Fertility Profile Determination in Bovine Spermatozoa: Marker Linked To NRR

Claudia Lalancette, Catherine Thibault and Nathalie Bissonnette¹

Dairy and Swine R&D Centre, Agriculture & Agri-Food Canada, Lennoxville QC J1M 1Z3. ¹Email: <u>bissonnettenath@agr.gc.ca</u>

It has been believed for a long time that sperm cells are only a vehicle of the haploid genome but recent evidence shows that these cells not only reflect the quality of past events (i.e. spermatogenesis) but also ship a complex cargo of RNA and proteins that may be crucial for an embryo's early development.

One of the final steps in spermatogenesis is cytoplasmic reduction, which is described as a step in which the unnecessary cytoplasmic components of the cell are rejected. Because the majority of the sperm RNA is ejected from the spermatozoa during cytoplasmic reduction, the residual RNA present in the mature spermatozoa is considered to be a remnant of spermatogenesis. However, a growing number of studies, mainly in humans, suggest that this RNA could be useful, if not in the post-fertilization stages then at least as markers to indicate whether spermatogenesis went wrong or well. In other terms, bovine expressed sequences in spermatozoa are not only a useless relic of spermatogenesis but can reflect the quality of the semen.

Our laboratory is studying the RNA populations present in bovine spermatozoa with the goal of determining whether these molecules can be used as fertility markers, within the context of the selection of the best bulls for the artificial insemination industry. Using the Suppressive Subtractive Hybridization molecular technique (SSH) for creating transcripts repertory or library for reporting differences among fertile bulls, we have selected and sequenced the differently expressed messenger RNA (mRNA) in the sperm cells of bulls that have demonstrated good/poor reproductive potential (based on their non-return rate, i.e. NRR). The preliminary results suggest primarily the presence of mRNA in bovine spermatozoa having a role in spermatogenesis and some transcripts that could also play a role during the initial steps of embryogenesis.

Implication: Verification of the status of fertility markers in semen will both help the artificial insemination industry (indicator of bull fertility or quality of a production lot) and make it possible to identify the genes and alleles that must be retained to improve the genetics of Canadian dairy herds.

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