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CABRERA DEMARION

Estimation of Genetic Parameters for Measures of Stayability in Beef Cattle LAP Lambert Academic Publishing

The variance and covariance components needed to estimate heritabilities of and genetic correlations among litter size, ovulation rate, scrotal circumference and body weight in Rambouillet sheep were estimated using REML (Restricted Maximum Likelihood) via an EM (Expectation-Maximization) type algorithm. Data were obtained from the University of Illinois Rambouillet flock located at the Dixon Springs Agricultural Center near Simpson, Illinois. There were 437 ram lambs with scrotal circumference records, 552 ewes with lambing records, 610 ewes with ovulation rate records and 998 lambs with body weight records. A bivariate animal model which included year of birth as a fixed effect and additive genetic value of animal and residual as random effects was employed. The inverse of the numerator relationship matrix was included in the mixed model equations. The heritability estimates from bivariate analyses were: .18, .20, .23, .34 and .10 for litter size, ovulation rate, scrotal circumference, 180 day body weight of females and 180 day body weight of males, respectively. The heritability estimate of litter size from a univariate analysis was 14%. Bias due to natural selection is suggested as the reason for the difference between the univariate and bivariate estimates. The genetic correlation between litter size and ovulation rate was near unity. Body weight in ewes had a moderate genetic correlation with both litter size (.22) and ovulation rate (.20), and a low residual correlation with both litter size (.03) and ovulation rate (.09). The genetic correlation between body weight in rams and scrotal

circumference was zero, while the residual correlation was .71. The genetic correlations of scrotal circumference with litter size and ovulation rate were $-.25$ and $+.20$, respectively. Comparison of direct, indirect and combined selection indices showed that, of the traits studied, ovulation rate was the most useful indirect selection criterion for genetic improvement of litter size. Expected response in litter size to indirect selection on ovulation rate was 93% as large as the expected response to direct selection on litter size. Selection based on an index of litter size and ovulation rate is expected to produce 132% as much response as selection on litter size.

Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics 1978.

Estimation of Genetic Parameters Estimation of Genetic Parameters Under Optimal and Suboptimal Environments for Body Weight in Chicken Using a Diallel Mating System Estimation of Genetic Parameters Using Molecular Markers and EM-algorithms Springer Science & Business Media

The present study was carried out to obtain information about the performance of maize inbred lines, genetic diversity, gene action and assessment of the combining ability of parental lines and their F1s by using diallel fashion. Cob length, number of kernels/row and no. of grains/cob could be the important selection criteria in the improvement of maize lines and hybrids for higher grain yield. The average inter-cluster was always higher than the average intra-cluster distance suggesting wider genetic diversity among the inbred lines of the groups. From W_r-V_r graph it has been noticed that expression of dominant and recessive alleles in the parents was influenced by environment as the same parent showed different positions on graphs. From this study, it is concluded that parents with recessive and dominant genes can also contribute towards high yield. Only 5 crosses had higher

grain yield. Of these crosses, P1xP2, P2xP5, P4xP5 and P5xP6 were considered promising hybrids and will be tested in yield trials for further evaluation.

Estimation of Genetic-parameters in the Oregon State University Hazelnut (Corylus Avellana L.) Breeding Population Estimation of Genetic Parameters Estimation of Genetic Parameters Under Optimal and Suboptimal Environments for Body Weight in Chicken Using a Diallel Mating System A 2 x 2 x 2N confounded diallel mating design (2 series, 2 males, N females per male per series) was used to obtain estimates of the genetic parameters in body weight traits in a noninbred population of New Hampshire chickens grown on 18% and 24% protein rations. Individual selection also was applied to evaluate the reliability of the genetic parameters obtained under each protein level. The analysis showed an extremely large contribution of series effects to the total variation in the traits which was attributed to the environmental influences from one series to the other and to the maternal environment. The component of variance due to series x male interaction was found to be small or zero under the 24% protein ration. An optimal environment may have given certain genotypes a greater opportunity to adapt to the environment. The higher estimates of the component of variance of series x female interaction for one-day body weight suggests the influence of maternal effects from one series to the other and from one dam to the other. Generally, estimates for the component of variance of male effects were higher under the 18% protein ration than under the 24% protein ration. Conversely, the component of variance of female effects showed higher values under the 24% protein ration than under 18% protein ration for most of the traits considered. ...Estimation of Genetic-parameters in the Oregon State University Hazelnut (Corylus Avellana L.) Breeding Population Heritability in the narrow sense and in the broad sense,

variance components and correlation coefficients are important genetic parameters in a breeding program. The estimates of these parameters can provide important information for a breeder in the selection of parents, the most efficient design for evaluation of seedlings and advanced selections and the choice of selection strategy to improve many target traits simultaneously. In addition, histograms showing the distributions of the traits in offspring may provide additional information about parent combinations for the improvement of target traits. The Oregon State University hazelnut breeding program is developing improved varieties for the kernel market. Estimates of genetic parameters for most traits of interest are not available. Seventy seven trees representing 41 genotypes and 35 progenies were used to investigate midparent values and progeny means for 17 traits, including 13 kernel and nut traits, and 4 phenological traits, for three years. Estimates for heritability in the narrow sense are all high, ranging from 0.56 for amount of kernel fiber, and 0.58 for date of opening of female flowers to 0.87 for percent kernel, 0.88 for nut compression index and 0.89 for nut depth. Therefore, progeny means can be predicted from mid-parent values and response to selection is expected to be rapid for the improvement of all traits. The analysis of variance components revealed that genotypic variance accounted for most of the phenotypic variance. Although significant, the genotype X year interaction only accounted for a very small part of the phenotypic variance. It suggested one year's evaluation of genotypes for all traits should be sufficient except for nut weight, kernel weight, number of nuts per cluster, fiber amount, nut maturity, time of catkin elongation, and time of opening of female flowers. Genetic and phenotypic correlation coefficients were large and positive for nut size traits (nut length, width, depth, nut weight and kernel weight). Phenological traits (date of opening of female flowers, time of catkin elongation and time of leafing out) were also highly and positively correlated. But most other traits were uncorrelated with each other. Therefore, selection of parents with round nuts of medium size, high % kernel, easily-blanched kernels, and early nut maturity is expected to rapidly improve the population for all of these traits. Histograms show that all traits have continuous variation. Transgressive segregation is very common. For all traits except blanching ability, parent combinations may be based on midparent values. For the improvement of blanching ability, both

parents should blanch easily. Because existing statistical packages do not allow easy calculation of genetic correlation coefficients for tree fruit and nut crops, the use of a spreadsheet to quickly estimate genetic correlation coefficients is demonstrated. Moment-type Estimation of Genetic Parameters and Their Variances for Calving Date and Production Traits from Hereford Data Using Multi-way Models Studies on the Estimation of Genetic Parameters Estimation of Genetic Parameters for Production Traits of Corn and Dual Purpose Sheep The Estimation of Genetic Parameters for Categorical Traits Estimation of Genetic Parameters in Two Maize Recurrent Selection Programs Characterization and Estimation of Genetic Parameters in the Interpopulation Formed by Crossing Two Populations of Maize Estimation of Genetic Parameters and Responses in Selection for Litter Size in Pigs Estimation of Genetic Parameters in a Commercial Pig Breeding Population Estimation of Genetic Parameters for an Ecuadorian Holstein Population Evaluation of Breeding Methods and Estimation of Genetic Parameters in Sugarcane Populations Estimation of Genetic Parameters and Sire Rankings for Holstein Linear Type Scores and Milk Production by Multiple Trait Analysis Estimation of Genetic Parameters from Generation Means Analysis in Eight Parent and Related Populations of Corn Characterization and Estimation of Genetic Parameters in the Interpopulations Formed by Crossing Unselected and Selected BSSS and BSCB1 Maize Synthetics Estimation of Genetic Parameters in Several Switchgrass (*Panicum Virgatum* L.) Populations Estimation of Genetic Parameters for Measures of Stayability in Beef Cattle Estimation of Genetic Parameters in Barley (*Hordeum Vulgare* L.) by the Techniques of Diallel Analysis and Its Modifications The Estimation of Genetic Parameters for Birth, 21 and 42 Day Weights of Duroc and Hampshire Swine Estimation of Genetic Parameters in Dairy Cattle Using an Animal Model and Implications for Genetic Improvement Estimation of Genetic Parameters of Meat and Milk Traits in Dual - Purpose Cattle Studies on the Estimation of Genetic Parameters and Gain from Selection in Yield Trials Effect of Scale of Measurement on Estimation of Genetic Parameters Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics Estimation of genetic parameters for various preweaning and postweaning beef cattle traits.

Characterization and Estimation of Genetic Parameters in the Interpopulations Formed by Crossing Unselected and Selected BSSS and BSCB1 Maize Synthetics

This book, suitable for numerate biologists and for applied statisticians, provides the foundations of likelihood, Bayesian and MCMC methods in the context of genetic analysis of quantitative traits. Although a number of excellent texts in these areas have become available in recent years, the basic ideas and tools are typically described in a technically demanding style and contain much more detail than necessary. Here, an effort has been made to relate biological to statistical parameters throughout, and the book includes extensive examples that illustrate the developing argument.

The Estimation of Genetic Parameters for Birth, 21 and 42 Day Weights of Duroc and Hampshire Swine

Heritability in the narrow sense and in the broad sense, variance components and correlation coefficients are important genetic parameters in a breeding program. The estimates of these parameters can provide important information for a breeder in the selection of parents, the most efficient design for evaluation of seedlings and advanced selections and the choice of selection strategy to improve many target traits simultaneously. In addition, histograms showing the distributions of the traits in offspring may provide additional information about parent combinations for the improvement of target traits. The Oregon State University hazelnut breeding program is developing improved varieties for the kernel market. Estimates of genetic parameters for most traits of interest are not available. Seventy seven trees representing 41 genotypes and 35 progenies were used to investigate midparent values and progeny means for 17 traits, including 13 kernel and nut traits, and 4 phenological traits, for three years. Estimates for heritability in the narrow sense are all high, ranging from 0.56 for amount of kernel fiber, and 0.58 for date of opening of female flowers to 0.87 for percent kernel, 0.88 for nut compression index and 0.89 for nut depth. Therefore, progeny means can be predicted from mid-parent values and response to selection is expected to be rapid for the improvement of all traits. The analysis of variance components revealed that genotypic variance accounted for most of the phenotypic variance. Although significant, the genotype X year interaction only accounted for a very small part of the phenotypic variance. It

suggested one year's evaluation of genotypes for all traits should be sufficient except for nut weight, kernel weight, number of nuts per cluster, fiber amount, nut maturity, time of catkin elongation, and time of opening of female flowers. Genetic and phenotypic correlation coefficients were large and positive for nut size traits (nut length, width, depth, nut weight and kernel weight). Phenological traits (date of opening of female flowers, time of catkin elongation and time of leafing out) were also highly and positively correlated. But most other traits were uncorrelated with each other. Therefore, selection of parents with round nuts of medium size, high % kernel, easily-blanched kernels, and early nut maturity is expected to rapidly improve the population for all of these traits. Histograms show that all traits have continuous variation. Transgressive segregation is very common. For all traits except blanching ability, parent combinations may be based on midparent values. For the improvement of blanching ability, both parents should blanch easily. Because existing statistical packages do not allow easy calculation of genetic correlation coefficients for tree fruit and nut crops, the use of a spreadsheet to quickly estimate genetic correlation coefficients is demonstrated.

Estimation of Genetic Parameters for Ultrasonic Backfat Measurements, Growth and Carcass Traits in Swine

A 2 x 2 x 2N confounded diallel mating design (2 series, 2 males,

N females per male per series) was used to obtain estimates of the genetic parameters in body weight traits in a noninbred population of New Hampshire chickens grown on 18% and 24% protein rations. Individual selection also was applied to evaluate the reliability of the genetic parameters obtained under each protein level. The analysis showed an extremely large contribution of series effects to the total variation in the traits which was attributed to the environmental influences from one series to the other and to the maternal environment. The component of variance due to series x male interaction was found to be small or zero under the 24% protein ration. An optimal environment may have given certain genotypes a greater opportunity to adapt to the environment. The higher estimates of the component of variance of series x female interaction for one-day body weight suggests the influence of maternal effects from one series to the other and from one dam to the other. Generally, estimates for the component of variance of male effects were higher under the 18% protein ration than under the 24% protein ration. Conversely, the component of variance of female effects showed higher values under the 24% protein ration than under 18% protein ration for most of the traits considered. ...

Estimation of Genetic Parameters and Time Trends in a Herd of Angus Cattle

Estimation of Genetic Parameters for Mature Weight in Hereford Females

Multi-trait Estimation of Genetic Parameters and Trends in a Closed Nucleus Population of Swedish Swine

Estimation of Genetic Parameters and Gains from a Partial Diallel Progeny Test of Longleaf Pine (Pinus Palustris Mill)

The Estimation of Genetic Parameters for Categorical Traits

Estimation of Genetic Parameters for Different Cardiovascular Defects in Meat-type Chickens

Estimation of Genetic Parameters in a Commercial Pig Breeding Population

Estimation of Genetic Parameters for Development of Alternative Selection Criteria for Increased Litter Size in Rambouillet Sheep

Estimation Of Genetic Parameters In Maize

Estimation of Genetic Parameters for Various Prewaning and Postweaning Beef Cattle Traits

Estimation of Genetic Parameters in Two Maize Recurrent Selection Programs

A Comparison of Models Used for Estimation of Genetic Parameters for Mature Weight of Hereford Cattle

Estimation of Genetic Parameters Under Optimal and Suboptimal Environments for Body Weight in Chicken Using a Diallel Mating System