Validation of genetic biomarkers and immune phenotypes as indicators of the immune response to E2-CD154 subunit classical swine fever virus (CSFV) vaccine.

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The objective of our study was to validate a set of genetic biomarkers and immunity phenotypes as indicators of immune response to the Porvac® E2-CD154 subunit CSFV vaccine. To achieve this goal, 120 8-week-old Duroc pigs were genotyped with a panel of 9 SNPs, previously described as associated with innate and adaptative immunity traits. Additionally, total concentration of IgG and *SOX13* gene expression levels were measured in blood. Based on the results, 2 genetically divergent groups of 13 pigs each were selected. After a week of acclimation, all animals were immunized with the commercial Porvac® vaccine on d 0 and 21. Sera samples were collected before vaccination and on d 14, 21, 28 and 35 post-vaccination. CSFV specific antibodies were measured by ELISA against the CSFV E2 glycoprotein (IDEXX) and seroneutralization tests. Association tests were performed with a threshold model including genetic biomarkers and immune phenotypes one at a time as explanatory variables. Results showed that divergent groups had significantly different specific CSFV E2-IgG levels at 21 d post-vaccination and neutralizing activity in the antibody response at 14 d post vaccination (23% of animals in the favorable group did not present neutralizing antibody titers to CSFV, compared with 47% in the unfavorable group). Animals in the favorable group had a higher frequency of the T allele for SNP rs319560097, which is associated with higher IgG plasma levels; the A allele for SNP rs342772739, associated with higher γδT cells and *SOX13* gene expression levels; the G allele for SNP rs713631040, associated with decreased CRP serum levels and the C allele for SNP rs80803525, associated with lower lymphocytes count in blood. In conclusion, our results suggest the existence of genètic variability in the immune response to CSFV vaccination and provide a set of biomarkers associated to it. This work was co-funded by the European Union's Horizon Europe Project 101136346 EUPAHW.

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