Bayesian Inference on Teat Numbers of Swine

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Swine breeders have attached considerable importance to teat number especially when teat numbers were less than litter size. Although teat number is a count trait, a mixed model was suggested for genetic analysis for teat numbers of swine because the model fits the field data better than the Poisson error model (Lee and Wang, 2000). Another concern is that a sample of parameter values can be easily obtained from a posterior density in a Bayesian approach using Gibbs sampling and then be used to estimate a moment of a lower dimensional marginal of the posterior. The purpose of this study was to estimate variance components for teat numbers of swine with the mixed model through the Bayesian approach.

Restricted Maximum Likelihood (REML) and Gibbs Sampling were implemented to estimate variance components for teat numbers in a swine population (N=16322) which includes Landrace (L, N=9898), Yorkshire (Y, N=1748), crossbreds of Landrace and Yorkshire (LY, N=1924), crossbreds of Landrace, Yorkshire and Chinese Indigenous Min pig (LYM, N=2685) and Min pig (N=67). The analytical model included breed and sex fixed effects and an additive genetic random effect. In Bayesian inference, the MTGSAM programs (Van Tassell and Van Vleck, 1996) were used to generate samples from posterior densities for variance components. Since there was no reasonable informative prior information, a weak Inverted Wishart (IW) prior distribution with shape parameter of 3 and various prior means, the posterior estimates. Using prior distributions with shape parameter of 3 and various prior means, the posterior means did not differ (P>.05) from REML estimates. When the shape parameters of 165 were used, different prior means influenced the posterior mean estimates.

Although use of flat priors for variance components empirically worked well, it is theoretically improper (Hobert and Casella, 1996). If there was no reasonable informative prior information, a prior close to the flat prior is recommended for variance components in Bayesian analyses.


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The REML estimates of $\sigma_a^2$, $\sigma_e^2$ and $h^2$ were $1.039\pm0.058$, $0.541\pm0.032$ and $0.655\pm0.026$ respectively. In analyses of subsets of data, a heterogeneity of variance components by breed and sex was observed. The estimates of $h^2$ were 0.658, 0.523, 0.800, and 0.573 respectively for L, Y, LY, and LYM, and 0.636 and 0.585 for males and females. The posterior mean estimates of $\sigma_a^2$, $\sigma_e^2$ and $h^2$ were $1.043\pm0.065$, $0.535\pm0.035$, and $0.660\pm0.028$, respectively, corresponding to the REML estimates.

The sensitivity analyses showed that the posterior mean estimates with a flat prior distribution are $1.035\pm0.068$, $0.540\pm0.038$ and $0.657\pm0.030$ for $\sigma_a^2$, $\sigma_e^2$ and $h^2$, without significant difference with REML estimates. Using prior distributions with shape parameter of 3 and various prior means, the posterior means did not differ (P>.05) from REML estimates. When the shape parameters of 165 were used, different prior means influenced the posterior mean estimates.