

# How immunogenetically different are domestic pigs from wild boars: a perspective from single-nucleotide polymorphisms of 19 immunity-related candidate genes

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**Abstract** The coexistence of wild boars and domestic pigs across Eurasia makes it feasible to conduct comparative genetic or genomic analyses for addressing how genetically different a domestic species is from its wild ancestor. To test whether there are differences in patterns of genetic variability between wild and domestic pigs at immunity-related genes and to detect outlier loci putatively under selection that may underlie differences in immune responses, here we analyzed 54 single-nucleotide polymorphisms (SNPs) of 19 immunity-related candidate genes on 11 autosomes in three pairs of wild boar and domestic pig populations from China, Iberian Peninsula, and Hungary. Our results showed no statistically significant differences in allele frequency and heterozygosity across SNPs between three pairs of wild and domestic populations. This observation was more likely due to the widespread and long-lasting gene flow between wild boars and domestic pigs across Eurasia. In addition, we detected eight coding SNPs from six genes as outliers being under selection consistently by three outlier tests (BayeScan2.1, FDI2, and Arlequin3.5). Among four non-synonymous outlier SNPs, one from TLR4 gene was identified as being subject to positive (diversifying) selection and three each from CD36, IFNW1, and IL1B genes were suggested as under balancing selection. All of these four non-synonymous variants were predicted as being benign by PolyPhen-2. Our results were supported by other independent lines of evidence for positive selection or balancing selection acting on these four immune genes (CD36, IFNW1, IL1B, and TLR4). Our study showed an example applying a candidate gene approach to identify functionally important mutations (i.e., outlier loci) in wild and domestic pigs for subsequent functional experiments.

**Keywords:** Wild boar . Domestic pig . Single nucleotide polymorphism . Positive selection . Balancing selection