Deciphering genetic factors of survival during PRRSV outbreaks

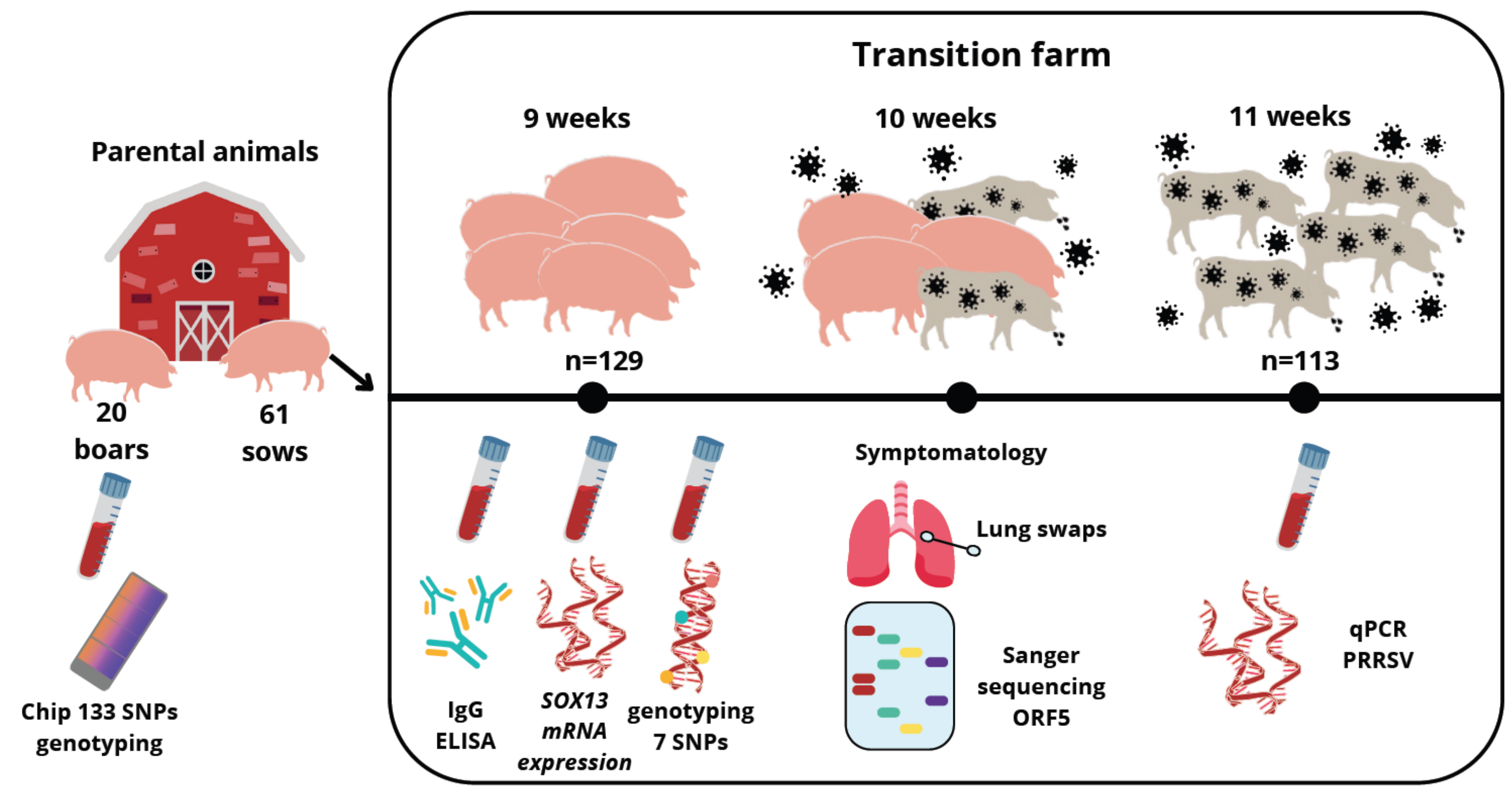
M. Ballester[1], T. Jové-Juncà[1], C. Hernández-Banqué[1], O. González-Rodríguez[1], L. Ganges[2], S. Gol[3], M. Díaz[3], R.N. Pena[4], R. Quintanilla[1], J. Tarrés[1]

[1]Animal Breeding and Genetics Program, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Spain. [2]Centre de Recerca en Sanitat Animal (CReSA), Unitat Mixta d'Investigació IRTA-UAB en Sanitat Animal, Campus Universitat Autònoma de Barcelona (UAB), Bellaterra, Spain. [3]Department of Research and Development, Selección Batallé S.A., Riudarenes, Spain. [4]University of Lleida, Lleida, Spain

INTRODUCTION

- Infectious diseases are a major threat to the sustainability and profitability of livestock production, global food security and public health.
- Breeding animals to produce more robust and disease-resistant pig populations becomes a complementary strategy to the more conventional methods of biosecurity and vaccination.
- **In this study we explored the ability of a panel of genetic markers and immunity parameters to predict the survival rates during a natural PRRSV outbreak.**

MATERIAL & METHODS



- Blood samples were collected from boars and healthy piglets (60± 2d) for phenotypic and genotypic analyses.
- Ten-week-old female Duroc pigs were naturally infected with the **highly pathogenic PRRSV-1** Rosalia strain.
- Blood samples were collected from eleven-week-old pigs for viral RNA quantification by qPCR.
- The risk of dying was analyzed with **survival analysis** using a semi-parametric proportional hazard model including pen, a polygenic effect and the different markers as explanatory variables.

$$h(t_{ij}) = h_0(t_{ij})exp(pen_j + u_i + s_{ik}\, a_k)$$

RESULTS

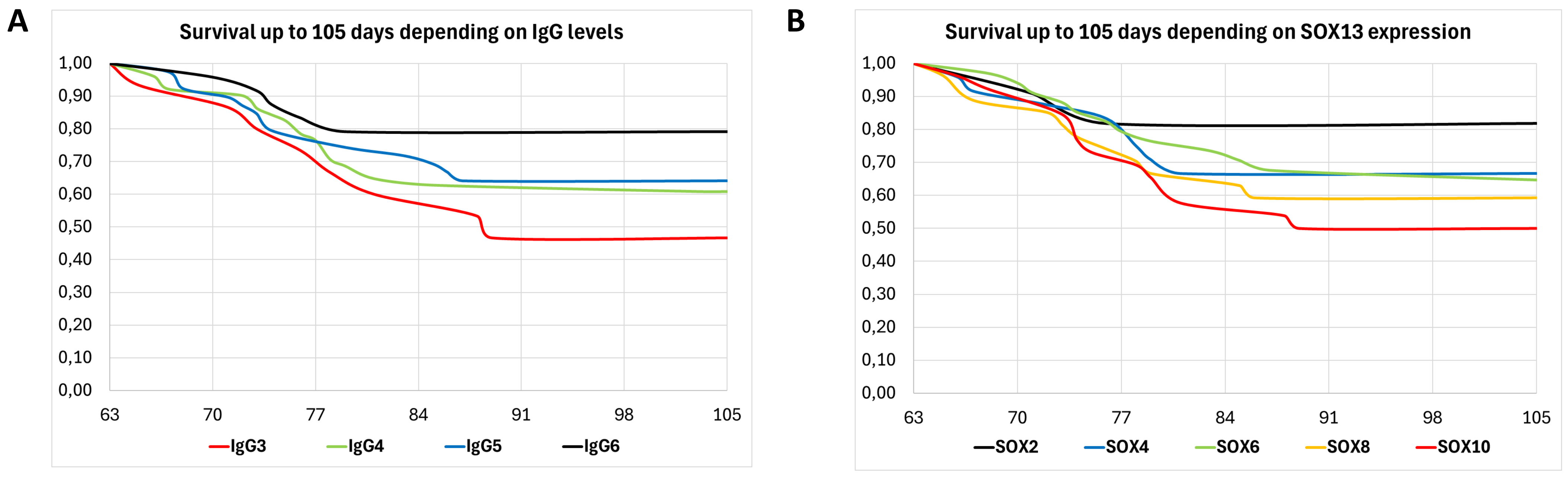


Figure 1. *Kaplan-Meier survival functions stratified by immunity parameters.* ***(A)*** *IgG levels were categorized as: IgG3=IgG<3.0, IgG4=3.0<IgG<4.5, IgG5=4.5<IgG<6.0, IgG6=IgG>6.0.* ***(B)*** *SOX13 mRNA expression levels were categorized as: SOX2=SOX13< 3.0, SOX4=3.0<SOX13<5.0, SOX6=5.0<SOX13<7.0, SOX8=7.0<SOX13<9.0, SOX10=SOX13>9.0.*

Table 1. *Description of genetic markers related to immunity traits associated with PRRS survival of daughters up to 105 days.*

	Allele (Frequency)			Survival up to 105 days for each genotype			
SNP	**Resistant**	**Susceptible**	**LRT[1]**	**Resistant**	**Heterozygous**	**Susceptible**	**Trait**
rs319560097	T (0.40)	C (0.60)	14.72 ***	1.00^a	0.58^b	0.62^b	IgG
rs81233340	A (0.92)	C (0.08)	8.42 **	0.69^a	0.35^b		CRP
rs338661853	G (0.85)	A (0.15)	13.61 ***	0.74^a	0.40^b		LYM_PHAGO_FITC
rs80904079	A (0.42)	G (0.58)	9.18 *	0.71^a	0.45^b	0.78^a	MCV, MCH
rs80803525	A (0.75)	G (0.25)	6.52 *	0.55^b	0.76^a	0.50^b	Lymphocytes
rs342772739	G (0.81)	A (0.19)	3.67 *	0.68^a	0.47^b		γδ T cells
rs323856019	C (0.83)	T (0.17)	4.53 *	0.73^a	0.55^b		Leukocytes

[1]P-value for the likelihood ratio test of models including or not each SNP: ***=P<0.001, **=0.001<P<0.01, *=0.01<P<0.05

[a,b,c]Estimates with different letter superscripts within a SNP row are significantly different at a nominal P<0.05

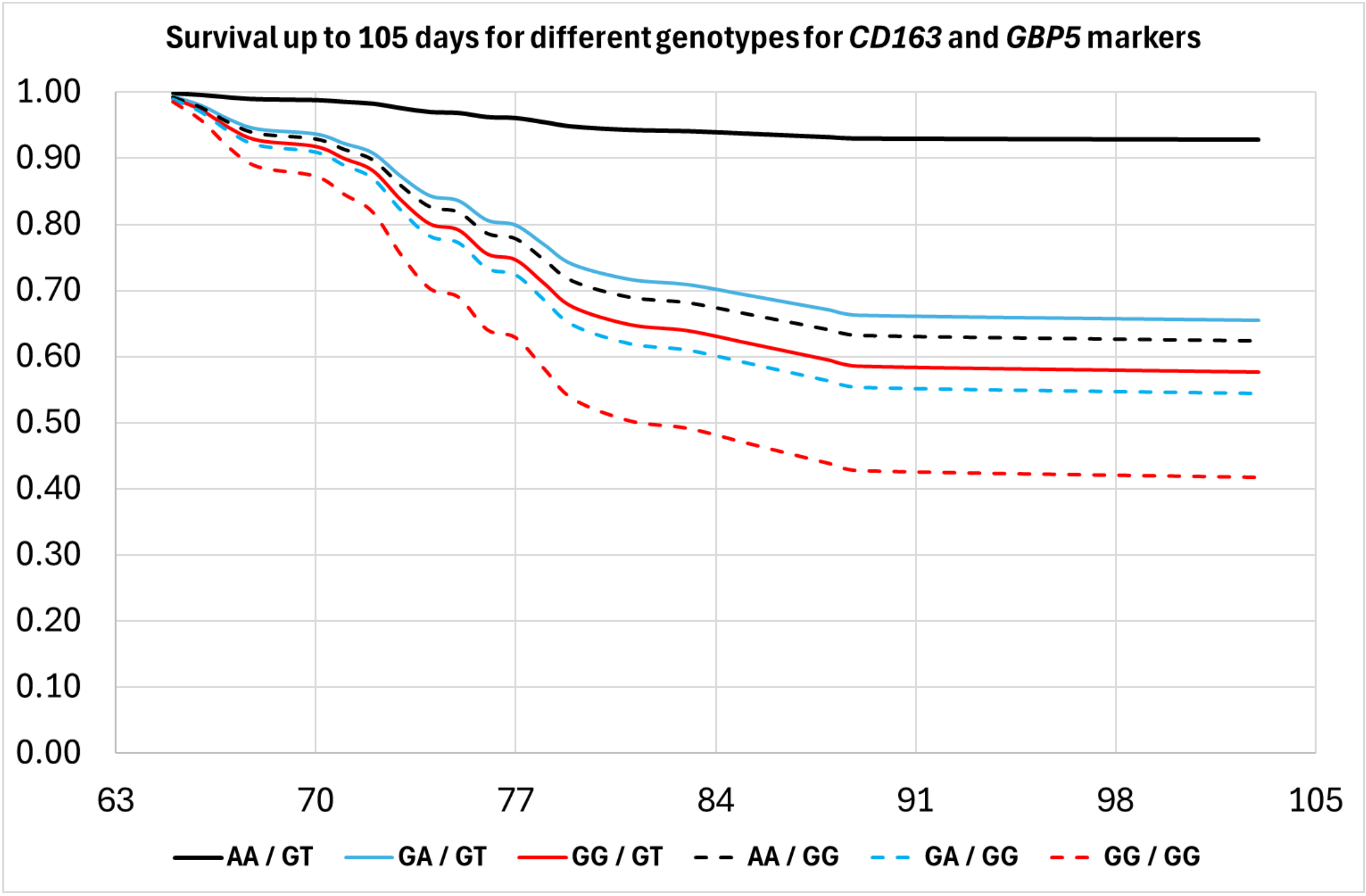


Figure 2. *Survival rate of pigs depending on the interaction between CD163 (rs1107556229) and GBP5 (rs340943904) genotypes.*

- ☐ After 6 weeks, the mortality of this outbreak reached 36,4% (47 deaths). Survival analysis showed that the risk of dying was significantly higher for animals with low IgG levels in plasma and/or high *SOX13* mRNA expression in blood (**Fig. 1**).
- ☐ The genotypes of the sires for SNPs associated with IgG plasma levels, CRP in serum, percentage of γδ T cells, lymphocyte phagocytic capacity (LYM_PHAGO_FITC), total number of lymphocytes and leukocytes, mean corpuscular volume (MCV) and mean corpuscular haemoglobin (MCH) (Ballester et al., 2020) were significantly associated with the number of surviving offspring (**Table 1**).
- ☐ SNPs located in *CD163* and *GBP5* genes were also associated to piglet survival (**Fig. 2**). The effects of these SNPs were polygenic and cumulative.

CONCLUSIONS: Our results confirmed the existence of genetic variability in survival after PRRSV infection and provided a set of genetic markers and immunity traits associated with PRRS survival

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