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9.4 SNP data in the detection of hybridization levels between wild boar and domestic pig in Europe

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Introgression of domestic genes into wild populations is considered to be a threat to biodiversity leading to loss of local adaptation and spread of human selected gene variants. Additionally, the contact between wild and domestic stocks can result in the transmission of infectious diseases. Thus, a better understanding of hybridization patterns in Europe might have important implications for conservation and management of both wild populations and local breeds, as well as for the contingency of infectious diseases.

We present the results for the analysis of 235 wild boar (WB; from 22 areas) and 149 domestic pigs (DP; 49 from 5 commercial lines and 100 from 9 local breeds) with the Porcine SNP60 Beadchip.

Principal component analysis shows a clear separation between domestic pigs and wild boar populations. The network analysis concordantly identifies two main clusters (corresponding to WB and DP) but, additionally, highlights the presence of several individuals, of both ancestries, with intermediate positions. This result was confirmed by Admixture analysis that detected the presence of hybrid individuals in both WB and local domestic pig breeds.

The introgression level varies considerably among populations, from non-detectable to very high. This result might be due to breeding practices, population history and WB management, but it arises questions on domestication and selective processes as well. Additional analyses to identify the presence of human or naturally selected genomes are needed to disentangle the observed results.

Keywords: wild boar, domestic pig, SNP, hybridization, introgression

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9.5 Assessing rates and patterns of hybridization between wild boar and domestic pig in Europe

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Introgressive hybridization between wild boar and domestic pig has unpredictable evolutionary consequences and has the potential to alter reproductive, immunological and behavioural traits, influencing individual fitness and possibly increasing species' invasiveness.

Though of great interest, reconstructing patterns of gene flow between wild and domestic form of *Sus scrofa* is arduous. In fact, hybridization patterns may differ greatly with respect to time (ancient vs. recent), source (intentional in captivity vs. unintentional in the wild), spread (extensive vs. occasional) and directionality (i.e. involved sexes of the two forms). This is likely to produce a puzzling scenario, where close populations may show contrasting signals of genetic introgression. Whether and how much this can impact the dynamics of local populations remains unproven. Diagnosing hybrids is the first step to address the issue. However, despite the availability of multiple molecular markers, with different inheritance systems and undergoing different selective pressures, the analysis on the extent and impact of introgressive hybridization in Europe remains challenging.

Here we show the outcome of the application of different genetic marker systems and the potentiality of newly developed markers across a range of European wild boar populations.

Maternally inherited mitochondrial DNA alleles are by large shared between wild and domestic stocks, and the most reliable indicator of introgression is commonly considered the presence of East Asian haplotypes, which are found at a very low frequency in European wild boar. Variation at the *MC1R* and *NR6A1* nuclear genes - influencing coat colour and number of vertebrae, respectively, and under strong artificial selection during domestication - revealed higher levels of a bidirectional gene flow. Unlike previously used Y-chromosome markers, which seem to suffer low variation, new polymorphic Y-linked microsatellites represent a promising tool to disclose the paternal contribution to gene flow, but should be tested on a larger sample of domestic and wild *Sus scrofa* to identify actual diagnostic alleles.

Keywords: wild boar, domestic pig, introgression, wild x domestic hybridization

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