

SIMPLE SELECTION METHODS FOR ANIMAL IMPROVEMENT IN CHINA

II, Selection for Two or More Traits— Selection Index

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A common way to make up a selection index is using variance-covariance matrices. (S.R.Searle, 1966.)

$$\underline{P} \underline{b} = \underline{G} \underline{a}$$

where, \underline{P} is the variance-covariance matrix of phenotypes, \underline{G} is the variance-covariance matrix of genotypes, \underline{a} is the matrix of economic value and \underline{b} is the matrix of weight factors need to be solved.

It is necessary to estimate parameters like standard deviation and heritability for each trait, phenotypic and genetic correlations between every two traits. The procedure of working out such an index is still rather complex.

The simplified selection index comes from the basic formula of breeding value, but we use a relative form in order to cancel the units of different traits.

$$A = \frac{h^2(P-\bar{P}) + \bar{P}}{\bar{P}} \times 100 \quad (1)$$

where, A is the relative breeding value for a single trait, P is the phenotypic value and \bar{P} is the population mean. Then, the selection index is

$$\begin{aligned} I &= w_1 A_1 + w_2 A_2 + w_3 A_3 + \dots \\ &= \sum_{i=1} w_i A_i \end{aligned} \quad (2)$$

where, I is the selection index, A_i is the relative breeding value and w_i is the weight factor for each trait.

Substituting phenotypic value and heritability into formula (2) We have

$$I = \sum_{i=1} w_i h_i^2 P_i / \bar{P}_i + \sum_{i=1} w_i (1-h_i^2) \quad (3)$$

Since all animals in the same herd have common $w_i (1-h_i^2)$, so that the rank of index values will not change if the second term of formula(3) is neglected. Then, we have

$$I = \sum_{i=1} w_i h_i^2 P_i / \bar{P}_i \quad (4)$$

For it is a simplified index, the weight factor of each trait is simply given out by breeders' experience or market price.

Sometimes breeders like to have an index which makes an animal of average lever at the index of 100. The formula need to be changed a little. That is

$$I = \sum_{i=1} a_i P_i / \bar{P}_i \quad (5)$$

where, a_i is the combined weight factor of w_i and h_i^2 , $\sum_{i=1} a_i = 100$.

Here is an example of making a simplified selection index for a sow. Assuming the following parameters are known.

Litter size born alive (No.) $\bar{P}_1=9$, $h_1^2=0.1$, $w_1=0.3$

Litter size at weanling(No.) $\bar{P}_2=8$, $h_2^2=0.2$, $w_2=0.3$

Litter weight at weanling (lb.) $\bar{P}_3=240$, $h_3^2=0.2$, $w_3=0.4$

First, we calculate the combined weight factors:

$$a_1 = (w_1 h_1^2) 100 / (w_1 h_1^2 + w_2 h_2^2 + w_3 h_3^2) = 17.65$$

$$a_2 = (w_2 h_2^2) 100 / (w_1 h_1^2 + w_2 h_2^2 + w_3 h_3^2) = 35.29$$

$$a_3 = (w_3 h_3^2) 100 / (w_1 h_1^2 + w_2 h_2^2 + w_3 h_3^2) = 47.06$$

where, $a_1 + a_2 + a_3 = 100$

Then, the index is

$$I = (17.65 P_1 / \bar{P}_1) + (35.29 P_2 / \bar{P}_2) + (47.06 P_3 / \bar{P}_3)$$

For the population mean of each trait is known, so that the index become

$$I = 1.96 P_1 + 4.41 P_2 + 0.196 P_3 \quad (6)$$

where, P_1 , P_2 and P_3 are phenotypic values of trait 1, 2 and 3 for every sow respectively.

Two points should be noticed when we use this simplified selection index:

(1) Since we do not consider the correlation between traits, it is better to combine two traits which have negative genetic correlation into one multiple trait. For instance, in egg production we may combine egg number and egg weight into total weight of eggs in a certain period.

(2) To those traits which need to be selected downwards, the weight factors should be given negative values. Such as the back fat thickness in pigs, and the age at first laying in chickens.

Also, a calculating diagram is presented for those farmers who are now still using abacuses. The steps of making a calculating diagram are as follows: (taking formula (6) for an example)

(1) Estimate the range of each trait

Supposing the litter size of born alive and the litter size at weanling are from 3 to 18, and the litter weight at weanling is from

170 to 320 lb., so that the ranges of trait P_1 , P_2 and P_3 are 15, 15 and 150 respectively.

(2) Calculate dividing coefficients

In order to match the range we take the length of each line as 150 units (say, mm.) The dividing coefficients of three lines are

$$L_{P_1} = 150 / (1.96)(15) = 5.102$$

$$L_{P_2} = 150 / (4.41)(15) = 2.268$$

$$L_{P_3} = 150 / (.196)(150) = 5.102$$

(3) Set a complementary line P_0

Assuming the distance between P_2 and P_3 is 100 units, the ratio of L_{P_2} on L_{P_3} is

$$a = L_{P_2} / L_{P_3} = 2.268 / 5.102 = 0.445$$

The distance from P_0 to P_3 is

$$d_{03} = 100 / (1+a) = 69.20$$

and distance from P_0 to P_2 is

$$d_{02} = 100 - 69.20 = 30.80$$

(4) calculate the dividing coefficient of complement line P_0
That is

$$L_{P_0} = L_{P_2} / (1+a) = 2.268 / 1.445 = 1.569$$

(5) Set an index line P_I

Assuming the distance between P_1 and P_0 is 100 units, the ratio of L_{P_0} on L_{P_1} is

$$b = L_{P_0} / L_{P_1} = 1.569 / 5.102 = 0.308$$

The distance from P_I to P_1 is

$$d_{I1} = 100 / (1+b) = 76.45$$

and the distance from P_I to P_0 is

$$d_{I0} = 100 - 76.45 = 23.55$$

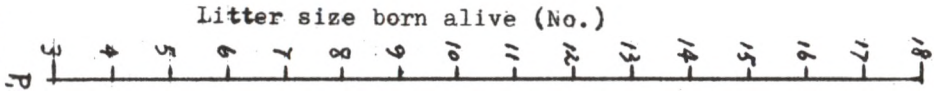
(6) Calculate the dividing coefficient of index line P_I
That is

$$L_{P_I} = L_{P_0} / (1+b) = 1.569 / 1.308 = 1.20$$

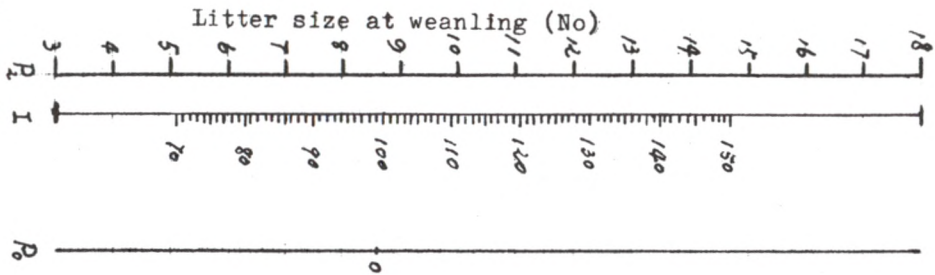
(7) Draw the calculating diagram

Set up the straight lines in the order of P_3 , P_2 , P_0 , P_1 and P_I according to the distance and length that we calculated above. Line P_1 , P_2 and P_3 are divided by their ranges equally, but no graduation on line P_0 .

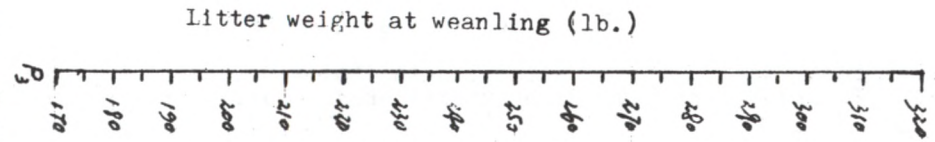
窝产仔数



断奶仔数



断奶窝重



(8) Find out the point of index value 100 on line P_I

First, we connect \bar{P}_2 and \bar{P}_3 , that is 8 and 240, on line P_2 and P_3 with a ruler, and get a intersection point, o , on line P_0 . Then, connect point, o and \bar{P}_1 that is 9 on line P_1 , and get a intersection point on line P_I . That point is the index value of 100.

(9) The index line P_I is divided by the dividing coefficient, 1.20, upwards and downwards from the point of 100.

(10) Measure an index value

Assuming the records of a sow are that $P_1=12$, $P_2=8$ and $P_3=250$. We put a ruler on the graduation of 8 and 250 on line P_2 and P_3 , and get a intersection point on the complement line P_0 . Then we connect that point with the graduation of 12 on line P_1 , and get a point on line P_I , 107.8 that is the index value of the sow. (approximate reading after the decimal place) If we calculate the index by formula (6), we shall have the same result.

$$I = 1.96(12) + 4.41(8) + .196(250) = 107.8$$

Notice for making a calculating diagram:

(1) It needs not to have a complement line in a diagram of two traits, but it needs to have two complement lines in a diagram of four traits. The number of complement line is $n-2$, where n is the number of trait in the selection index.

(2) To those traits which are selected downwards, the line of phenotypic value should be put upside down. That means the lower the phenotypic value, the higher the index.

REFERENCES

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Wu, C., 1977. Heredity and Breeding, 4: 32-34; 5: 31-34.
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