

Abstract 15:

Resilience through knowledge: Molecular characterization of Pig IPECJ-2 and Chicken CRL cell lines

Jani de Vos^{1*}, Richard Crooijmans¹, Martijn Derks¹, Susan Kloet², Martien Groenen¹, Ole Madsen¹

¹ Animal Breeding and Genetics Group, Wageningen University & Research, The Netherlands

² Leids Universitair Medisch Centrum, The Netherlands

* Corresponding author. E-mail: jani.devos@wur.nl

The Functional Annotation of Animal Genome (FAANG) consortium is driven by a scientific community and aims to provide functional annotation of the genome for farm and companion animals. Functional annotation of genomes in farm animals contributes to animal breeding. Knowledge of functional genomic sequences is essential to obtain insight in traits of interest as well as biological processes such as intestinal absorption, immunity, protein interaction and tumor growth. Cell lines are useful models to assay and investigate these elements in detail. In this study we investigated two cell lines which are of interest due to the uniqueness of the cells being promoted as being neither transformed nor tumorigenic in nature and the functions of the cells. The IPECJ2 cell line in pigs is an intestinal epithelial cell line which can be used to investigate e.g. intestinal transportation. The Chicken SL-29 cell line is derived from embryonic (10 days gestation) untransformed fibroblast cells and is used to gain insight into immune function. The functional genome of cell lines can be different in comparison to tissues thus it is important to characterize these cell lines. Genome structure results showed aneuploidy of various chromosomes and multiply structural variants such as duplications, insertions and deletions. Gene expression analyses showed higher gene expression for genes located on chromosomes with aneuploidy, in comparison to diploid chromosomes. In conclusion, this study establishes the molecular characteristics at various levels of each cell line to use as a reference in future research not only within the FAANG community, but the scientific community.