282 Comparison of Student's *t*, LASSO, and multiple shrinkage methods for the prediction of genomic breeding values. C. Maltecca* and J. P. Cassady, *North Carolina State University*, *Raleigh*.

The objective was to compare 4 different approaches for predicting genomic breeding values (GEBV). First an implementation of the Bayes-A (M1) was used. The second method was an extension of Bayes-A (M2) with scale and degrees of freedom of the mixing inverted Chi-square distribution treated as unknown and estimated from the data. Third (M3) a Laplace prior was employed to obtain LASSO estimates of SNPs effects. Finally a semi-parametric approach was investigated (M4) which allowed shrinkage of each coefficient toward multiple prior means with unknown location. A Dirichlet process prior was put on the mean and scale parameters in order to create few groups with different degree of shrinkage. Hierarchical modeling was employed for all the methods. We simulated 8000 SNPs and 12 QTL. Genotypes for 2000 individuals were generated in age order over 4 generations with the first 500 representing the training generation. All individuals were assigned a phenotypic value by adding a random residual to the true breeding value obtained as the sum of each marker effect. This was done in order to mimic estimated breeding values with different accuracies. Two different average levels of accuracy (0.95, 0.85) of the phenotypes were simulated. Five replicates of each scenario were performed. On average M2, M3, and M4 performed better that M1 in estimating markers effects and predicting GEBV in subsequent generations. The average increase in accuracy (measured as correlation between true and estimated GEBV in the next generation) was of .031(±0.004), .034(±.008) and .036(±.011) (M1 prediction accuracy 0.85 ±.011); .042(±.012), .048(±.009), .051(±.014) (M1 prediction accuracy 0.78 ±.013); .052(±0.015), .051(±0.018), .048(±0.017) (M1 prediction accuracy 0.71 ±.012) for M2, M3 and M4 over M1 for the first, second and third generation after training, respectively for phenotypes accuracy of 0.95. M3 and M4 performed on average better than M2 at higher phenotypic accuracy but failed to converge in some replicates at lower phenotypic accuracy. M2 was the least computationally demanding, and M4 was the most computationally demanding.

Key Words: GEBV, Bayesian methods, multiple shrinkage

283 Equivalent mixed model for joint genetic evaluation considering molecular and phenotypic information. N. Gengler*[1,2] and F. Colinet[1], [1]*Gembloux Agricultural University*, *B-5030 Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *B-1000 Brussels, Belgium*.

Currently efforts are underway to introduce molecular information into genetic evaluation systems. A particular situation is genomic selection however simpler cases exists where major genes are known and used by breeders. A new alternative strategy for the prediction of gene effects and especially their smooth integration into genetic evaluations based on an equivalent method was developed from existing theory. Underlying hypothesis were based on the idea that knowledge of genotypes will not affect overall additive genetic variance but only change expected values of genetic effects for animals with known genotypes. The developed equations were modified to allow that not all animals were genotyped. As the underlying mixed model is open a very large range of models can be used in situations including random regression models, multiple-trait, maternal effects and multiple-across-country-evaluation models. Computations involved successive solving of two mixed models, with the use of an linear extrapolation to speed up convergence of gene effects. The method was tested for several known major genes and QTL, e.g. for the mh gene in the dual-purpose Belgian Blue population in Belgium. Modifications of the method could also be developed to be useful in the context of genomic selection.

Key Words: molecular Information, joint estimation, genomic selection

284 Effect of estimation approach and number of QTLs in accuracies of genomic breeding values for simulated data. G. Gaspa[1], E. L. Nicolazzi[2], R. Steri[1], C. Dimauro[1], and N. P. P. Macciotta*[1], [1]*Dipartimento di Scienze Zootecniche, Università di Sassari*, *Sassari, Italia*, [2]*Istituto di Zootecnica, Università Cattolica del Sacro Cuore*, *Piacenza, Italia*.

Accuracies of estimated genomic breeding values (GEBVs) in simulated data depends both on the relative efficiency of the methodology used but also on the assumptions made for the simulation. A key issue is represented by the number of QTLs related to the genome length and to the density of SNP markers. In this study two scenarios of number of QTLs, 10 or 20, for a genome size of 1 M length and with 1000 SNPs were tested. Initial allelic frequencies for both SNPs and QTLs were sampled from a uniform distribution. QTL effects were sampled from a gamma distribution (shape parameter 0.42). After 50 generations of random mating, two training (2,000 individuals) and three prediction (3,000 individuals) generations were created. Phenotypes of training individuals were generated by adding random noise to the true breeding value (TBV). Heritability was set at 0.5. The estimation step was performed by fitting phenotypes of training individuals with a mixed linear model that included the fixed effect of the mean and the random effect of: i) the genotype of all 1,000 SNP markers (ALL); or ii) the scores of the first 200 principal components extracted from the correlation matrix of the SNP genotypes (PCA). Estimates were then used to predict GEBVs in the prediction generations. Accuracy of prediction was evaluated as correlation between TBVs and GEBVs. Each scenario was replicated 10 times. Average accuracy of prediction for the training generations was 0.90 (standard deviation 0.04) and 0.86 (0.03) for BLUP or PCA calculations, respectively, when 10 QTLs were simulated. Values raise to 0.94 (0.02) and 0.87 (0.01) in the scenario with 20 QTLs. In the prediction generations, the PCA approach resulted in a higher accuracy of prediction in both scenarios: 0.66 (0.09) vs 0.53 (0.07) and 0.72 (0.06) vs 0.61 (0.07) for 10 and 20 QTLs respectively. Moreover, the decreasing trend of accuracy in the prediction generations was less pronounced reduced in the PCA approach. Both the number of QTLs considered and the mathematical approach used had an influence in the accuracy of GEBVs.

Key Words: genomic selection, number of QTLs, principal component analysis