Mammary nutrigenomics in lactating goats

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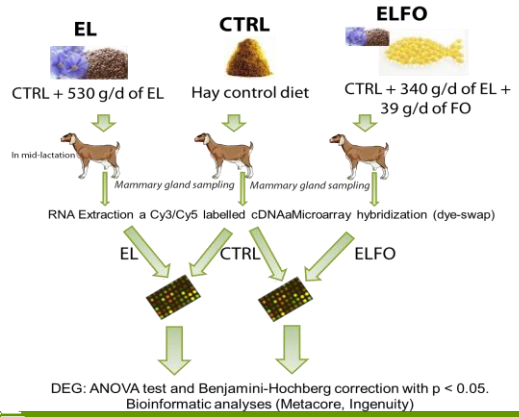
Hypothesis:

Nutrition is a major factor that regulates ruminant milk components synthesis particularly fatty acid (FA) composition which is an important determinant of milk nutritional quality for human consumers. Thus, in ruminants, nutritional strategies were developed with dietary supplementations such as plant oils or seeds rich in n-3 polyunsaturated FA to increase the milk nutritional value. In goats, a previous study[1] reported the effects of a supplementation of natural grassland hay (CTRL) with extruded linseeds (EL) alone or in combination with fish oil (ELFO) on milk fat and FA profile. Compared with the CTRL, ELFO tended to lower milk fat yield, whereas EL increased milk fat content and secretion. ELFO was effective for enriching milk cis-9,trans-11 CLA and trans-11 18:1 concentrations, whereas EL, compared with CTRL decreased milk 10:0 to 16:0[1]. In the mammary gland (MG), the milk components biosynthesis involves a large number of genes which nutritional regulation is not totally known in ruminants. **Thus our objective was to evaluate the effects of dietary EL alone and in combination with FO on MG gene expression in goats.**

Materiel & Methods:



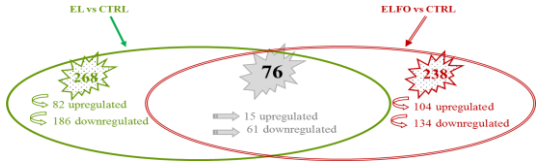


Fig.1: Repartition of DEG in goat MG

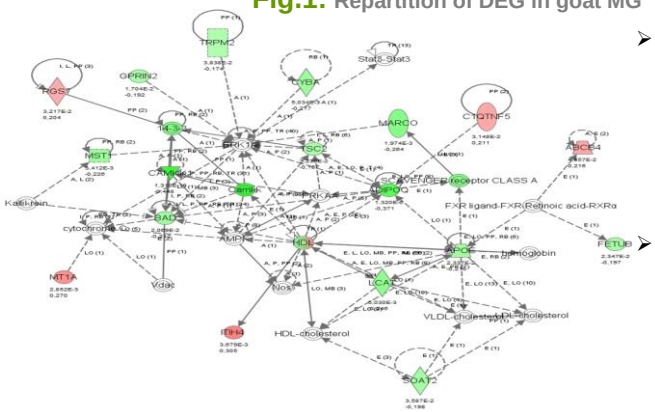


Fig.2: **Lipid metabolism network** based on MG DEG from goats feed with **EL *vs* CTRL** diet, obtained from Ingenuity.

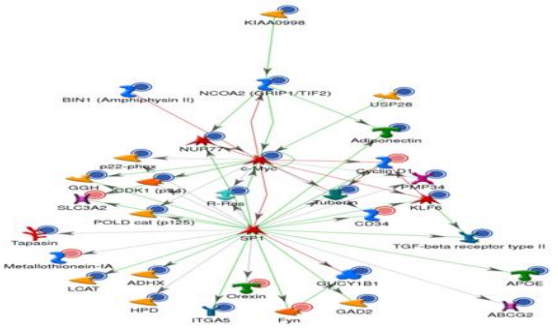


Fig.3: **SP1 network** based on DEG in the MG with the **EL *vs* CTRL** obtained from MetaCoreTM.

Results & Discussion:

- Transcriptomic analyses revealed **344** and **314** differentially expressed genes (**DEG**) with the **EL and ELFO compared with the CTRL** diet, respectively (Fig.1).
- The two major altered categories of genes belong to '**cell cycle, proliferation, differentiation and death**' (ca. 13% of the DEG) and to '**protein metabolism and transport**' (ca. 13.5% of the DEG) classes. Moreover, the '**cellular lipid metabolism and transport**' class comprised 2.6% and 3.8% of the DEG identified with EL (Fig,2) and ELFO compared to CTRL diet, respectively.
- mTOR signaling pathways was pointed out through the down regulation of genes as *IL7*, *DGKD* and *PLD*. Pleiotropic role of mTOR emerged this last years. So, in this study, the down-regulation of this set of genes could be the reflect of a mammary *de novo* lipids biosynthesis reduction through mTOR signaling pathways in line with the decrease of C8:0, C10:0 and C12:0 previously reported[1] with the same EL and ELFO diets. This hypothesis must be confirmed by further investigations.
- Both EL vs CTRL and ELFO vs CTRL analyses pointed out, notably, one **network** focused **on ESR1** known to be involved in mammary development and mammary cell differentiation[2] and one focused on the transcriptional factor **SP1** (Fig. 3) known to modulate the expression of genes involved in milk component biosynthesis as the alphaS1 casein gene[3] and the delta9 desaturase gene[4].

Conclusions:

The comparison of dietary induced variation of gene expression using transcriptomic approach highlighted different networks (ESR1 and SP1) and signaling pathways such as (mTOR) which must be considered and need further investigations to precise their respective role.

References: *[1]: Bernard et al (2014) Animal FirstView, 1-12.; [2]: Schams et al. (2003) J. Endocrinol. 177 (2): 305-17; [3]: Martin et al. (2002) RND 42(5): 433-59; [4]: Pauciullo et al. (2010) Mol Cell Probe 24(6) 407-10.*

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