

6th World Congress on **Biotechnology**

October 05-07, 2015 New Delhi, India

Protein profile of seminal plasma of Murrah buffalo bulls

Brijendra Mani Yadav, S K Maurya and Shiv Kumar Yadav
Narendra Deva University of Agriculture & Technology, India

Artificial insemination in cattle and buffalo is the common practice and to keep the success at high, the quality of the semen must be good. Seminal plasma is a complex secretion composed by fluids from accessory sex glands, epididymis and testicles and its molecular composition is capable of modulating sperm function. Proteins are the most abundant organic compounds in seminal plasma and play a crucial role in processes related to fertilizing capacity of sperm and can be considered as potential molecular markers of fertility. This study was carried out to assess the protein profile of the Murrah buffalo seminal plasma by using SDS-PAGE and to correlate them with the semen characteristics. Semen samples were collected by a bovine artificial vagina from 8 Murrah buffalo bulls maintained at College of Veterinary Science, N. D. University of Agriculture & Technology, Kumarganj, Faizabad. Semen characteristics were measured using standard procedures. Seminal plasma was separated after centrifugation of semen at 5000 rpm for 10 min. The supernatants were collected and precipitated using nine volumes of cold ethanol and the proteins recovered. These seminal plasma proteins were separated on a 12% SDS-PAGE using standard procedure. A total of 22 protein bands could be identified by the fractionation of seminal plasma protein on the SDS-polyacrylamide gels. Some of these bands were more prominent in some samples. A protein fraction of 25.8 kDa was significantly correlated with progressive motility of sperm. The semen samples that had greater sperm viability showed a prominent fraction of 58 kDa protein in the SDS-PAGE.

brijendravet09@gmail.com

Proteome profiling of Sahiwal cow saliva

Gautam Kumar, A K Mohanty and Sudarshan Kumar
¹National Dairy Research Institute, India
²Bruker Daltonics, India

Saliva has emerged as an ideal diagnostic sample to explain various types of pathophysiology mainly because of ease in its collection and strong correlation between local and systemic changes. In the present study we have profiled the proteome of cow saliva and analyzed their functional significance. To profile the protein, the saliva collected from 3 healthy Sahiwal cows (*Bos indicus*) on their day of AI. Protein was extracted from 3 animals. Equal amount of protein from each animal was pooled and resolved on 12% SDS-PAGE. The complete lane was divided into 7 major pieces according to the intensity of bands, the gel pieces were digested with trypsin and bRPLC were carried out. The compound lists of all the nLC MS-MS/MS fractions were converted into MASCOT Generic Files (MGF) in ProteinScape software. A total of 441 proteins were obtained using Mascot enabled IPI bovin database of proteins from 12 pooled bRPLC fractions, out of which 338 proteins were unique proteins identified in this study for the first time. IgG, MUC19, albumin, Ovostatin2, Lactotransferrin and lactoperoxidase are the top representatives of the list. The PANTHER based GO classification reveals that 39% proteins are involved in catalytic activity, 29% in binding, 12% in structural and 52% in metabolic processes which is true to the biological functions and role of the saliva in cows. Out of these 441 proteins, 91 proteins were secretory in nature. Thus, these results provide a wide data set of bovine salivary proteome that may serve as important biomarkers in different physiological contexts. The saliva undoubtedly is a very excellent non-invasively collected sample which represents the physiological state of animals.

kumarsudershan@gmail.com