

Spermatozoal Transcriptome Profile as Marker for Bull Fertility and Sperm Motility: A Potential Tool to Evaluate Semen Quality

Bissonnette, N., Levesque-Sergerie, J.-P., and Boissonneault, G.

Agriculture and Agri-Food Canada, Sherbrooke, Canada J1M 1Z3

Email: bissonnettenath@agr.gc.ca

Fertility represents significant costs to the dairy industry and is still a major concern for dairy producers. In the past, most dairy cattle breeding programs focused on increasing production, which can have deleterious side effects on health and fertility in both female and male bovines. Efforts are made to evaluate bull fertility in order to offer semen of the highest quality value. In a previous study, we had analyzed the sperm transcript content and found that bulls with different non-return rate, a measure of field fertility, contain a different profile (Lalancette et al. 2007, *Biology of Reproduction*, in press). Since motility is a prerequisite of high quality semen, we verified if spermatozoa collected from fresh semen and presenting different motility indexes could also display different transcriptome profiles that could eventually be used as a hallmark of high semen quality.

Results: The transcript panel of bull spermatozoa isolated from highly and subfertile bulls (Lalancette et al. 2007), comprising 3216 EST, has been used to construct a microarray by automated spotting. The transcript content of fresh spermatozoa isolated at the bottom fraction 90% (highly motile) of a Percoll step gradient was compared by microarray hybridization to the transcript extracted from the spermatozoa harvested at the 70%–90% interface (motile but less vigorous normal sperm cells). Spermatozoa derived from the same ejaculated bull semen, but displaying subtle yet different motility, contain different transcript abundance. Among the genes of which expression was confirmed by real-time PCR, we validated some well-known transcript —notably that of protamine 1 (PRM1), whose encoded proteins are architectural and required for an adequate genome packaging. Uncharacterized gene such as a gene encoding a protein similar to human metalloproteinase was among the differentially expressed genes. Interestingly, expression of this candidate was predicted in December 2006 by automated computational analysis and was found and for which no bovine ortholog sequence has yet been reported.

Implications: Analyzing the spermatozoal transcriptome would not only be helpful in determining bull fertility but could also be used in a semen quality analysis. Whereas this specialized cell has long been considered a vehicle that contains only a half-genome, it also contains remnant transcripts of spermatogenesis, whose profile can be used as a signature for semen quality.