Transcriptomics–genomics data integration and expression quantitative trait loci analyses in oocyte donors and embryo recipients for improving in vitro production of dairy cattle embryos

In this paper we first provide a brief review of main results from our previously published studies on genomewide gene expression (transcriptomics) in donor and recipient cattle used in in vitro production (IVP) of embryos and embryo transfer (ET). Then, we present novel results from applying integrative systems genomics and biological analyses where transcriptomics data are combined with genomic data in both donor and recipient cattle to map expression quantitative trait loci (eQTLs). The eQTLs are genetic markers that can regulate or control the expression of genes in the entire genome, via complex molecular mechanisms, and thus can act as a powerful tool for genomic and gene-assisted selection. We identified significant eQTLs potentially controlling the expression of 13 candidate genes for donor cow quality (IVP parameters; e.g. cyclin B1 (CCNB1), outer dense fiber of sperm tails 2 like (ODF2L)) and 19 candidate genes for recipient cows quality (endometrial receptivity; e.g. ER membrane protein complex subunit 9 (EMC9), mannosidase beta (MANBA), peptidase inhibitor 16 (PI16)). Annotation and colocation of detected eQTLs show that some of the eQTLs are in the same genomic regions previously reported as QTLs for reproduction-related traits. However, eQTLs and the candidate genes identified should be further validated in larger populations before implementation as genetic markers or used in genomic selection for improving IVP and ET performance.