Topic 2: Genetics of reproduction traits (important genes and heritability)

Practical example

Welcome to the lecture on quantitative genetics, which is a part of module 1 and was created within the ISAGREED project. The lecture is focused on solving practical examples from the field of quantitative genetics, calculating basic genetic parameters, heritability coefficient and repeatability coefficient. Let's look at the first example. There are 10 female California rabbits in the sample set and we know the number of live births for each mother. Our task is to calculate the basic genetic parameters, mean, standard deviation, mean error, and coefficient of variation, based on which we can determine the variability of this trait. We have to realize that it is a quantitative trait that has continuous variability, is measurable, and can be expressed by a number or value. In the table, we have specific data for our sample set. The total number of females in the set is 10, n = 10. For each female, we know the number of litters, which we denote by the symbol x. The total number of cubs observed in the sample set, that is the sum of x, in our case is 80. Based on these data, we can calculate the arithmetic mean, which is obtained as a quotient of the total number of cubs in the sample set and the number of females in this set. 80 divided by 10 equals 8, which is the average number of cubs in the observed set. For the calculation of other genetic parameters, we need auxiliary calculations. In the third column, the difference between the number of cubs of individual females and the average number of cubs in the set is given, and in the last column, these values are squared. From the available values, we calculate the variance, which expresses the diversity of the data in the monitored file. Variance is typical for quantitative traits that have continuous variability and different manifestations. By substituting into the formula, we get the result 3.33. This number is dimensionless and is essentially the first step to other indicators of variability. By taking the square root of the variance, we calculate the standard deviation, which is the average deviation from the mean and is expressed in the same unit as the observed trait. In our case, the standard deviation from the average is 1.82 cubs. In the next step, we estimate the mean error from the standard deviation, which is calculated as the quotient of the standard deviation and the square root of the number n. After substituting the values into the formula, we get a result of 0.58. The unit is the same as in the previous calculation, the value represents the number of cubs. The last quantity calculated is the coefficient of variability, which is a relative measure of variability and is expressed as a percentage. We calculate the coefficient of variation as the ratio of the standard deviation and the arithmetic mean. Hold generally that the higher the value of the coefficient of variation, the greater the variability in the number of young between individual females. In our case, its value reached 22.75%. Based on the calculations, we found that the average number of pups in the litter is 8 plus or minus 0.58, where plus or minus value is the mean error, the standard deviation s is 1.82 pups, and the value of the coefficient of variation V is 22.75%. In the next example, we have to calculate the value of the heritability coefficient using the half-sibling method for the number of pups in the first litter of Arctic foxes. The table shows the basic data on the size of the litter x, daughters j, by mothers i. The number P represents the number of mothers, n is the total number of daughters and ni is the number of daughters of a specific mother i. In this example, we know the size of the litter of three daughters of each mother, so the value of ni is 3. The number xij represents the number of cubs of each daughter. The sum xij is the sum of the cubs of all the daughters. In the next column, these values are squared, and at the end, the sum of these values is shown again. The number xi represents the number of young daughters per mother, in the next column these values are squared and in the last column, this number is divided by the number of daughters for each mother, which in our case is the number 3. Using ANOVA, or analysis of variance, we calculate the genetic variance between half-sibling groups and variance due to environmental influences within groups. In the first step, we calculate the sum of squared deviations Sg and Se, which express the degree of deviations from the mean between groups and within groups of mothers. In the next step, we calculate the degrees of freedom for individual sums of squares. We calculate Fg as p minus 1 and Fe is equal to n minus p. From these values we calculate the value of the mean square. The between-group and within-group mean-square values are 3 and 2.6, respectively. Subsequently, we can calculate the genotypic variance, sigma g, and the variance caused by the environment, sigma e. The resulting value of phenotypic variance is the sum of genotypic and environmental variance. Based on the analysis of variance, we calculate the intraclass correlation coefficient, which is the proportion of the genotypic variance and phenotypic variance and expresses the degree of similarity between related individuals. In the last step, we calculate the heritability coefficient, which is 4 times the intraclass correlation coefficient and in our case reached the value of 0.16. Based on the calculated heritability coefficient, we can conclude that the number of litters is a low heritability trait and its phenotypic variability is mainly influenced by the environment. In this example we have to calculate the coefficient of repeatability of number of piglets, including its mean error. The numbers of all piglets born to 250 sows for their first four litters were monitored. We know the sum of squares of deviations from the mean between groups, it means between individual mothers , the sum of squares of deviations within groups , and overall in the observed group. The way we calculate the sum of squares is explained in the previous example. Subsequently, we calculate the degrees of freedom. The degrees of freedom for calculating between-group variability is equal to the number of sows minus one. The degrees of freedom for the calculation of variability within the groups are equal to the difference between the number of observed litters and the number of sows. We know from the assignment that we observed 250 sows and 4 litters for each sow, which is a total of 1000 observed litters. For total variability, the degrees of freedom are equal to the number of monitored litters reduced by 1. Finally, we calculate the value of the mean squares as the ratio of the sum of squares and the degrees of freedom. The variability between groups of sows consists of environmental and genetic variance. The environmental variance, sigma E, takes into account the differences within individual groups, in other words, it takes into account the differences in the number of piglets in the observed litters for a particular sow. Genetic variance, sigma G, is estimated based on differences in litter size between groups of sows. The variability caused by the environment is not further partitioned but is equal to the environmental variance sigma-e. Subsequently, we calculate the genetic variance as the difference of between-group and within-group variability divided by the number of repetitions per sow, in our case, it is the number 4, because we monitored 4 litters for each sow. Phenotypic variance is the sum of genotypic variance and environmental variance. Based on the detected variances, we calculate the repeatability coefficient, which in our case reached a value of 0.1424. Finally, we calculate the mean error of the repeatability coefficient, which is at the level of 0.0317. The found repeatability coefficient is low. which means that the similarity between repetitions in the number of piglets born is also very low. Therefore, the number of piglets in the first litter is not authoritative for the number of piglets in the second and subsequent litters. Thank you for your attention.