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Genetic connectedness and genotype-by-environment interaction in a maternal pig line across countries

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Introduction

To perform efficient selection among animals raised in different management units, we must be able to compare estimated breeding values (EBV) across farms, regions or countries. Although BLUP enables fair comparisons of EBV, the accuracy of these comparisons depends on the level of genetic connectedness between management units: the lower the connectedness, the lower the accuracy of EBV comparisons. The degree of genetic connectedness depends on the genetic relationships or relatedness among individuals across management units (Kennedy and Trus, 1993; Mathur *et al.*, 1998). It is mainly achieved through the exchange of genetic material, particularly the use of common sires across units. Several methods have been proposed to evaluate connectedness. The coefficient of determination (CD) of EBV contrasts is widely recognized as a robust and interpretable measure, as it accounts for data structure, amount of information, and genetic relationships (Laloë, 1993).

From a different perspective, when comparing EBV from different management units, genotype-by-environment (G×E) interactions can be a potential source of inefficiency if the difference between genotypes depends on the environment in which it is measured (Knap and Su, 2008). In the presence of G×E, genetic superiority expressed in one environment may not translate into equivalent genetic progress in another, even when connectedness is high. Ignoring relevant G×E can reduce the accuracy of EBV and limit genetic gain. G×E across countries can be investigated using multi-trait animal models, where country-specific phenotypes are treated as correlated traits, and genetic correlations are used to assess potential re-ranking of animals.

At the pig nucleus-farm level, environmental variation can persist despite standardized management, due to differences in nutrition, management practices, and other uncontrolled factors. Therefore, evaluating whether a single breeding program can operate efficiently across countries requires jointly assessing genetic connectedness and G×E. The objective of this study was to quantify genetic connectedness and G×E among countries for five economically important traits: age at 100 kg (AGE), number of functional teats (NFT), birth weight (BW), backfat thickness at 100 kg (BFT), and number of piglets born alive (NBA) in a maternal pig line evaluated in France, China, and Thailand.

Materials & Methods

Animals and data. Data were obtained from a commercial maternal pig line evaluated in nine nucleus farms: seven in France, one in China, and one in Thailand. Animals were born between 2010 and 2024 in France, between 2016 and 2024 in China, and between 2023 and 2024 in Thailand. The Chinese and Thai farms were established through the importation of live animals from France and operate under the same genetic selection program, with consistent trait definitions and similar management practices. Genetic connectedness among countries is

maintained through regular exchange of semen from France to Asia and the population is considered a single genetic population distributed across management units in France and Asia. No sires are exchanged directly between China and Thailand, and no sires were used in the three countries.

The dataset (for AGE, NFT, BW, BFT and NBA) comprised 149,531 records from France, 92,385 from China and 15,326 from Thailand. Contemporary groups were defined by farm and batch (including year of birth), and groups with fewer than 10 animals were excluded. For BFT, records from Thailand were excluded due to limited data availability. The pedigree included 305,845 animals traced back six generations.

A total of 14,019 animals were genotyped using the Porcine SNP60 Illumina BeadChip. After quality control, 43,817 SNPs and 13,829 genotyped animals were retained for analyses.

Measures of genetic connectedness. To study the genetic connectedness between animals from different countries, we computed the CD of contrasts of EBV (Laloë, 1993). The CD represents the reliability of EBV contrasts between countries and accounts for data structure, amount of information, and genetic relationships. Pairwise CDs were estimated between France, China, and Thailand for the period 2023–2024, and additionally between France and China for the period 2016–2024. Average additive genetic relationships were obtained from pedigree based relationship matrices.

Genetic differentiation between populations was also evaluated using Wright's fixation index (Fst), computed from genomic data for all country pairs.

Analysis of genotype-by-environment interaction. Genotype-by-environment (G×E) interactions across countries were evaluated using multi-trait animal models, in which country-specific phenotypes for each trait were treated as correlated traits. Single-step genomic BLUP (ssGBLUP) models were fitted for AGE, BW, BFT, NFT, and NBA.

The models included relevant fixed effects (sex, parity, contemporary group, and trait-specific covariates) and random effects accounting for additive genetic, common litter, permanent environmental, and residual effects, depending on the trait.

Variance components were estimated using the EM-REML algorithm implemented in the BLUPF90+ software suite (Misztal *et al.*, 2014; Lourenco *et al.,* 2022). Connectedness analysis was performed using Gibbs sampling. Genetic correlations between countries were used to assess the presence of biologically relevant G×E interactions. Those below 0.80 were considered indicative of meaningful G×E.

Results

Genetic connectedness. Across all traits and periods evaluated, average coefficients of determination (CD) ranged from 0.61 to 0.86 (Table 1), indicating a good level of genetic connectedness among France, China, and Thailand. For the 2023–2024 period, CD values were consistently higher between France and China (average 0.80) than between France and Thailand (average 0.70). AGE showed the largest difference in CD between these two comparisons. For the longer period (2016–2024), NBA presented the lowest CD value (0.69).

Average additive genetic relationships between countries during 2023–2024 were low but consistent with effective connectedness, with values of 0.034 between France and China, 0.027 between France and Thailand, and 0.014 between China and Thailand. Pairwise Fst values were also low (0.006–0.020), confirming limited genetic differentiation among the three populations, with slightly higher differentiation between China and Thailand, as expected due to the absence of direct sire exchange.

Table 1. Coefficient of determination (CD) of contrasts of EBV among countries: France, China and Thailand for specified time periods.

Trait[1]	France - China 2016-2024	France - China 2023-2024	France - Thailand 2023-2024	China - Thailand 2023-2024
AGE, kg	0.84	0.84	0.65	0.79
NFT	0.86	0.86	0.71	0.82
BW, kg	0.81	0.81	0.63	0.76
BFT, mm	0.80	0.65	-	-
NBA	0.69	0.61	0.81	0.61

[1]AGE, the age at which the animal reached 100 kg; NFT, Number of functional teats; BW, Birth weight; BFT, backfat thickness at 100 kg; NBA, Number of piglets born alive

Genotype-by-environment interaction. Genetic correlations across countries were generally high (Table 2). For NFT, correlations ranged from 0.95 to 0.98, indicating no evidence of G×E interaction. For NBA, correlations ranged from 0.81 to 0.97, also suggesting limited G×E. In contrast, BW showed lower and more variable genetic correlations (0.53 to 0.83), while AGE and BFT exhibited moderate correlations ranging from 0.70 to 0.79 and a correlation of 0.77 between France and China, respectively. No evidence of biologically relevant G×E interaction was observed, except for BW. These results indicate that across-country genetic evaluations are reliable for most traits in this maternal pig line.

Table 2. Genetic correlations from a multitrait genetic analysis using ssGBLUP, where the same trait measured in different countries is treated as a different but correlated trait

Trait[1]	France-China	France-Thailand	China-Thailand
AGE, kg	0.79±0.04	0.77±0.05	0.70±0.11
NFT	0.95±0.02	0.96±0.03	0.97±0.06
BW, kg	0.67±0.07	0.83±0.06	0.53±0.16
BFT, mm	0.77±0.06	-	-
NBA	0.81±0.04	0.90±0.02	0.97±0.01

[1]AGE, the age at which the animal reached 100 kg; NFT, Number of functional teats; BW, Birth weight; BFT, backfat thickness at 100 kg; NBA, Number of piglets born alive

Discussion

The coefficient of determination (CD) values obtained across all traits and periods indicated a high level of genetic connectedness among the three countries. Yu *et al.* (2018) proposed the upper limit of sufficient CD value (0.7 to 0.9) that gives a reasonable prediction accuracy while maintaining genetic diversity in a population. Average CD values were consistently above this threshold, indicating that EBVs can be reliably compared across countries. These results reflect the structure of the breeding program, in which animals across countries belong to a single population, share a common breeding goal, and are connected through the regular use of common sires (AI). The low Fst values (below 0.02) further confirmed the close genetic relationship between pigs from different countries, consistent with their shared ancestry and historical and ongoing genetic exchange.

While genetic connectedness ensures the accuracy of EBV comparisons, it does not prevent the existence of G×E interactions. Biologically significant G×E interactions, and re-ranking of animals between environments, occur when the genetic correlations fall below 0.80 threshold (Robertson, 1959). Genetic correlations across countries were generally high for most traits, indicating limited G×E interaction.

Birth weight (BW) was the only trait showing evidence of biologically relevant G×E, with moderate genetic correlations between some country pairs. This result is consistent with the

known sensitivity of BW to environmental conditions and management practices. Although management protocols were standardized across countries, residual differences in climate, handling, may have contributed to this pattern.
Similar patterns have been reported in pig populations, with the magnitude of G×E interactions varying according to the trait studied and the population (Godinho *et al*.,2019; Song *et al.,* 2020; Bussiman *et al.*, 2025).
Differences in data structure across countries, particularly the more recent establishment of the Thai nucleus farm, may have affected the precision of genetic parameter estimates involving Thailand. These factors could partially explain the larger standard errors observed for some genetic correlations. As additional data from this environment become available, more robust conclusions regarding G×E interactions involving Thailand will be possible.

Conclusions

The results showed high genetic connectedness across countries, indicating that animals from different countries share sufficient genetic links to support across-country genetic evaluations. There was no evidence of a biologically significant G×E interaction resulting in economically significant reranking of animals for most of the studied traits, except for BW. Overall, the existing international breeding program should be efficient regardless of the environment in which animals are raised and perform, hence separate national breeding programs are not necessary.

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