

# Comparaison de l'expression des gènes du tissu adipeux entre les porcs Large White et Basque

Annie VINCENT (1,2), Isabelle LOUVEAU (1,2), Joanna WYSZYNSKA-KOKO (1,2), Bénédicte LEBRET (1,2), Marie DAMON (1,2)

(1) INRA, UMR 1079 SENAH, 35590 Saint-Gilles ; (2) AgroCampus-Ouest, UMR 1079 SENAH, 35000 Rennes

Annie.vincent@rennes.inra.fr

Avec la collaboration technique de Nathalie BONHOMME (1,2), Patrick ECOLAN (1,2), Sandrine TACHER (1,2), Christine TREFEU (1,2) et le personnel de l'élevage et de l'abattoir (1,2)

## Gene expression in subcutaneous adipose tissue: differences between Large White and Basque pigs

Body fat accumulation influences the economical value and product quality in pig production. To enhance our knowledge of the mechanisms underlying fat accumulation, subcutaneous adipose tissue gene expression was studied in two extreme pure breeds of pigs: Large White (LW; conventional, high lean meat content) and local Basque pigs (B; low growth performance and high fat content) (Q-PorkChains European Program). All phenotypic analyses were performed on pigs with live weight of 35 kg and 145 kg. For transcriptomics analysis, a custom microarray with 15 028 oligonucleotides (Agilent) was developed, targeting transcripts expressed in pig adipose tissue. Comparison of gene expression in adipose tissue of LW and B pigs revealed that 1108 and 1474 genes were differentially expressed at 35 kg and 145 kg, respectively (adjusted p value <0,1). To highlight breed-specific differences, we focused our investigations on the 359 genes that were common to both stages. Some genes related to lipid and oxidative metabolisms were expressed more in LW than in B pigs. The finding that genes known to be involved in the immune response were over-expressed in B pigs compared with LW pigs support the notion that adipose tissue may play a significant role in the regulation of the immune system. Further gene ontological investigations should improve our knowledge on mechanisms related to fat accumulation.