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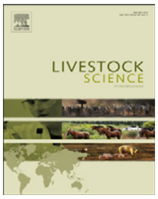

Meta-analysis of genetic parameter estimates for reproduction, growth and carcass traits of pigs in the tropics

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ABSTRACT

The design of swine breeding programs for the tropics requires knowledge of genetic parameters for economically important traits determined under tropical conditions. A literature review found a total of 468 heritability (h^2) estimates, 368 genetic correlations and 254 phenotypic correlations for 35 traits across 117 peer-reviewed articles published from 1974 to 2009 and covering tropical Africa, Southeast Asia, the Caribbean and Latin America. A model that incorporated between and within study variance component was used to obtain weighted means and variances for all parameter estimates. Weighted means and standard errors of direct and maternal heritability, common litter effects and the correlation between direct and maternal effects are given for various reproduction, growth and carcass traits. The weighted means and confidence intervals for the genetic and phenotypic correlations between the trait groups are also given. Weighted least-squares analyses of the h^2 estimates were performed by fitting a number of fixed effects and covariates for each trait as appropriate for the data. Breed, data origin, estimation method, data age and location of study were found to be significant ($P<0.05$) for majority of the traits analysed. These results indicate the relevance of having local, population-specific genetic parameter estimates for the tropics. The weighted mean estimates of genetic parameters presented here are recommended for use when reliable estimates are not available for a specific tropical pig population. This is quite appropriate because it uses the vast resource of published genetic parameter estimates effectively.

1. Introduction

Genetic parameters such as heritability, genetic and phenotypic correlations and other components of total phenotypic variance have wide applications in genetic and animal breeding research. Accurate estimation of genetic parameters in every population of interest requires large across-generation data sets with reliable pedigree information which are not always available. The development of animal mixed models using REML and Bayesian procedures (Sorensen and Gianola, 2002; Thompson, 2008) and the advances in computing capacity have all resulted in the publication of what are expected to be better estimates of these parameters. The advances in procedures have allowed for estimation of maternal heritability, common litter effects and the correlation between direct and maternal genetic effects for many traits.

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Over the last four decades, several estimates of genetic and phenotypic parameters for pig production traits determined under tropical conditions have been published. These estimates were derived using a variety of methods, are of variable quality in terms of sample size used to estimate them, and have contradictory results. Under these circumstances, swine breeders and researchers may have difficulty making sense of the literature estimates or taking stock of the knowledge base. This can have negative consequences on breeding decisions and can hinder genetic progress.

The motivation for this study was the need for a quantitative synthesis of previous findings in order to provide summary estimates of genetic parameters for the development of breeding objectives for swine genetic improvement in tropical developing countries. A statistical method known as "meta-analysis" was utilised (Sutton et al., 2000). Koots et al. (1994a) summarised estimates of genetic parameters for beef production traits using a fixed effects meta-analysis method and identified significant study characteristics that affect estimates. A random effect meta-analysis model was used to obtain weighted estimates of genetic parameters in sheep (Safari et al., 2005) and in beef cattle (Giannotti et al., 2005). No such review has yet been carried out for pigs raised in tropical environments where management systems are unstable and genetic parameter estimates are highly variable and show lack of consensus.

Using a fixed-effect method to combine estimates of genetic parameters makes the assumption that each published estimate is estimating the same underlying true parameter (i.e. no heterogeneity between published estimates) (Barron et al., 2008) and any difference observed is due to chance factors or sampling variation within each study. If this assumption is invalid, as shown by Koots et al. (1994a), then a preferred alternative method would be to fit a random effects meta-analysis model. A random-effects model assumes that each estimate from the various studies is estimating different underlying true parameters, and takes into account the extra variation implied in making this assumption. This underlying true parameter is assumed to vary at random and its effect is believed to be normally distributed. Hence, this model accounts for the between and within-study sources of variation and has been proposed as a more conservative method of meta-analysis that yields results that can be generalised (Berkey et al., 1995; Barron et al., 2008; Sutton et al., 2000; Safari et al., 2005).

The objective of this study was to use a random-effect meta-analysis model to arrive at consensus estimates of genetic and phenotypic parameters of economically important traits of pigs determined under tropical conditions and to test for factors that can affect these parameters in the tropics.

2. Materials and methods

2.1. Description of study scope and traits

A systematic search of the literature using electronic and non-electronic media was conducted to identify all references reporting estimates of genetic and phenotypic parameters for pig production traits in the tropics. A total of 117 peer-reviewed articles with full description of methods and published between 1974 and 2009 were reviewed. These papers reported original research that was carried out in Southeast Asia, Latin America, the Caribbean and Tropical Africa. These regions lie in the tropics between latitude 23.5° north and latitude 23.5° south of the equator. The climate is hot and humid all year round with daytime temperature above 25 °C and relative humidity of 85%, on average. The annual rainfall usually exceeds 2000 mm.

Traits included in the study were those considered to be economically important for pork production in the tropics and are likely to be included in breeding objectives. These traits were grouped into three broad categories: reproduction, growth and carcass. See Table 1 for a list of trait abbreviations. Reproduction traits included litter size at farrowing (LSF), number born alive (NBA), litter size at 21 days (LS21), litter size at weaning (LSW), litter weight at farrowing (LWF), litter weight at 21 days (LW21), litter weight at weaning (LWW), pre-weaning average daily gain

Table 1
List of traits studied, abbreviations used and units of measurement.

Traits	Abbreviations	Units
Reproduction		
Litter size at farrowing	LSF	Piglets
Number born alive	NBA	Piglets
Litter size at 21 days	LS21	Piglets
Litter size at weaning (5–8 weeks)	LSW	Piglets
Litter weight at farrowing	LWF	kg
Litter weight at 21 days	LW21	kg
Litter weaning weight (5–8 weeks)	LWW	kg
Pre-weaning daily gain	PDG	g/d
Pre-weaning mortality	MOR	Piglets
Maternal ability	MA	Ratio
Survival rate	SRT	%
Age at first farrowing	AFF	d
Age at first conception	AFC	d
Gestation length	GLT	d
Weaning to service interval	WSI	d
Farrowing interval	FIT	d
Daily feed intake during lactation	DFI	kg
Growth		
Average daily gain	ADG	g/d
Individual birth weight	IBW	kg
Individual weight at 21 day	IW21	kg
Individual weaning weight (5–8 weeks)	IWW	kg
Post weaning individual weight ($\leq$ 6 months)	PIW	kg
Mature weight (> 6 months)	MWT	kg
Days to 90 kg weight	D90	d
Feed conversion ratio	FCR	ratio
Average daily feed intake	ADFI	kg/d
Carcass		
Back fat ultrasonically measured	BFU	mm
Back fat adjusted for live weight	BFA	mm
Back fat thickness on carcass	BFT	mm
Per cent lean meat	LEAN	%
Carcass weight	CWT	kg
Carcass length	CLT	cm
Dressing percentage	DPT	%
Loin eye area	LEA	cm^2
Ham yield	HYD	kg