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Morphological markers to select populations of oocytes with different cultural needs for dedicated pre-maturation protocols

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Abstract

Oocyte's chromatin gradually becomes more compacted during the final stage of oocyte development and the level of chromatin compaction is considered a marker of oocyte differentiation (Luciano *et al.*, 2014). Moreover, several studies demonstrate that in vitro pre-maturation treatments (Pre-IVM), aimed to improve the developmental capability of immature oocytes, might behave differently depending on the oocyte metabolic status, when it is isolated from follicle (Luciano *et al.*, 2011).

This study aims at identifying correlations between cumulus-oocyte complex (COC) morphology and oocyte chromatin configuration and secondly at testing the hypothesis that only fully grown oocytes at earlier stages of differentiation with loosely compacted chromatin (GV1) can benefit from Pre-IVM treatment.

COCs were collected from bovine 2-6mm ovarian follicles, and further divided in three groups according to their morphology (Class-1, 2 and 3) as previously described (Blondin & Sirard, 1995).

Analysis of chromatin configuration revealed that only Class-1 COC was enriched in GV1 oocyte, while Class-2 and 3 presented a similar distribution of GV1, GV2 and GV3 oocytes, where GV2 and 3 oocytes are characterized by increased chromatin compaction (Lodde *et al.*, 2007).

Then COCs were divided into two groups, one containing Class-1 COCs and the other containing Class-2 and 3 COCs and subjected to pre-IVM for 6 hours in presence of cilostamide and 10-4 UI/ml rhFSH. Finally, COCs underwent standard in vitro maturation (IVM) for 22 hours, in vitro fertilization and embryo culture. Blastocyst rate and embryos cell number were assessed at day 7. Pre-IVM positively affected developmental competences of Class-1, while in Classes 2 and 3 Pre-IVM had detrimental effects.

In conclusion COCs morphology could be used as a non-invasive approach to select population of oocyte with different cultural needs. These data could be useful in setting-up dedicated IVM protocols considering specific genes and pathways to improve IVP efficiency.

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