

Translational Research in Veterinary Science Vol. 5 No. 1-2 (2022) p. 11

Miętkiewska K.,^{1,2} Herudzińska M.,¹ Tul O.,^{1,2,3} Zvenihorodska T.,^{1,2,3} Jaśkowski J.M.,¹ Pareek Ch.S.^{1,2}

1) Department of Basic and Preclinical Sciences, Institute of Veterinary Medicine, Faculty of Biological and Veterinary Sciences, NCU, Torun, Poland.

2) Division of Functional Genomics in Biological and Biomedical Research, Centre for Modern Interdisciplinary Technologies, NCU, Torun, Poland.

3) Department of Surgery and Obstetrics, Faculty of Veterinary Medicine, Poltava State Agrarian University, Poltava, Ukraine.

The aim of presented study is to investigate the single cell transcriptome of bovine blastocysts in Polish HF cows using the advanced next-generation genome sequencing (NGS): the scRNA-seq technology. The experiment design of in vivo experiment was performed by collecting a total of 24 embryos from local Polish HF cattle herd using the mobile laboratory unit and field veterinarian skills. The experiment design of in vitro experiment will be performed using standard in vitro fertilization (IVF) protocol and laboratory procedures. In this presentation, we will provide the preliminary information on the experiment design and laboratory procedures utilized in vivo and in vitro experiment of bovine embryos, as well as to discuss the challenges in field veterinarian skills during embryo collection and the bioinformatics analysis to analyze the large set of generated scRNA-seq data from experiment.

Keywords: single-cell, transcriptome, NGS

Acknowlegement:

The research work was financially supported by the preludium NCN project (UMO 2020/39/O/NZ9/00621), entitled "Analiza transkryptomu i epigenomu w ocenie dojrzewania oocytów i kompetencji rozwojowych zarodków przedimplantacyjnych u bydła rasy polskiej HF".