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Characterization of 3D genomic interactions in fetal pig muscle

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Genome sequence alone is not sufficient to explain the overall coordination of nuclear activity in a particular tissue. Studies have shown the important role played by nuclear organization on gene expression regulation (Bickmore & Van Steensel 2013). Moreover, genomic long-range intra- and inter-chromosomal interactions are involved in the activation of tissue- specific gene networks (Fanucchi et al. 2013). **Here we present an overview of the pig genome architecture in muscle at two late developmental stages.** The maturation process occurs between the 90th day and the end of gestation (114 days). To characterize this key period for survival at birth, we profiled chromatin interactions genome-wide with in situ Hi-C (High Throughput Chromosome Conformation Capture) in muscle samples collected at 90 and 110 days of gestation, specific moments where a drastic change in gene expression has been reported (Voillet et al. 2014). About 200 million read pairs per library were generated (3 replicates per condition). This allowed to (a) produce an experimental Hi-C protocol optimized on frozen fetal tissues, (b) reveal the first Hi-C contact heatmaps in fetal porcine muscle cells, (c) profile Topologically Associated Domains (TAD) defined as genomic domains with high levels of chromatin interactions (Pombo & Dillon 2015). About 82% of the Hi-C reads could be mapped on the reference genome using the new assembly version *Sus scrofa* v11, from which, after filtering, 49% of valid read pairs have been used to infer the genomic interactions in both developmental stages. In addition, ChIP-seq experiments are being performed to map the binding of the structural protein CTCF, which is known to regulate genome structure by promoting interactions between genes and distal enhancers (Hnisz et al. 2016). By integrating the results from the previous differential analysis of gene expression (Voillet et al. 2014) and our results in nuclear organization (Hi-C data and ChIP-seq data), we will report general differences between both developmental stages in terms of transcription and structure.