Indrajit Ganguly, J Biotechnol Biomater 2012, 2:6
http://dx.doi.org/10.4172/2155-952X.S1.008

OMICS Group Conferences
Accelerating Scientific Discovery

3rd World Congress on
Biotechnology

September 13-15, 2012 Hyderabad International Convention Centre, Hyderabad, India

Expressions of sperm-specific genes in normal and motility impaired semen producing crossbred Frieswal (HF X Sahiwal) bulls

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Mature spermatozoa harbour thousands of mRNA transcripts. These untranslated mRNA may perhaps serve as a marker for the spermatogenesis since many of them might directly or indirectly be involved in fertilization, early embryo cleavage, poor semen quality and fertility. The present research was undertaken to elucidate differential representation of few sperm specific genes in normal (% initial progressive motility: 57.61 ± 1.41) and motility impaired (% initial progressive motility: 18.45 ± 1.61) semen producing crossbred Frieswal (HF X Sahiwal) bulls. We obtained spermatozoa by subjecting the semen samples to discontinuous (40:80) Percoll gradient centrifugation. Total RNA was extracted from sperm pellets using hot Tri reagent and cDNA was synthesized. Genomic DNA contamination of the samples was tested by PCR using intron spanning primers specific to bovine deleted azoospermia-like (DAZL) and protamine 1 (PRM1) genes. Absence of epithelial cell, germ cell and leukocyte contamination of sperm RNA was tested by using primers specific to molecular markers like CDH1, KIT, and CD45 antigen, respectively. We detected the expressions of the sperm-specific genes, PRM1, PRM2, TPN1 and TPN2 by RT-PCR, and tried to associate with sperm motility. The presence of transcripts like PRM1, PRM2, DazL, TPN1, TPN2 and PPIA were demonstrated in the ejaculated spermatozoa. The normal group showed significantly higher level of PRM1 mRNAs expression as compared to the motility impaired semen producers ($P<0.05$) indicating putative role of the gene and semen quality (initial progressive motility). Although, the normal semen producing group showed comparatively higher amount of TPN2 mRNAs transcripts as compared to motility impaired group, however, transcript level was not significantly different ($P>0.05$) between the groups. Moreover, the difference of PRM2 transcript levels was not significant ($P>0.05$) among the groups and almost identical representation was observed in both the groups for TPN1transcripts.

Biography

Indrajit Ganguly has completed his Masters from National Dairy Research Institute (Deemed University), Karnal, Haryana and Ph.D from Indian Veterinary Research Institute (Deemed University), Bareilly, UP. He did postdoctoral studies at CCMB, Hyderabad. He joined Indian Council of Agricultural research as a Scientist in the year of 2008. Currently he is working as a Senior Scientist in the DNA Fingerprinting Unit, National Bureau of Animal Genetic Resources, Karnal, Haryana-132001, India. He has published many papers in reputed journals. His research area includes molecular understanding of male fertility, disease resistance and conservation & utilization of Animal Genetic Resources.

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