Genetic Evaluation for Disease Resistance and Tolerance in Pigs using Reproduction Records

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ABSTRACT: A method for detection of disease outbreaks was developed using reproduction records from several countries. The outbreaks detected using statistical approaches were confirmed using clinical signs and available diagnostic tests for PRRS and other diseases. The method was used for a) outbreak detection using phenotypic data, b) genetic parameter estimation during disease and healthy periods using a bivariate approach, and c) genetic parameter estimation for a range of challenges using a random regression approach. Data consisted of 3,518,222 records from 447 farms. There were higher variances due to permanent-environment and service-sire effects during disease phases. The additive genetic variance increased as overall challenge load increased. Heritability was highest at extremes of the challenge and non-challenge phases. Genetic correlations decreased as the contrast in challenge load increased. Results suggest usefulness of random regression approach in selection for disease resistance and tolerance.
Keywords: reproduction; disease; genetic parameters; random regression

Introduction

In many livestock species, genetic selection is conducted in high-health environments, typically in nucleus farms, while the progeny is destined to live under commercial conditions, and therefore more exposed to diseases and other challenges. It is then important to know the effectiveness of such selection. This could be useful in optimizing the selection within genetic lines according to challenges in target production environment or using specific lines for specific environments.

Genetic selection for disease resistance and tolerance requires estimates of genetic parameters based on large volumes of data and pedigrees records. In most farm animal species, it is difficult to organize challenge trials with specific pathogens to obtain useful data such as pathogen burden. On the other hand, large volumes of performance records could be readily available from periods of disease that occur in commercial farms. These data could be used to study variation among sows with respect to disease tolerance and resistance, as suggested by Lewis et al. (2009) and Rashidi et al. (2014).

This investigation was conducted to develop a method for detection of challenge phases using reproduction records and evaluate its usefulness for genetic parameter estimation and selection decisions.

Materials and Methods

Data. A total of 3,518,222 records from 908,591 sows from 447 farms in Europe and North and South America were used. The records included number of piglets born alive (NBA), stillbirths (STB), mummified (MUM) and number of weaned piglets (NWP). The records on STB and MUM were summed together as number of lost piglets (NLP). The data were divided in three datasets namely: training, test and validation datasets. Firstly, the training dataset consisting of 57,135 reproduction records from 10,910 sows from a commercial farm in PRRS endemic area of Canada was used to develop a method for outbreak detection using a variable called "Challenge load (CL)". Secondly, different models for developing CL were compared using the test dataset from 15 farms in the Netherlands containing 263,274 records from 65,826 sows. Thirdly, data from rest of the farms were used in the validation dataset for testing effectiveness of CL for a range of challenges across continents. The entire dataset was then used for estimation of genetic parameters.

Estimation of challenge load (CL) in training dataset: This was based on several confirmed disease outbreaks of PRRS in the test dataset. All the pigs during a PRRS outbreak were considered exposed to the disease and were assigned a value of 100, while those during rest of the periods were given a value of 0. A linear regression model was used to derive the weights for the traits NWA, NLP and NWP for prediction of CL. The model also included fixed effects of parity, year, day length and random effects of sow and year-week of farrowing.

Identification of disease outbreaks. Predicted CL was analyzed with a linear model including the above factors. Weeks of a year within a farm were considered as challenge periods when the ratio of year-week solution exceeded the threshold of 2.326 (1% truncation point of normal distribution) as suggested by Rashidi et al. (2014).

Estimation of genetic parameters in healthy and disease phases with a bivariate model. The entire data set was divided into disease and healthy phases using the above approach of outbreak detection. Only 3% of records belonged to disease challenge periods. Hence, only reproduction records from sows that had records both in disease and healthy periods were used. In this analysis, expression of the same trait in disease and healthy phases were considered as two different traits. Consequently, bivariate analysis was used within each of the reproduction trait (NBA, NLP and NWP). Fixed effects of farm, parity, year etc. and random effects of animal, permanent

environment and service sire were used for estimation of variance components.

Genetic parameters for a range of challenges. A random regression approach was used for this purpose (Calus and Veerkamp (2003); Li and Hermesch (2012)). CL was used as covariate for animal and permanent environment effects. Slopes of individual reaction norms were estimated using Legendre polynomials. Ten classes of increasing challenge load, based on the CL, were created to account for the effect of heterogeneity of variances. Each of these classes had ~92,000 records. The analysis was conducted with ASReml version 3.0 (Gilmour et al. (2009)).

Results and Discussion

Testing and validation of Challenge load (CL): Out of 15 outbreaks of PRRS in the test dataset, 14 outbreaks were detected using CL while the use of NBA, NLP and NWP as single traits allowed detection of six, five and 12 outbreaks respectively. Results of further validation using CL in farms from Europe and America are given in Table 1. A majority of outbreaks detected was confirmed as PRRS (28 out of 41 outbreaks). The other 13 outbreaks were related with other infectious agents such as Leptospira or infectious diarrhea, and feed quality issues.

Table 1. Validation of outbreaks detected using CL

Country	Number of farms	Outbreaks detected	Outbreaks confirmed
Canada	13	2	2
Germany	47	1	1
Spain	38	5	5
Hungary	7	2	1
Italy	7	5	3
Netherlands	295	23	20
Portugal	11	4	4
Russia	14	6	5
Total	**431**	**48**	**41**

Genetic parameters during healthy and disease phases using a bivariate model. Variance components due to all random effects in the models for NBA and NLP were estimated separately during healthy and disease phases. These estimates are given as percentage of the phenotypic variance in Table 2.

The results suggest an increase in total phenotypic variance due to diseases. The additive genetic variance (Va) was also higher resulting in a higher heritability of NLP during disease periods. Availability of higher genetic variance as a result of disease was also observed by Lewis et al. (2009). One of the reasons could be that the genetic differences among sows for piglet losses are not fully expressed during healthy periods but they are more clearly revealed during the disease challenge. There was a higher permanent environmental variation during disease periods for NBA and NLP. Interestingly, the service sire effect was also higher during disease than during healthy periods. This could be partly due to the non-genetic effect of the service sire arising from semen quality, or genetic effect of the service sire or the combined genetic effect of the service sire and piglets in the litter.

Table 2: Variance components as percentage of total phenotypic variances.

	Number born alive		Number lost pigs	
	Health	Disease	Health	Disease
σ_a^2/σ_p^2*	8	8	7	11
σ_{pe}^2/σ_p^2	7	9	6	12
σ_{ss}^2/σ_p^2	2	3	1	4
σ_e^2/σ_p^2	82	80	86	74
σ_p^2	9.27	12.25	2.65	4.07

σ_a^2 =Additive genetic variance, σ_p^2 =Total phenotypic variance, σ_{pe}^2 = Variance due to permanent environment of the dam, σ_{ss}^2 = Variance due to service sire, and σ_e^2 = residual variance. * Heritability.

Genetic parameters for a range of challenges using random regression model. Very often the interest is not to genetically select for specific diseases but to select for higher resistance or tolerance to a broad range of diseases or challenges. As part of the validation, it was observed that CL also identified periods of challenges other than PRRS, in some countries. Partly, this is expected as CL is mainly based on drops in reproductive output which could be due to PRRS, but due to other diseases, extreme climates or even feed or management issues. In this regard, it was of interest to investigate whether CL could be used as a covariate to estimate genetic parameters at increasing levels of challenges. In this approach, the residual variance class (class 10) with highest CL had majority of sows with a confirmed disease challenge. The results are summarized in Figure 1.

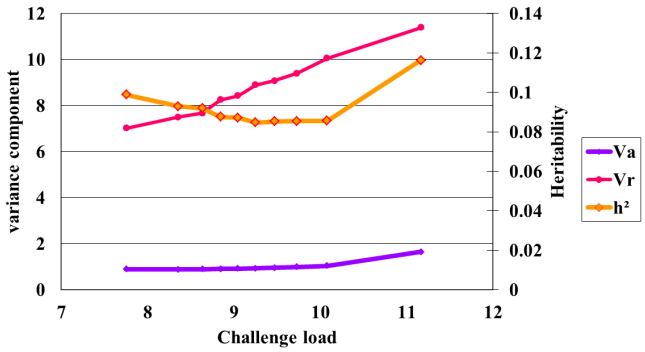

Figure 1: Estimates of additive genetic variance (Va), residual variance (Vr), and heritability (h^2) for NBA with increasing levels of challenge load estimated through CL.

There was an increase in residual variance (Vr) for NBA as the level of challenge increased. The additive genetic variance (Va) increased from 0.89 to 1.65 as CL increased from 7.8 to 11.2. The heritability of NBA was highest (0.12) at the highest challenge load, followed by the lowest challenge load (0.10). A comparison between the level of predicted CL and proportion of records during healthy periods based on outbreak detection is given in

Table 3. In general, the proportion of records during healthy periods increased from class 1 to 10, as the CL increased. In spite of this, a majority of the records were during healthy periods in classes 1 to 8. The intermediate level of disease was in the class 9 with 47% of records during disease periods. At this level of disease challenge, the heritability was 0.086.

We used both a bivariate analysis (no assumptions on the variance components in different environments) and a random regression approach (fitting a function through variance components in different environments) to see whether the results are similar in order to make sure that the function describes the real situation well and does not create artifacts.

Comparison of results of the bivariate analysis (Table 2) and random regression analysis (Figure 1) for NBA revealed similar changes in variance components. The main difference is that the bivariate analysis requires a clear distinction between disease and health, while the random regression approach supports gradual progression with increasing level of challenge. In the latter analysis, use of CL also accounts for the level of challenge where clinical symptoms are not fully expressed. Consequently, even records with an intermediate CL contribute to the estimation of the tolerance of a disease with a high CL. In reality, clear distinction between disease and health periods just based on reproduction is arbitrary as it is difficult to set clear boundaries of onset of a disease and complete recovery. Furthermore, production systems do not have a constant CL, but it varies considerably over time. The random regression approach associates an observation to the correct challenge load and better than possible with classes of herd-year-season or a bivariate approach. The random regression approach also allows for estimation of variance components and heritabilities for a range of levels of an environmental variable in a single analysis constituting a powerful tool for selection for resistance or tolerance to disease.

Correlations between the ten classes of CL are given in the Table 3. In general, the genetic correlations decreased with increasing contrast in CL. For example genetic correlation of class 1 (CL=7.8) with class 2 (CL= 8.4) was 0.97 while it was 0.42 with the class with highest CL (CL=11.2). This implies that selection of sows in the high health environment could result in substantially lower response than direct selection in the target environments.

Table 3: Genetic correlations between different classes of challenge load for number born alive.

CL	*H%*	**Challenge load class**								
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
7.8	***99***									
8.4	***96***	.97								
8.6	***98***	.95	1.0							
8.8	***96***	.93	.99	1.0						
9.0	***95***	.91	.98	.99	1.0					
9.3	***93***	.89	.97	.99	.99	1.0				
9.5	***85***	.86	.96	.98	.99	.99	1.0			
9.7	***73***	.83	.93	.96	.97	.98	.99	1.0		
10.1	***53***	.77	.89	.93	.95	.96	.97	.99	1.0	
11.2	***20***	.42	.61	.66	.70	.74	.77	.81	.85	.89

*CL: Challenge load
*H%: Percentage of observations in healthy environment within the class

Conclusions

This study suggests that reproduction records can be used to identify periods of disease outbreaks. This allows for estimation of genetic parameters during disease challenge phases and selection of specific lines for tolerance to specific diseases. The concept can be extended to challenges other than diseases as well, to breed for enhanced general robustness. Reaction norms of animals in response to CL could then be used in a selection index to identify animals with higher robustness within a line.

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