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Genomic regions associated with resilience indicators and medical treatments in Swiss Large White and Landrace pigs

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Introduction

The breeding of pigs that are resilient to environmental stressors is becoming increasingly important. One key characteristic of resilient pigs is a reduced need for medical treatments (Berghof *et al*., 2019). Resilience indicators can be derived by quantifying deviations from feed intake patterns using data from automated feeding stations (Gorssen *et al*., 2023). Previous studies have shown that such deviations are moderately heritable and genetically favourably correlated with resilience-related traits such as mortality and number of medical treatments (Putz *et al*., 2019, Gorssen *et al*., 2024). Importantly, the heritability is higher for deviations from expected feed intake than the number of therapeutic treatments that pigs receive (Gorssen *et al*., 2021; Guy *et al*., 2018; Putz *et al*., 2019). However, the genetic architecture of these deviation traits remains largely unknown.

Here, we investigate the genetics of resilience indicator traits derived from automated feeding station data and the number of medical treatments in Swiss Large White (SLW) and Swiss Landrace (SLR) pigs. First, heritabilities and genetic correlations are estimated. Second, associated genetic regions are identified by a genome wide association study (GWAS).

Materials & Methods

Animals, data collection and phenotype definition. The pigs described in this study were kept in compliance with Swiss legislations. Feeding station data were available from the performance testing station of SUISAG, a Swiss pig breeding company. Daily records of feed intake, feeding duration and frequency were recorded for 12,230 SLW and 2,523 SLR pigs that were tested between 2017 and 2024. The data was standardized for a uniform age trajectory between 75-155 days. Medical treatment records and pedigree data were available for all pigs. Resilience was estimated as the natural logarithm transformed variance (lnvar) of differences in observed versus predicted trait values via linear regression on feed intake ($lnvar_{FI}$), feeding duration ($lnvar_{dur}$) and frequency ($lnvar_{freq}$), as described in Gorssen *et al*. (2023). For medical treatments, the number of individual therapeutic treatments per pig received during the finishing phase were summed (TRT), discarding group treatments and prophylactic treatments like vaccinations, castration and deworming.

A subset of the phenotyped cohort consisting of 2,827 SLW and 1,514 SLR pigs had medium density microarray-derived genotypes. Per-breed quality control was performed at the individual level (call-rate>0.95, duplications, sex and parentage check) and per-variant (minor allele count>30, no deviation from Hardy-Weinberg proportions (p>0.0001)) with PLINK v1.09. Afterwards, genotypes were imputed to the sequence-level. For SLW, imputation was done using Beagle v5.4 and an in-house reference population. For SLR, imputation was done with the online SWine IMputation haplotype reference panel (Ding *et al*., 2023). Imputed sequence variants with a minor allele frequency below 1% were discarded. After quality control, there were 21,329,612 autosomal imputed sequence variants for 2,436 SLW pigs and 14,423,064 imputed sequence variants for 1,508 SLR pigs.

Estimation of genetic parameters and genome-wide association study. Genetic parameters were estimated per breed using gibbsf90+ software accounting for animal (genetic), pen (random), sex and farm of origin (fixed), the arrival weight and number of daily records (covariate) using a ssGBLUP approach taking into account both pedigree and genotypes. Posterior means and 95% highest posterior density (HPD) intervals were obtained from 500,000 samples, a burn-in of 50,000 and thinning interval of 1,000. Heritabilities were estimated with a single-trait model, genetic correlations in bivariate models. GWAS between autosomal imputed sequence variants and the traits were performed using GCTA-software, accounting for the same effects as described above and the first four principal components calculated from the genomic relationship matrix.

Results & Discussion

The resilience traits $lnvar_{FI}$, $lnvar_{dur}$ and $lnvar_{freq}$ were approximately normally distributed based on visual inspection of the histograms. TRT exhibited a Poisson-like distribution, with 75.0% of pigs receiving no treatments and a mean TRT of 0.82 per pig (SD=1.96).

Heritability estimates for $lnvar_{FI}$, $lnvar_{dur}$ and $lnvar_{freq}$ were moderate (SLW: 18.0-35.8%; SLR: 21.3-32.1%; Table 1), in agreement with values reported previously in different pig populations (Gorssen *et al*., 2024, Putz *et al*., 2019). Heritability for medical treatments was lower (SLW: 7.4%; SLR: 11.6%), but also comparable to literature (Putz *et al*., 2019, Guy *et al*., 2018). Although Pearson correlations were significantly positive between $lnvar_{FI}$ and TRT (r_p=0.26 in both breeds; Table 1), genetic correlation estimates had wide 95% HPD intervals that included zero (r_g=0.36 for SLW and r_g=0.19 for SLR; Table 1). Similarly, Putz *et al*. (2019) reported moderate positive genetic correlations between the number of treatments and deviations in feed intake, but with large standard errors (r_g=0.52±0.48). The highly skewed distribution of TRT, with a large proportion of untreated animals, may contribute to the relatively low heritability estimates and large posterior uncertainties of genetic correlations. These results show that feed intake variability and TRT are lowly to moderately heritable and could be implemented in breeding programs to improve resilience. However, there is a low to moderate genetic relationship between $lnvar_{FI}$ and TRT, and the large uncertainty of estimates precludes firm conclusions.

Table 1. Heritabilities (in %, diagonal), phenotypic correlations (below diagonal) and genetic correlations (above diagonal) of resilience traits and number of treatments (TRT). The 95% highest posterior density estimates are given between brackets. Resilience traits were estimated as log-transformed variance (lnvar) of deviations in observed versus expected feed intake ($lnvar_{FI}$), duration ($lnvar_{dur}$) and frequency ($lnvar_{freq}$)

	Swiss Large White				Swiss Landrace			
Trait	$Lnvar_{FI}$	$Lnvar_{dur}$	$Lnvar_{freq}$	TRT	$Lnvar_{FI}$	$Lnvar_{dur}$	$Lnvar_{freq}$	TRT
$Lnvar_{FI}$	18.0% (14.4 to 22.6)	0.47 (0.33 to 0.58)	-0.15 (-0.27 to -0.03)	0.36 (-0.17 to 0.82)	23.2% (16.7 to 31.4)	0.68 (0.51 to 0.82)	0.04 (-0.23 to 0.30)	0.19 (-0.76 to 0.82)
$Lnvar_{dur}$	0.59	35.4% (30.9 to 40.0)	0.11 (0.01 to 0.21)	0.14 (-0.34 to 0.63)	0.60	32.1% (25.6 to 38.8)	0.36 (0.15 to 0.55)	-0.02 (-0.89 to 0.61)
$Lnvar_{freq}$	0.01	0.14	35.8% (31.7 to 39.2)	-0.35 (-0.99 to 0.29)	0.14	0.26	21.3% (16.1 to 26.7)	0.52 (-0.27 to 0.98)
TRT	0.26	0.28	0.08	7.4% (0.1 to 20.1)	0.26	0.26	0.07	11.6% (0.1 to 30.5)

The GWAS revealed a region on SSC1 in SLW significantly associated with $lnvar_{FI}$ (1:270,760,166, $p=2.2x10^{-12}$) and $lnvar_{dur}$ (1:270,518,583, $p=1.1x10^{-11}$), near the genes *ASS1* and *FUBP3*. This QTL was previously associated with production traits such as mean feed intake, daily gain and lean meat content in SLW suggesting it has pleiotropic effects (Nosková *et al*., 2023). Moreover, Wang *et al*. (2025) found a suggestive association in this region for

$lnvar_{dur}$ (1:270,386,804; P=1.2x10^{-6}) in a combined population of Duroc, Landrace, and Yorkshire pigs. For SLR, no significant associations were found for $lnvar_{FI}$, $lnvar_{dur}$ and $lnvar_{freq}$. The absence of significant associations for resilience indicators in Swiss Landrace may reflect limited statistical power due to a smaller sample size rather than a substantially different genetic architecture. The GWAS for TRT identified a significant region on SSC2 in SLW (2:30,002,033, p=4.8x10^{-8}) near *MPPED2* (Fig. 1B and 1D). A variant near *MPPED2* had previously been implicated at a suggestive significance threshold (p=3.6x10^{-5}) with E2 antibody levels in piglets 21 days after vaccination for classical swine fever (Mehrotra, 2022). Although not surpassing the genome-wide threshold, the suggestive association on SSC7 for TRT (7: 92,974,421, P=9.3x10^{-7}) in SLW is noteworthy as well. The nearby gene *ZFP36L1* has been implicated in overproduction of pro-inflammatory cytokines and immune dysregulation in a mouse model (Cook *et al*., 2022).

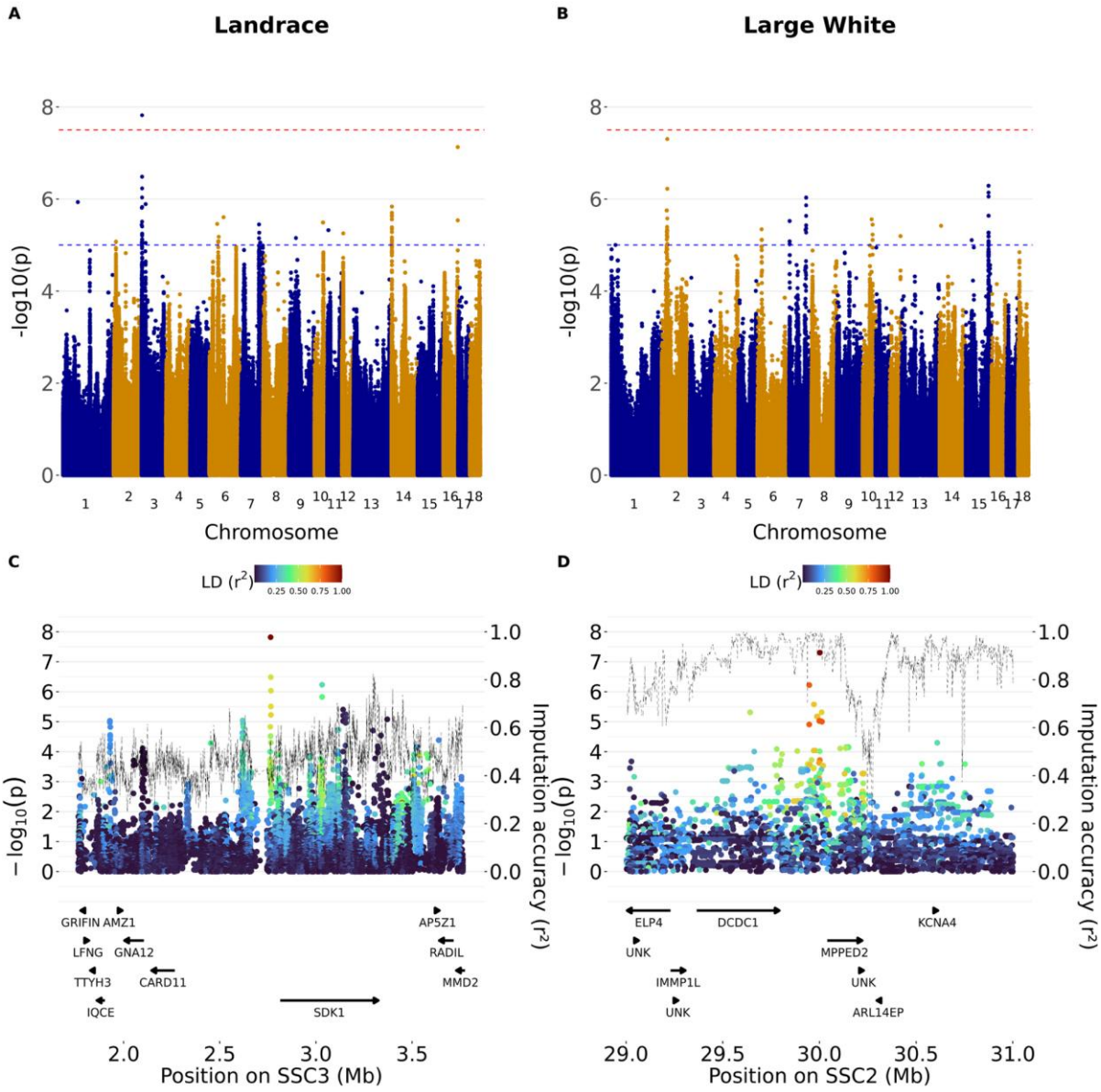

Figure 1. SNP-based Manhattan plots for number of treatments in 1,508 Swiss Landrace pigs (A) and 2,436 Swiss Large White pigs (B). The negative logarithm of the p-value is given on the left y-axis, the chromosomal location in Mb on the x-axis. The red and blue horizontal lines indicate the genome-wide (P<5x10^{-8}) and suggestive (P<1x10^{-5}) significance threshold. Panels C and D show the zoomplot for the strongest association per breed. Imputation accuracy is

given as a dashed line (right y-axis) and the linkage disequilibrium (r^2) with the top variant is coloured according to the legend.

A significant association for TRT was also found on SSC3 in SLR (3:2,764,444, P=1.3x10^{-8}) near *SDK1* (Fig. 1A and 1C). The *SDK1* gene is a member of the immunoglobulin superfamily and was previously linked to pigs' antibody response after PRRSV vaccination in Yorkshire gilts (P=4.7×10^{-6}; Icedo-Núñez *et al*., 2025). Although the GWAS analysis showed a clear peak in association near *SDK1*, it should be noted that imputation accuracy was generally low in the SLR population (around 0.50; Fig. 1C). This probably indicates that the reference population of the online SWIM imputation server contains Landrace pigs that are substantially diverged from the Swiss Landrace population (Ding *et al*., 2023). It should be noted that TRT reflects both underlying disease susceptibility and management decisions, which may dilute direct genetic signals for immune-related traits.

Conclusions

Our results provide new insights into the genetic architecture of resilience-related traits and medical treatment incidence in pigs. The moderate heritabilities of feed intake–based resilience indicators in both SLW and SLR support that they are potentially useful traits to improve robustness in pig breeding programs. However, the low heritability of medical treatment number and the large uncertainty of genetic correlations with resilience indicators suggest that indirect selection on feed intake variability alone is unlikely to substantially reduce therapeutic interventions. GWAS revealed breed-specific genomic regions associated with resilience indicators and medical treatments. A pleiotropic region on SSC1 was significantly associated with feed intake and feeding duration variability in SLW, corroborating earlier findings for production-related traits. For medical treatments, significant associations near *MPPED2* in SLW and *SDK1* in SLR highlight genes with plausible links to immune function, although imputation accuracy and limited sample size warrant cautious interpretation.

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