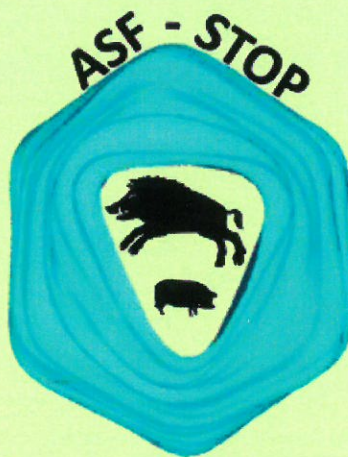




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Hybridization levels in European *Sus scrofa*, comparison between genetic and survey data

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Outdoor farming has been traditionally implemented in some European rural areas, but was mostly limited to backyard or small farming systems, however we are now observing an increment in this practice, as a result of both increased attention to animal welfare and consumers interest in organic food. At the same time, Europe is showing interest in rewilding projects. This combination might expand the wildlife-livestock interface, with enhanced sanitary risk and hybridization.

Hybridization events between the domestic pig (*Sus scrofa domestica*; hereafter DP) and the wild boar (*Sus scrofa*; hereafter WB) have been reported in several European countries and might provide insight on human practices that can lead to increased, although spatially delimited, risk of contagion. The markers most commonly used to investigate this aspect are mitochondrial DNA (mtDNA), MC1R and microsatellite (STR). All of them present some advantages and some disadvantages. MtDNA and MC1R can be easily compared among laboratories, while STR require calibration. Furthermore, STR can only detect recent hybridization events, while MC1R and mtDNA can also identify more ancient episodes. On the other hand STR and MC1R are biparentally inherited, thus representing the whole population, while mtDNA only shows the maternal lineage. In recent years the development and decrease in price of genomics techniques have allowed the implementation of genomic markers (like whole genome sequencing or Single Nucleotide Polymorphisms - SNP) for the study of genomic ancestry and hybridization. SNP markers are easily comparable between laboratories, biparentally inherited and allow the simultaneous study of loci neutral and under selection.

Here we present a comparison based on data from several European countries of genetic hybridization levels, detected with SNP markers, with data on hybridization perception, collected through an online survey. The survey covers 29 countries, with a major contribution from academic researchers (70%) but not negligible answer rate from the non-academic component (28%). Genetic data are based on 235 WB from 22 areas 149 DP (49 from 5 commercial lines and 100 from 9 local breeds) analysed with the Porcine SNP60 Beadchip (64,232 SNP).

Although data are not perfectly comparable, due to incomplete overlap of sampled areas and differences of methods, results show some interesting aspects. Genetic data show a clear separation between WB and DP, with a limited number of hybrids in both populations. The introgression level varies considerably among populations, from non-detectable to very high. Perceived presence of hybrids, based on phenotypic characteristics or historic data, is usually higher and widespread than that observed with SNP data, especially in the WB population.

Participants that stated hybridization was a past issue, often still report the presence of introgressed phenotypes in WB (50%) or both WB and DP (29%).

These results show the importance of considering both available information and hard data as they might help interpretation of outcomes or complement each other. At the same time, they point out the need to investigate further the genomes of hybrids individuals, as they might show the presence of regions under selection introgressed from one of the two forms into the other that might help better understand selection, introgression and genetic basis of WB invasiveness and that would be useful in the development of contingency or management plans.