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DNA methylation analysis in sperm from infertile/subfertile boars

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Male infertility is an increasing health challenge for our societies, either for human or livestock's populations. As diffusion of the genetic progress goes through sires, male infertility consequently slows the improvement of animal selection schemas and farms' productivity. In the french pig sector, more than 35% of boars selected on agronomical criteria and to be diffused through Artificial Insemination Centers (AICs) are culled for bad sperm quality (including concentration, morphology and motility).

We propose here to study the epigenetic marks in the sperm and somatic DNA from fertile and subfertile/infertile boars at two different levels. First, we started the production of genomewide methylome maps from fertile boars. Then, taking advantage of our collection of sperm and somatic cells from fertile and infertile boars, we compared DNA methylation levels at specific loci reported to be altered in infertile humans. Combining these studies, our aim is to define specific or common epigenetic signatures of farm animals' infertility. These epigenetic signatures will be an additional parameter to evaluate the sperm quality and will finally help to lower the number of potentially infertile males introduced in the selection schemas. Moreover acquisition of epigenetic information on germ cells may help to introduce epigenetic factors within genomic selection models.

Key words:

Infertility, epigenetics, sperm, DNA methylation