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IV Encontro de Estudantes de Doutoramento em **Ambiente e Agricultura**
IV PhD Students Meeting in **Environment and Agriculture**

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Pólo da Mitra, Universidade de Évora

Book of abstracts

Comparative RNAseq analysis of backfat tissue from local pig breeds

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Alentejano (AL) and Bísaro (BI) are the main local pig breeds in Portugal, but have no information comparing their transcriptomic activity. AL belongs to the Iberian branch, presenting lower growth rates, precociously high adipogenic activity and higher levels of unsaturated fatty acids (FAs) while BI pig is from the Celtic group, sharing ancestors with higher growth rate and leaner commercial breeds.

This work intended to explore the genome function of AL and BI to better understand the underlying physiological mechanisms associated with body fat accretion, lipid composition and meat quality. Dorsal subcutaneous fat (DSF) samples were collected from AL and BI fattening pigs, with ~150kg BW at slaughter. Total RNA was obtained and sequenced for transcriptome analysis. Bioinformatic analyses using three different tools (Cufflinks, EdgeR and DESeq2) were performed.

A total of 367, 137 and 155 differentially expressed genes (DEGs) (q -value<0.05, $|\log_2 FC|>0.8$) were found using the Cufflinks, EdgeR and DESeq2 pipelines, respectively, between AL and BI DSF samples. EdgeR and DESeq2 shared a total 121 DEGs (~71% overlap) while Cufflinks showed divergent results (2.7% overlap with EdgeR and 5.5% with DESeq2).

A functional enrichment analysis of the candidate DEGs was performed using Ingenuity Pathway Analysis. Synthesis of lipid, depletion of glycogen, mass of organism and accumulation of oleic acid were revealed as main involved functions (p -value<0.05) though no directional activation state was observed ($-2 < Zscore < 2$). Potential upstream regulators that explain the obtained results such as *TCF7L2* and *RIPK2* were predicted to be activated and inhibited in AL, respectively. Moreover, 4 causal networks with *RIT2*, *KL*, *FLCN* and *RIPK2* as master regulators were inhibited in AL while another with *PPARGC1B* was activated.

These results present the first high-throughput transcriptomic data involving these local breeds and can help explain the metabolic differences that occur in the adipose tissue and shed light into specific meat quality traits.

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