Additive effects of 19 porcine SNPs on growth rate, meat content and selection index

S. Kamiński¹, H. Help², T. Suchocki³, J. Szyda³,⁴

¹University of Warmia and Mazury, Department of Animal Genetics, Olsztyn, Poland
²AsperBiotech, Tartu, Estonia
³Institute of Natural Science, Wrocław University of Life Sciences, Wrocław, Poland
⁴Department of Animal Genetics, Wrocław University of Life Sciences, Wrocław, Poland

Abstract. A total of 306 boars (108 Large White and 198 Landrace) were genotyped for 52 candidate SNPs to determine which of the polymorphisms influence growth rate, meat content and selection index. The effects of SNPs were estimated by a mixed linear model including a random additive polygenic animal effect, fixed effects of SNPs including additive, and pairwise additive-by-additive epistases, year*season of birth, breed and RYR1 genotype. In order to estimate all possible pairwise SNP combinations without overparameterising the model a stochastic approach was adopted. A total of 1 350 replications of the model were generated, each containing five randomly selected SNPs. The final estimates of the fixed effects of the model equaled an average out of the replications. The hypothesis of a nonzero effect of SNP was tested by the Wald test. Among 4 257 estimates calculated, many significant (P<0.01), but mostly minor effects (below 1 phenotypic standard deviation) were recorded. The selected SNPs will be further investigated to determine which may be used in MAS.

Keywords: additive effect, epistasis, growth rate, meat content, pig, SNP.

Introduction

Although carcass traits in commercial breeds of pigs have already reached relatively high levels, their molecular background remains mostly unknown. Many studies search for SNPs significantly influencing genetic variation of these traits. Using a molecular approach, several polymorphisms, namely the missense mutation in RYR1 (Fujii et al. 1991), and in PRKAG3 (Milan et al. 2000), have shown major effects on lean meat content and meat quality, as well as the point mutation in intron 3 of IGF2 (Van Laere et al. 2003) underlying a major QTL for muscle growth and lean meat content. Pig growth rate seems to be correlated with feed intake, as it was shown by Kim et al. (2000) in case of the melanocortin 4 receptor gene (MC4R) and by Houston et al. (2006) for the cholecystokinin type A receptor gene (CCKAR). For many SNPs related to pork quality (reviewed by Brym and Kamiński 2006), association studies have been less successful than expected in detecting causal genetic variants. For most SNPs investigated to date, their effects on traits were estimated for single polymorphisms without considering their genetic background. The development of array technology facilitated genotyping of many SNPs simultaneously in the same sample of animals. It opened new possibilities to estimate effects of many SNPs and taking into account epistatic effects, which increases the precision of additive effect estimation. In this report we use this new opportunity, based on data generated by the mini-chip SNiPORK consisting of SNPs, which were mostly indicated by other authors as associated with pork yield and quality (Kamiński et al. 2008).
The aim of this study was to estimate additive effects of the 52 SNPs precorrected for the additive polygenic background for their further utilisation in MAS and genomewide breeding value prediction, as well as to reveal which of the 52 candidate SNPs have significant additive and epistatic effects on growth rate (GR), meat content (MC) and selection index (SI) in order to identify potential candidate genes.

Materials and methods

A total of 108 Large White and 198 Landrace boars were included in the study. Boars were born between 2002 and 2006, and sampled randomly from a single herd when they reached the age when daily gain and meat content are officially measured. All boars were genotyped for 52 SNPs by the method described earlier (Kaminski et al. 2008) to determine which of them or their combinations influence growth rate, meat content or selection index. All these traits were measured and calculated following obligatory and standardized instructions controlled by the Regional Animal Breeding Centers.

GR is standardized at the age of 180 days and is estimated by the formula:

\[ GR = \frac{616974 Z - 0.0127 W^2 + 6.2843W - 102.72}{W} \]

where \( Z \) is body weight (kg) on the day of measurement and \( W \) is the age (in days) on the day of measurement.

MC is measured between the 170th – 210th day of boar’s life and is calculated as follows:

\[ MC = -0.4776 P_{2ST} - 0.4593 P_{4ST} + 0.3486 P_{4MST} + 48.9829 \]

where \( P_{2ST} \) is standardized backfat thickness at point P2 (behind the last rib, 3 cm from the middle line of the back), \( P_{4ST} \) is standardized backfat thickness at point P4 (behind the last rib, 8 cm from the middle line of the back) and \( P_{4MST} \) is the height of loin at point P4. GR and backfat thickness were transformed and adjusted to day 180 of boars’ life and 110 kg of body weight.

SI is calculated using the following formula:

\[ SI = 0.1556 GR + 3.1023 MC - 179.4935 \]

The effects of SNPs were estimated by the following mixed model:

\[ y = X_{\beta} \beta + X_{\mathbf{q}} q + Z \alpha + e, \]

where \( y \) is a vector of trait values (GR, MC or SI), \( \beta \) is a vector of fixed effects comprising: a general mean, an animal’s birth year × birth season class (10 classes), an animal’s breed (Large White and Landrace), an animal’s RYR genotype class (NN or Nn), \( q \) is a vector of fixed SNP effects comprising an additive, dominance and pairwise additive-by-additive epistatic effects, \( \alpha \) is a vector of random polygenic effects of animals assuming \( \alpha \sim N(0, \sigma^2\alpha) \) with \( \sigma^2\alpha \) being a component of the total additive genetic variance attributed to polygenes; \( e \) is a vector of random errors assuming \( e \sim N(0, \sigma^2e) \) with \( \sigma^2e \) denoting the error variance, \( X_{\beta}, X_{\mathbf{q}} \) and \( Z \) are corresponding design matrices. Both variance components were assumed as known (i.e. were not estimated) with \( \sigma^2\alpha = 0.3\sigma^2_\gamma \) and \( \sigma^2e = 0.7\sigma^2_\gamma \). Corresponding elements of \( X_{\beta} \) are set up following the parameterization of Álvarez-Castro and Carlborg (2007), where codes for additive effects are given by:

\[
\begin{align*}
X_{\beta1} &= \left\{ \begin{array}{ll}
0 &-P(12) - 2P(2) & \text{for SNP genotype 11} \\
1 &-P(12) - 2P(2) & \text{for SNP genotype 12} \\
2 &-P(12) - 2P(2) & \text{for SNP genotype 22}
\end{array} \right. \\
X_{\beta2} &= 1 - P(12) - 2P(2) & \text{for SNP genotype 11} \\
X_{\beta12} &= 0 - P(12) & \text{for SNP genotype 12} \\
X_{\beta21} &= 0 - P(12) & \text{for SNP genotype 22}
\end{align*}
\]

for dominance effects by:

\[
\begin{align*}
X_{\beta1} &= \left\{ \begin{array}{ll}
0 &-P(12) - 2P(2) & \text{for SNP genotype 11} \\
1 &-P(12) - 2P(2) & \text{for SNP genotype 12} \\
2 &-P(12) - 2P(2) & \text{for SNP genotype 22}
\end{array} \right. \\
X_{\beta2} &= 1 - P(12) - 2P(2) & \text{for SNP genotype 11} \\
X_{\beta12} &= 0 - P(12) & \text{for SNP genotype 12} \\
X_{\beta21} &= 0 - P(12) & \text{for SNP genotype 22}
\end{align*}
\]

where \( P(ij) \) is the frequency of SNP genotype \( ij \) estimated from the data, and for the additive by dominance epistasis by:

\[
x_{\beta1} = X_{\beta1\beta}, \ X_{\beta1\beta} = x_{\beta1}, \ x_{\beta1} = x_{\beta1}, \ x_{\beta12} = x_{\beta1\beta}, \ x_{\beta12} = x_{\beta1\beta}, \ x_{\beta21} = x_{\beta1\beta}, \ x_{\beta21} = x_{\beta1\beta}, \ x_{\beta22} = x_{\beta1\beta}, \ x_{\beta22} = x_{\beta1\beta},
\]

where \( X_{\beta1\beta} \) represents the parameterization for an additive effect of \( i \)-th SNP.

Parameters of the model were estimated based on solving mixed model equations (Henderson 1963).

Note that it is a standard parameterisation, where an additive effect is equal to half of the difference between the two homozygotes (11 and 22), while the dominance effect represents a difference between a heterozygous genotype (12) and the mean of both homozygotes. In the case of fitting the additive effects only this model is equivalent to models proposed previously by Kao and Zeng (2002) and Zeng et al. (2005). Moreover, for allele frequencies \( P(1)=P(2)=0.5 \) it is furthermore equivalent to Cockerham (1954).

The above model was evaluated 1 350 times, but each time out of 52 SNPs a set of 5 SNPs was randomly selected for \( \mathbf{q} \). A final estimate of each effect of the model was an average of the estimates obtained during the 1 350 evaluations. A null hy-