

SELECTION FOR RECESSIVE FAVORABLE GENES ON QUANTITATIVE TRAITS*

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SUMMARY

If a quantitative trait is affected by polygenes in which recessive brings beneficial effect. In that case, ordinary selection methods such as individual selection, family selection will not be efficient. Sometimes it may lead to a wrong selection. In order to show the existence of recessive favorable genes in quantitative traits, a comparison of purebred and crossbred selection has been done in an experiment on *Drosophila*. It is the result that selection on crossbred is more efficient than on purebred. The method of selection for recessive favorable genes is presented in this paper. It can be applied to improve performances of local breeds, especially to those traits which had been selected for a long time but still got very little progress.

INTRODUCTION

Methods of selection that we are using very often in animal breeding are individual selection and family selection. The former is based on individual's performance and the latter is based on performances of its relatives. Generally speaking, individual selection is used for high heritability traits and family selection for low heritability traits. The methods are available for most quantitative traits and have got quite good results, but for a few traits like litter size in pigs still very little progress have been achieved after long term selection. The reason of that may be due to the influence of recessive favorable genes.

HYPOTHESIS

Usually the effects of polygenes can be divided into three parts: additive, dominance and epistasis. In the situation of natural selection the population remains dominant genes which are mainly favorable to animal themselves but unfavorable to human being because of low output of production. On the contrary, recessive genes in quantitative traits are mainly favorable to human being. They contribute more meat, milk, wool and eggs to us, but it is no good at all to animal themselves. If we consider a local breed which has not been selected systematically. In that case, the natural selection becomes more important, and the population leaves more dominant unfavorable genes. Let us take two individuals, X and Y, from the population for an example. Their genotypes are assumed to be AABbCcDd for X, and aaBBCCDD for Y. We use capital letters representing dominant genes which contribute half unit of production at each locus, and use small letters representing recessive genes which contribute one unit of production when the locus is homozygous. Therefore the output of individual X is

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$0.5 + 0.5 + 0.5 + 0.5 = 2.0$ units and of individual Y is $1.0 + 0.5 + 0.5 + 0.5 = 2.5$ units. Individual X has more recessive favorable genes (three) but less output, and individual Y has less recessive favorable genes (two) but higher output. In the case of mass selection, X will be cutted out and Y be remained. Even if in family selection such as sib test or progeny test, the recessive favorable genes are covered by dominant genes. Still, it will not be selected correctly.

In order to solve this problem, a highly selected breed (or line) need to be taken for test cross. Under the hypothesis, the breed should have a high frequency of recessive favorable genes that is to have very good performance on the trait which is going to be improved in another breed.

Suppose the corresponding loci in high performance breed are recessive homozygotes, say aabbccdd. The test crosses of individual X and Y will be (1) AABbCcDd x aabbccdd and (2) aaBBCCDD x aabbccdd respectively. There are eight genotypes in offspring of test cross (1): AaBbCcDd, AaBbCcdd, AaBbccDd, AaBbccdd, AabbCcDd, AabbCcdd, AabbccDd and Aabbccdd. Assumed as before, dominant genes contribute half unit at each locus, and recessive genes contribute one unit when it is homozygous at a locus. The average output of offspring in test (1) therefore is 2.75 units. For test cross (2), since that is only one genotype, aaBbCcDd in offspring, so the average output is 2.5 units. Then we can find out individual X is better than Y.

Of course, individuals taken from a highly selected breed are not necessary homozygous in all loci. They may be Aabbccdd or aaBbCcdd. The test cross still can be done although more offspring be required.

VERIFICATION OF THE HYPOTHESIS

According to above hypothesis, if a quantitative trait is mainly affected by recessive favorable genes, the response of selecting on crossbred should be better than on purebred. To prove that, an experiment was designed as follows:

Material and method

1. Material used: *Drosophila melanogaster*
2. Trait observed: Number of bristles (ocellar)
3. Lines of *Drosophila*: (1) Wild type in which the number of bristles varied from 6 to 9. It was the line needed to be improved. (2) Low bristle line in which the number of bristles mostly was zero. It was the line that had already been highly selected.
4. Direction of selection: Selected downwards that was to select less bristles every generation to simulate as reducing backfat thickness in pigs or days period of frist laying in chickens. It also could be selected upwards to simulate higher lean meat percentage, more piglets per litter, higher milk yield, more egg numbers and so on. In that case, a high bristle line would be needed for test crossing.
5. Selection method: (1) Selected on crossbred. 10 wild type males were taken at random from the population and each male mated with 5 females of low bristle line. The same 10 males, after they had mated with low bristle line females in two days, each one mated with 5 wild type females to produce next generation. But only two families which selected on the base of crossbred family mean would be the parents of next generation. (2) Selected on purebred. 10 wild males each one mated with 5 females from the same population. Two out of ten families were selected each generation according to their lowest family means of bristle number.

Result

The experiment lasted 11 generations of selection. Mean, variance, covariance, heritability and genetic correlation had been calculated. From the figures in Table 1 the result of selection on crossbred was better than on purebred. It proved the existence of recessive favorable genes in certain trait.

Table 1 Average number of bristles in each generation

Generation	Selected on crossbred	Selected on purebred	Difference
0	6.57	6.68	-0.11
1	6.78	6.83	-0.05
2	6.41	6.33	0.08
3	5.88	6.15	-0.27
4	5.43	5.84	-0.41*
5	5.51	5.89	-0.38*
6	5.37	5.70	-0.33
7	5.03	5.48	-0.45*
8	4.19	4.87	-0.68**
9	4.24	4.58	-0.34
10	3.67	4.60	-0.93**
11	3.12	3.87	-0.75**

* $P < 0.05$;

** $P < 0.01$

DISCUSSION

1. As compared generation 11 with generation zero, the number of bristles reduced 53% by selection on crossbred and 42% on purebred. It seemed that both selections were efficient. Selection on crossbred was even better than selection on purebred that was because of the effect of recessive favorable genes.

2. It is important to know whether a quantitative trait is mainly effected by recessive favorable or not. A test cross between high producing breed and low producing breed is suggested. If the average yield of F_1 is closer to high producing breed, that is the effect of dominant favorable or heterosis. If the average yield of F_1 is closer to mid-parent, that is the effect of additive. And if the average yield of F_1 is closer to low producing breed, that is the effect of recessive favorable (or dominant unfavorable).

3. In order to achieve a better result of selection on crossbred such as in a scheme of reciprocal recurrent selection, following conditions are required:

(1) The existence of recessive favorable genes in the trait which is going to be selected.

(2) A higher correlation between the selection on crossbred and on purebred.

- (3) Large number of offspring in each family.
- (4) Large number of families in the selection scheme to reduce inbreeding level because it may rise rapidly after several generations.

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