



Analysis of polymorphisms in the *FUT1* and *TAP1* genes and their influence on immune performance in Pudong White pigs

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ABSTRACT. *FUT1* and *TAP1* have been identified as candidate genes that offer resistance against Escherichia coli F18 infection, with the AA genotype in *FUT1* and the GG genotype in *TAP1* conferring resistance. In order to confirm polymorphisms at *FUT1* M307 and *TAP1* G729, and evaluate their influence on immunity performance in Pudong White pigs, we performed polymerase chain reaction-restriction fragment length polymorphism analysis, measured immune indices, and compared the results with those observed in Large White pigs. The AA genotype of *FUT1* was first discovered in Pudong White pigs and has not been found in other Chinese domestic pig breeds. The frequency of the AA genotype in Pudong White and Large White pigs was 0.018 and 0.052, respectively. The GG genotype of *TAP1* was also detected in the two breeds, with a frequency of 0.708 and 0.695, respectively. Chi-square fitness analysis of both genes showed that these loci deviated from Hardy-Weinberg equilibrium in the two breeds ($P < 0.05$). No significant differences were observed in

interleukin-6 (IL-6) and IL-10 levels among the three genotypes at *FUT1* and *TAP1* in the two breeds ($P > 0.05$). Individuals for all genotypes of *TAP1* in both pig breeds had similar TNF- α levels ($P > 0.05$), implying that Pudong White pigs may have the same ability for hepatocyte inflammatory response and B cell differentiation as Large White pigs. These differences have a degree of influence on Pudong White pig's immune ability to resist F18 or other infections.

Key words: *FUT1*; *TAP1*; Disease resistance; Pudong White pig; Immune indexes; Polymorphism