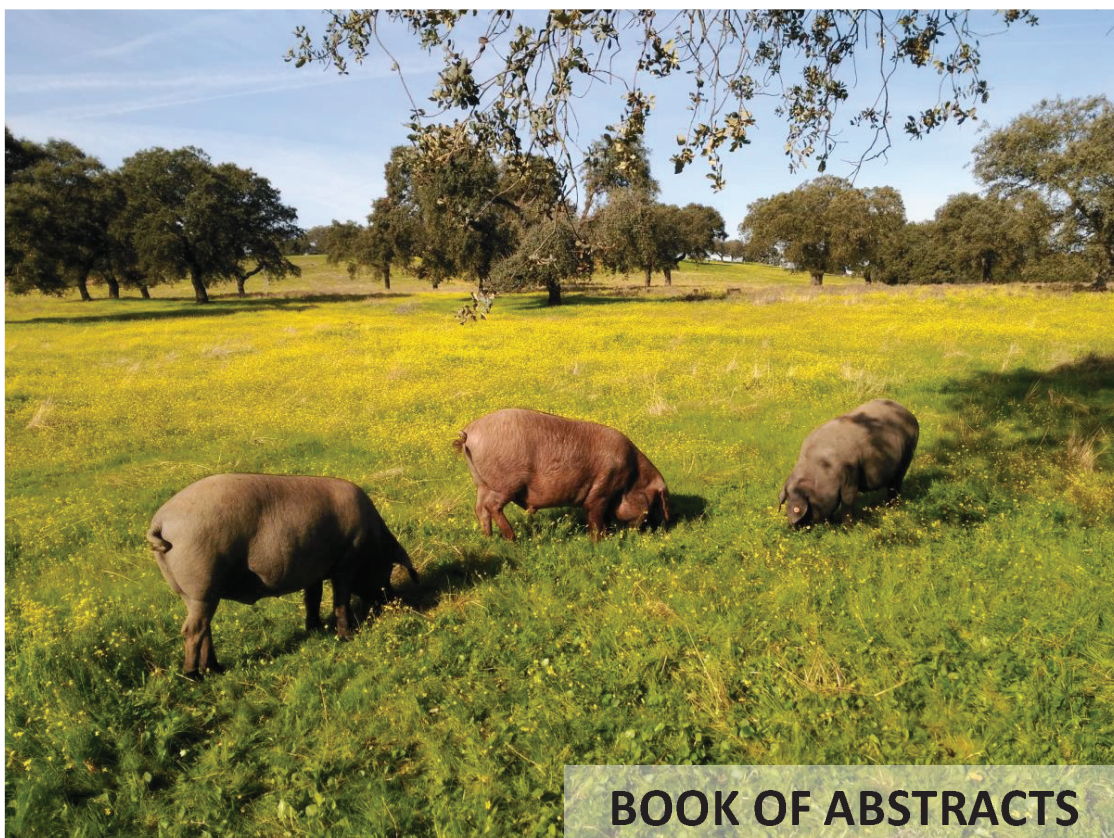


 **4<sup>th</sup> FATTY PIG**  
Science & Utilization  
International Conference  
**NOVEMBER 2017, Badajoz (SPAIN)**



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MINISTERIO  
DE ECONOMÍA, INDUSTRIA  
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 **INIA**  
Instituto Nacional de Investigación  
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International Conference**

23-25 November, 2017, Badajoz (Spain)

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- Front cover: Iberian pigs during *montanera* in the *dehesa*. From left to right, Retinto, Torbiscal and Lampiño strains. Javier García Gudiño (CICYTEX; IRTA).
- Back cover: Blond Mangalitzta piglet and sow. Francisco I. Hernández García (CICYTEX).

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## **DIVERSITY ACROSS MAJOR AND CANDIDATE GENES IN EUROPEAN LOCAL PIG BREEDS (S2OC01)**

C. Óvilo, R. Bozzi, F. García, Y. Núñez, C. Geraci, A. Crovetto, J. García-Casco J, E. Alves, M. Skrlep, R. Charneca, R. Quintanilla, G. Kusec, J. Riquet, M.J. Mercat, C. Zimmer, V. Razmaite, J.P. Araujo, C. Radovic, R. Savic, M. Candek-Potokar, L. Fontanesi, A.I. Fernández, M. Muñoz

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In the frame of the European TREASURE\* project, the genetic characterization of 20 local pig breeds is being performed with genetic and genomic tools. The objectives are the study of genetic diversity in these populations and the identification of useful markers for authentication, traceability, conservation and breeding programs. In first place, a candidate gene approach has been applied and the most relevant genes and mutations associated with pig productive, meat quality, reproductive and disease resistance traits have been prioritized and analyzed. Two OpenArray® chips of 32 and 16 SNPs were designed and genotyped in 48 animals from each one of 20 breeds included in the project (Alentejana, Apulo Calabrese, Basque, Bísaro, Black Majorcan, Black Sicilian, Black Slavonian, Casertana, Cinta Senese, Gascon, Iberian, Krskopolje, Lithuanian indigenous wattle, Mangalitsa, Mora Romagnola, Moravka, Old Lithuanian White, Sarda, Schwäbisch Hällisches, Turopolje). Forty SNPs located in 34 genes were successfully genotyped (MC1R, TYRP1, NR6A, PCK1, RYR1, IGF2, MC4R, PHKG1, SCD, GBP5, TAS2R39, TAS2R4, MUC4, ESR1, CYP2E1, LEP, CAST, MTTP, CYB5A, FTO, PPARGC1A, CAPN1, PPARC, CTSL, LEPR, PRKAG3, ACACA, KIT, ACSL4, ADIPOQ, FASN, AHR, FUT1, MSTN). Results provide relevant information

regarding genetic diversity and segregation of SNPs responsible for specific production and quality traits. Coat color and morphological trait-genes, showing low level of segregation, and fixed SNPs may be useful for traceability. On the other hand, we detected SNPs which may be useful for breeding programs. For instance, we observed predominance of unfavorable alleles for disease resistance and boar taint genes in most breeds, and segregation of many genes involved in meat quality, fatness and growth. These results joint with ongoing genomic assays, will provide essential information regarding genetic diversity, structure, selective signatures and biological processes responsible for specific production and quality traits.

**Keywords: fatty pig, candidate gene, diversity, allele frequency**

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