and by a method developed for multiple-trait models by Strabel and Misztal (2001) (accf90 program; M2). In both methods the only fixed effect considered was the contemporary group (CG). D1 was a simulated data set containing 30,250 animals, 5,000(250) base dams(sires) and 5 generations (G) of 5,000 animals, 3 measurements (M) per animal, distributed in 15 CG (GxM combination). The sex rate in non base animals was 1 M:4 F. D2 was a data set of 1,812,871 records of Gelbvieh animals in 199,168 CG. Initial analyses involved D1, where the exact accuracies were also computed by inversion (M3). Regression coefficient, intercept and R2 of direct accuracies when M1 was regressed on M3 at 205 days (Weaning Weight) for males were 0.95, 0.03 and 0.99. The same quantities of M2 on M3 were 0.96, 0.04 and 0.99, and of M1 on M2 were 0.98, 0.00 and 0.98. The corresponding numbers for females were 1.06, -0.01, 0.99 (M1 on M3), 1.09, 0.00, 0.99 (M2 on M3), and 0.98, 0.00, 1.00 (M1 on M2). For maternal effects both methods showed similar performance and errors. Both M1 and M2 overestimated accuracies for base dams with many offspring. Using data set D2 without distinction of sex and retaining only animals with computed accuracy >= .6 for M1, similar statistics for M1 on M2 were 1.05, -0.06, 0.97 (1.13, -0.14, .96) for direct (maternal) effects. Computing requirements for D2 were 8 CPU min. and 878 Mb. of RAM with M1 and 7 min. and 326 Mb. with M2. A multiple trait accuracy algorithm is useful for computing accuracy of a RR linear spline model when there is at most one observation per trait and no interest on other ages than those defining traits.

Key Words: Accuracy, Beef Cattle, Linear Splines

418 Equivalent mixed model equations for genomic selection. D. J. Garrick*, *Colorado State University*, *Fort Collins*.

Henderson's mixed model equations are used for genetic evaluation from pedigree and performance information. Equations are solved for factors influencing a trait (eg direct genetic, maternal genetic, maternal permanent environment). Assumptions to obtain BLUP include the var-cov matrix between effects on one animal (eg G0) and the var-cov matrix of additive effects between animals (numerator relationship or A matrix). These var-cov matrices are commonly full rank, and their inverses are used in computations. Widespread implementation has occurred because A-1 is sparse and can be easily made directly from pedigrees. Genetic merit is assumed to result from an infinitesimal number of genes of small effects. An incidence matrix is used to relate genetic merit to phenotypes. This indicator matrix contains one or more unit elements that identify the animals own additive and any other effects. The number of equations increases each evaluation, in proportion to the number of new animals. Genomics has delivered an apparently very different approach to selection. Genetic merit can be considered the finite sum of perhaps tens of thousands of effects, physically located at some place on the genome whose transmission can be traced through genetic markers or haplotypes. Genomic selection might involve mixed model equations that ignore animal effects but include haplotype effects. Pedigree relationships are not necessarily required, the dense markers being used to trace identity by descent (IBD) at each locus and these IBD probabilities being used to construct incidence matrices. Such equations would not increase according to the number of new animals added over time, only the number of new markers or haplotypes. Total genomic merit of candidates would be obtained by summing up many relevant haplotype effects.

An equivalent model can be written that does not explicitly fit haplotype effects but total genomic effects for each animal. This demonstrates the similarity between total genomic selection and conventional A matrix evaluation. The animal-based formulation may be computationally attractive in the short-term when there are more haplotype effects than animals with markers.

Key Words: Genetic Evaluation, Equivalent Models

419 Detection and use of single gene effects in large animal populations. N. Gengler*[1,2], S. Abras[1], M. Szydlowski[1], and R. Renaville[1], [1]*Gembloux Agricultural University*, *Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Belgium*.

Unbiased estimation of single gene effects can only be achieved by estimating them simultaneously with other environmental and polygenic effects in mixed inheritance models. As in large animal populations the vast majority of animals are however not genotyped, missing genotypes have to be estimated. Currently used methods as iterative peeling or MCMC are unpractical for large datasets. Recently an alternative method to estimate missing gene content, defined as the number of copies of a particular allele was developed. Unknown gene content is approximated from known genotypes based on the additive relationships between animals. In this study the proposed method was tested for the detection of candidate gene effects for bovine transmembrane GHR on first lactation milk, fat and protein test-day yields in Holsteins. The GHR gene was estimated to show moderate to small gene substitution effects of 295 g/day for milk, -8.14 g/day for fat yield and -1.83 g/day for protein yield for a phenylalanine replacement by a tyrosine (frequency 23.3%). Only 961 mostly recent sires out of 2,755,041 animals were genotyped. The accuracy of the procedure was then estimated by doing 15 simulations using gene dropping and adjustment of the observed 12,858,741 records using the estimated parameters. The new method to estimate missing gene content resulted to be functional and accurate as relative bias in the estimation of allele frequency was very low (0.2%) as were the biases for moderate allele substitution effects (milk: 3.7%; fat yield: 3.3%). Biases were larger for traits with smaller substitution effects (protein yield: 55.3%). The new method has the potential to allow even in very large animal population with few genotyped animals reliable estimation and use of moderate to large single gene effects.

Key Words: Single Gene Effects, Large Population, Estimation of Gene Content