

# congenomics 2016

Conference on Conservation Genomics

3 – 6 May 2016 | Campus de Vairão, Portugal | CIBIO-InBIO

ABSTRACT BOOK

congen.



View metadata, citation and similar papers at [core.ac.uk](http://core.ac.uk)

brought to you by  
provided by VBN  
CORE

**FT08** Laura Iacolina

## Hybridization among wild boars, local breeds and commercial breeds - preliminary results

Laura Iacolina<sup>1</sup>, Jana Bakan<sup>2</sup>, Vlatka Cubric-Curik<sup>3</sup>, Szilvia Kusza<sup>4</sup>, Ragne Oja<sup>5</sup>, Urmas Saarma<sup>5</sup>, Massimo Scandura<sup>6</sup> and Cino Pertoldi<sup>1</sup>

- (1) Department of Chemistry and Bioscience, Aalborg University, Aalborg, Denmark
- (2) Department of Phytology, Technical University of Zvolen, Zvolen, Slovakia
- (3) Department of Animal Science, University of Zagreb, Zagreb, Croatia
- (4) Faculty of Agricultural and Food Sciences and Environmental Management, University of Debrecen, Debrecen, Hungary
- (5) Department of Zoology, Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia
- (6) Department of Science for Nature and Environmental Resources, University of Sassari, Sassari, Italy

[li@bio.aau.dk](mailto:li@bio.aau.dk)

*Sus scrofa* is one of the most widespread mammal species and it is heavily managed throughout its range in both its domestic and wild form. The wild boar is one of the most relevant game species in Europe but it is also considered a pest as it can produce economically important crop damages. Hybridization with the domestic pig is known to occur in Europe, however the degree and extent of the phenomenon is not fully understood yet. Introgression is considered to be a threat to biodiversity and could lead to loss of local adaptation or introgression in the wild population of human selected genes. A better understanding of the hybridization levels at European scale would provide an important tool for the development of management plans aimed at reducing human conflict but also at preserving biodiversity and genetic differentiation. Additionally, this information would provide new perspectives on infection routes for pig diseases and zoonoses. Here we report the first results of an ongoing study using genome wide SNPs data. Concordantly with previous studies we found variable levels of introgression from non-detectable to quite high according to sampling location. Interestingly, we also observed gradients in variability levels among the analysed wild and domestic populations. This preliminary results will be further investigated to address the possible presence of hybrid zone(s) in Europe and the possible implications for conservation and management of both wild populations and local pig breeds, as well as the development of contingency plans for infectious pig diseases.