



## **An online phenotype database: first step towards breeding programs in local pig breeds**

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**Small variation in diet energy content affects muscle gene expression in Iberian pigs**Y. Núñez<sup>1</sup>, L. Calvo<sup>2</sup>, R. Benítez<sup>1</sup>, J. Ballesteros<sup>1</sup>, J. Segura<sup>3</sup>, J. Viguera<sup>4</sup>, C. López-Bote<sup>3</sup> and C. Ovilo<sup>1</sup><sup>1</sup>INIA, A6, Madrid, Spain, <sup>2</sup>Incarlopsa, Tarancón, Madrid, Spain, <sup>3</sup>UCM, A6, Madrid, Spain, <sup>4</sup>IMASDE, Pozuelo, Madrid, Spain; [nunez.yolanda@inia.es](mailto:nunez.yolanda@inia.es)

Modulation of dietary energy content may be a tool to influence pork fat quantity and quality. The metabolic response to different diets depends on individual factors as genetic background, age or sex and treatment factors as intensity or duration. The aim of this study was to analyse the effects of small variations in the energy content of growing and finishing diets on ham muscle transcriptome in Iberian commercial crossbred pigs. One hundred and fifty animals of both sexes (82 females and 68 males) were employed. These were subjected to three dietary protocols: a control diet with low energy in growing and finishing periods (LL, n=44), a low energy diet in growing and high energy diet in finishing (LH, n=54) and a high energy diet in both growing and finishing periods (HH, n=52). High and low energy diets were isoproteic and differ in energy and fat content (5% higher digestible energy in H diet). Scarce effects of the diets were observed at the phenotypic level with a trend for higher and quicker fattening in the animals fed high energy in growing period, especially in males. Animals were sacrificed with a mean live weight of 158 kg. Biceps femoris muscle samples from 30 animals (5 males and 5 females from each treatment) were collected for transcriptome analysis with RNAseq technology. Differential expression analyses showed 8 genes differentially expressed (DE) between HH and LL and 23 DE genes between LH and LL, when both sexes were jointly analysed. The differential expression results obtained in the separate analysis of males and females suggested a strong interaction diet×gender. For example, in males relevant genes involved in lipid metabolism, such as *SCD* and *PLIN1*, were DE between HH and LL, and other ones involved in glucose metabolism were DE between LH and LL, such as *PPP1R3B* and *PKD4*; which were not DE in females. These interaction effects may be related with the phenotypic results and should be further explored. Results show interesting diet effects, conditional on sex, on the expression of relevant genes after slight modifications of diet composition in different periods.

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**An online phenotype database: first step towards breeding programs in local pig breeds**M.J. Mercat<sup>1</sup>, E. Zahlan<sup>1</sup>, M. Petig<sup>2</sup>, H. Lenoir<sup>1</sup>, P. Cheval<sup>1</sup>, M. Čandek-Potokar<sup>3</sup>, M. Škrlep<sup>3</sup>, A. Kastelic<sup>4</sup>, B. Lukić<sup>5</sup>, J. Nunes<sup>6</sup>, P. Pires<sup>6</sup> and B. Lebret<sup>7</sup><sup>1</sup>IFIP-Institut du Porc, La Motte au Vicomte, 35651 Le Rheu, France, <sup>2</sup>BESH, Haller Str. 20, 74549 Wolpertshausen, Germany, <sup>3</sup>KIS, Hacquetova ul. 17, 1000 Ljubljana, Slovenia, <sup>4</sup>KGZS-Zavod NM, Šmihelska cesta 14, 8000 Novo mesto, Slovenia, <sup>5</sup>PFOS, TRG SV TROJSTVA 3, 31000 Osijek, Croatia, <sup>6</sup>IPVC, Praça General Barbosa, 4900 Viana do Castelo, Portugal, <sup>7</sup>PEGASE, INRA, Agrocampus-Ouest, 35042 Rennes, France; [benedicte.lebret@inra.fr](mailto:benedicte.lebret@inra.fr)

In order to further allow implementation of breeding programs in local pig breeds, with selection objectives defined for each local breed, we aimed at developing a standardised recording of carcass and meat quality traits. These data have to be connected with herdbooks to estimate genetic parameters of the traits (heritabilities and genetic correlations) which are necessary to define breeding objectives. Today the situation is very different from one local breed to another. No or very few phenotypes are recorded in some of them, while breeding programs already exist for a few breeds. To promote phenotyping, a dedicated database and a website were developed in the frame of the TREASURE project. First, the required variables have been collected for six local breeds: Basque (FR), Bísaro (PT), Crna slavonska (HR), Gascon (FR), Krškopoljski (SI) and Schwäbisch-Hällisches (DE). In total 74 variables have been identified dealing with animal herdbook information (10), rearing and growth (22), carcass (22) and meat quality (20) attributes. The database is compatible with the various identifiers used in the different countries: animal IDs, breed, farm... codifications. Major attention has been paid to the description of measurement methods of traits. Thus, each carcass and meat quality phenotype is associated to a method description representing 35 additional variables. The website can be easily translated into several languages. The website and database are currently on test until the end of the TREASURE project. All the breeds studied in TREASURE are free to use these tools. The database can be duplicated so that each partner can host its own data. Funded by European Union H2020 RIA program (grant agreement no. 634476).