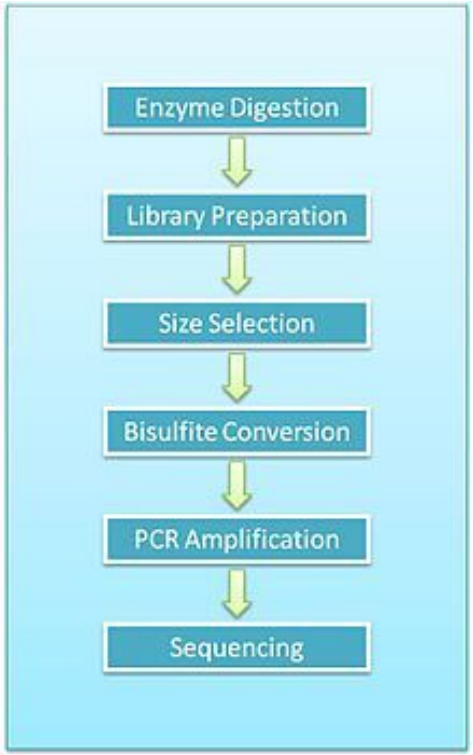
Introduction. miRNA



Introduction. piwiRNA



Reduced representation bisulfite sequencing: RRBS



What is already known?

- 52 differentially methylated regions (DMRs) in sperm were identified that distinguished lowest and highest peripubertal serum TCDD concentrations (RCS, Pilsner et al., 2018)
- Peripubertal exposure to toxicants (like dioxins) and smoking affects the methylation of sperm DNA at the age of 18 (last year project, Y.Kornienko)

What is needed to be known?

- How does smoking influence the DNA methylation and changes the profile of miRNA and piwiRNA of peripheral blood leukocytes at the age of 18?
- How are associated epigenome changes of sperm and leukocytes in the same study participants?

Project objectives

Data:

- Before filtration: 41 samples, 6 547 551 CpGs (coverage: >= 10X) *
- After filtration - 2 datasets: *
  1) 36 samples, 19466 CpGs *
  2) 36 samples, 2277623 CpGs *
- miRNA and piwiRNA profiles for 20 samples

Steps:

- A-clustering: done for CpGs which presented in all samples *
- GEE-model: x - smoking, y - CpGs
- GEE-model: x - smoking, y - piwiRNA/miRNA profile
- Final step: connection between CpG and piwiRNA/miRNA profiles

Thanks for your attention!
Any questions?