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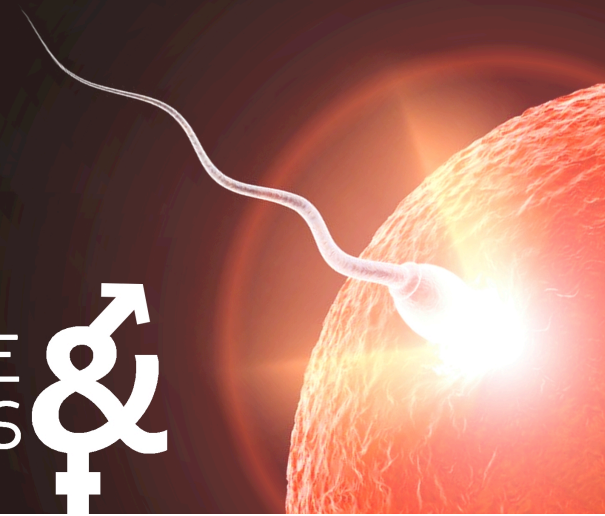
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ABSTRACTS &



## What makes a good egg ? Molecular mechanisms defining egg developmental competence in teleost fish.

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Egg quality (i.e. the egg's ability to be fertilized and subsequently develop into a normal embryo) is highly variable in the wild or under aquaculture conditions. Yet, the egg components – and associated molecular processes – responsible for its developmental competence remain poorly understood. In teleost fish, in which a high fecundity can be observed in comparison to other vertebrate models, it is possible to sample individual egg clutches in which both developmental success assessment and analytical studies can be performed in parallel. Several types of approaches have been conducted to draw the molecular portrait of a developmentally competent fish egg by studying its composition in terms of maternal mRNAs, miRNAs, and proteins. Correlative studies have shown a link between the abundance of specific mRNAs and/or proteins in the eggs and the overall developmental success of the corresponding egg clutches. In rainbow trout (*Oncorhynchus mykiss*), a correlation between developmental success and the abundance of nucleoplasmin (npm2) mRNA in the egg was previously established. In zebrafish (*Danio rerio*), a model species with transparent eggs and rapid development, a knock-down (KD) approach showed that maternally-inherited npm2 mRNA was crucial to allow developmental success beyond zygotic genome activation (ZGA). Similar approaches at the proteome and miRNA repertoire levels have yielded interesting results that are currently being further analyzed. Taking advantage of the wide diversity of fish models (over 30000 species), future studies will be designed to identify key molecular mechanisms that could be shared by evolutionary distant species.

Rennes du 13 au 15 avril 2015

## GAMATOX Project: impact of cancer treatments on semen characteristics, sperm DNA fragmentation and sperm aneuploidy: a multicenter prospective study from the CECOS Network

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Testicular Germ Cell Tumor (TGCT) is the most common cancer in young men and TGCT incidence has increased in several countries over the past 50 years. Hodgkin lymphoma (HL) and non-Hodgkin lymphoma (NHL) affect also young men who wish to procreate. Prognosis of these cancers has improved very markedly over the last decades due to the treatment mainly based on chemotherapy and radiotherapy. Several late adverse effects of chemotherapy or radiotherapy have been described but mainly in retrospective studies and very few studies, with discrepant results, have explored sperm DNA fragmentation and sperm aneuploidy following such treatments.

In this context, we performed the national multicenter prospective research project "GAMete MAle TOXicity" (GAMATOX I) which enrolled patients with testicular germ cell tumors (n= 129), patients with Hodgkin Lymphoma or no Hodgkin lymphoma (n=75). Patients performed semen samples before cancer treatment and 3, 6, 12, 24 months after the treatment ending. Routine semen analyses were performed according to the WHO recommendations in each center while specific analyses for the sperm DNA fragmentation and the sperm aneuploidy were centralized in Toulouse, Grenoble and Rouen centers. All samples were registered with the GERMETHEQUE biobank (France). Results were explored according to each cancer type and each treatment regimen. Predictive factors for sperm recovery following treatment were studied by multivariate analyses.

Treatments have drastic effects on spermatogenesis and the capacity and the time needed to recover were dependant of the type of treatment and of pretreatment sperm characteristics. Compared to control group of normal men pretreatment alterations existed in certain cancer groups. Sperm DNA fragmentation and sperm aneuploidy were increased following treatment but were also increased before treatment in lymphoma group.

The results of the GAMATOX I project were relevant for the counseling of cancer patients, before and after treatment, about the risks for the male gamete and the progeny. However, the new genome and epigenome technology explorations will be applied in the next project: GAMATOX II, in order to define more precisely the alterations induced by such treatment and to evaluate the period safety after the end of treatment.

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