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Reshaping of Good Mondelian Characteristics in Fine Breed of Yellow Cattle

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Abstract: Using probability matrix, the efficiencies of 4 different breeding systems, animal cloning, superovulation and embryo transfer, breeding of hybrid animals with desirable phenotype in themselves and multiple testcross, in maintaining general genetic diversity were probed while restoring Mondelian characteristics of fine breed in cattle. The results showed that the ratio between the cull rates of neighboring generations was also the ratio between inbreeding increment and the loss of genetic diversity under different systems. In the restoration of characteristics of the fine breed, system is far higher in efficiency than system III. Using the wild type and 3 mutation types of *Drosophila melanogaster* as subjects, the selection and breeding process were simulated and the results conformed to theoretic investigation. The findings demonstrated that, in the project to rescue fine breeds in cattle, the multiple testcross system is a better way to reshape the good Mondelian breed characteristics.

Key words: Fine breed of yellow cattle, rescue of breed, good mondelian, characteristic of breed

INTRODUCTION

To restore and promote the good characteristics of the well-known 5 fine breeds, Qinchuan, Luxi, Jinnan, Nanyang and Yanbian, selection within the breed is the basis of rescuing these fine breeds so as to cultivate modern breeds of beef cattle in China. The project involves over 20 Mondelian traits related to adaptability, meat quality and breed traits. With the intrinsic fine features as standards, the homozygosis of relevant gene loci is the selection target of these traits (Chang and Miao, 1988; Chang *et al*., 2003). Since, the 5 good breeds are limited in present scale (Chang, 2001), all the other gene loci should be kept the general genetic diversity while making specific gene loci homozygosized.

Maintenance of population genetic diversity: For the inbreeding coefficient F of a population is, in the sense of traceable pedigree, the mean value, for the whole group, of the probability of a pair of allelic genes of every individual being reproduced from the same gene of their common ancestor. The other value, the random mating index, corresponds to the gene heterozygosity (H) representing genetic diversity in a population, therefore, the inbreeding increment

$$\Delta F = 1 - P_t \cdot P_{t-1}^{-1}$$

of 2 neighboring generations (t-1, t) is an indicator of the loss of genetic diversity.

Provided that linkage and genetic co-adaptation is not considered, the influence of the selection at the few specific loci on the whole genome takes place at random. Therefore, the filial population of cattle may be regarded as samples from parent gamete group. The increment of inbreeding coefficient between the 2 generations will be related to gene frequency q and its sampling variance $\sigma^2_{\Delta q}$ and will be ultimately dependent on the scale of cattle population N and sampling rate of:

$$\Delta F = \sigma^2_{\Delta q} \cdot q^{-1}(1-q)^{-1} = \frac{q(1-q)(1-f)[2-(N-1)]^{-1}}{q(1-q)}$$
$$= (1-f)[(2(N-1)]^{-1}$$

From the angle of breeding science, f and (1– f) are, respectively percentage of animals used for breeding and percentage of the cull.

There are 4 possible ideas about the basic breeding system of the rescue endangered breeds: animal cloning (I), superovulation and embryo transfer (II, MOET in the broad sense), breeding of hybrid animals with desirable phenotype in themselves (III) and multiple testcross (IV). If we use f_1, f_2, f_3 and f_4 and S_1, S_2, S_3 and S_4 to, respectively stand for percentage of animals used for

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breeding and percentage of the cull of one generation under the 4 systems, for the reeds with a certain scale, the percentage of the cull has the following ratio under different systems:

$$\frac{S_x}{S_y}=\frac{(1-f_x)}{(1-f_y)}=\frac{(1-f_x)[2(N-1)]^{-1}}{(1-f_y)[2(N-1)]^{-1}}=\frac{\Delta F_x}{\Delta F_y}$$

Against the background of the breeding technology of yellow cattle in China, the last two systems have similar percentages of the cull ($S_3 \approx PS_4$). Provided that the technological costs are sufficiently compensated and the necessity is embodied, $S_1>>S_2>>S_3$. If the percentages of the cull under the systems of animal cloning and MOET are, respectively 1,000 and 50 times that of multiple testcross, the loss of genetic diversity in the first two groups is also 1,000 and 50 times that of the last.

Progress of homozygosis at specific loci: Strict phenotypic selection with a generation may realize the homozygosis of recessive genes. The problem lies in the homozygosis of many dominant genes, which are not linked. If the donors are identified phenotypically in cloning of animal embryos and somatic cells, it will be inevitable that the population continues its character segregation after it enters into the normal reproduction process. The progress of homozygosis under MOET system depends on the selecting methods aiming at specific loci. Breeding of hybrid animals with desirable phenotype in themselves is in essence phenotypic selection plus mating like to like for phenotype and its level of homozygosis was already quantitatively analyzed at the end of the last century (Yang, 1979; Chang *et al*., 1988). The so-called multiple testcross system refers to the practice in which a group of multiple recessive type of female animals or several groups of recessive type of female animals at different loci, or a group or several groups of heterozygous female animals containing recessive genes at many loci carry out testcross at various loci on reserved male animals. Replacement sires of multiple dominant type of homozygosis are selected through many generations and female are only typically selected at the beginning of testcross. No selection at these loci shall take place later on.

Homozygosis progress under multiple testcross system: For n dominant genetic types, there are n+1 possibilities in the number of homozygosized loci. If j and i stand, respectively for number of heterozygous loci (j= 0, 1, 2, … n; I = 0, 1, 2, … n) of the maternal and filial generations, the following (n+1)(n+1)-dimensional probability matrix may be established by the corresponding relationship between them, under the condition of bull mating of n dominant homozygosis:

$$A=\begin{bmatrix}
1 & \frac{1}{2} & \cdots\cdots & (\frac{1}{2})^j & \cdots\cdots & (\frac{1}{2})^n \\
0 & \frac{1}{2} & \cdots\cdots & j(\frac{1}{2})^j & \cdots\cdots & n(\frac{1}{2})^n \\
\vdots & 0 & & \vdots & & \vdots \\
\vdots & \vdots & & \vdots & & \vdots \\
\vdots & \vdots & & C_j^i(\frac{1}{2})^j & \cdots\cdots & C_n^i(\frac{1}{2})^n \\
\vdots & \vdots & & \vdots & & \vdots \\
\vdots & \vdots & & \vdots & & \vdots \\
\vdots & \vdots & & (\frac{1}{2})^j & & \vdots \\
\vdots & \vdots & & & & \vdots \\
\vdots & \vdots & & 0 & & \vdots \\
\vdots & \vdots & & \vdots & & \vdots \\
\vdots & \vdots & & \vdots & & \vdots \\
\vdots & \vdots & & \vdots & & \vdots \\
0 & 0 & \cdots\cdots & 0 & \cdots\cdots & (\frac{1}{2})^n
\end{bmatrix}$$

$$a_{(i+1)(j+1)}=C_j^i(\frac{1}{2})^j$$

As far as restoration of breed features is concerned, the worst situation is that all the existing n dominant types are n heterozygosis (the male animal of n dominant homozygote can only be obtained from its next generation). Column vector may be established for the ratio of various categories classified by the next generation dominant type in accordance with the number of homozygosized loci.

$$b=\begin{bmatrix}
(\frac{1}{3})^n \\
n(\frac{1}{3})^{n-1}(\frac{2}{3}) \\
C_n^2(\frac{1}{3})^{n-2}(\frac{2}{3})^2 \\
\vdots \\
\vdots \\
C_n^{n-1}(\frac{1}{3})(\frac{2}{3})^{n-1} \\
(\frac{2}{3})^n
\end{bmatrix}$$

Therefore, after t generations, the probability of various individuals in the cattle populations shows as follows:

$$P_t = A^t b \quad (1)$$

Solve the characteristic equation of matrix A and the characteristic value is:

$$\lambda = 1, \frac{1}{2}, \frac{1}{4}, \ldots\ldots \frac{1}{2^n}$$

Put the characteristic vallues into linear transformation equation A x = λ x and the corresponding characteristic vector is obtained. Standardize the characteristic vector and the result:

$$\lambda = 1 \quad [1 \ 0 \ \cdots\cdots]^T$$

$$\lambda = \frac{1}{2} \quad [\frac{1}{\sqrt{2}} \ -\frac{1}{\sqrt{2}} \ 0\cdots\cdots]^T$$

$$\lambda = \frac{1}{2^j} \quad \left[(-1)^0[\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}} \quad (-1)^1 j[\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}} \cdots (-1)^i C_j^i[\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}} \cdots\cdots (-1)^j C_j^i[\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}}\right]^T$$

$$\lambda = \frac{1}{2^n} \quad \left[[\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}} - n[\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}} \cdots\cdots (-1)^i C_n^i[\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}} \cdots (-1)^n[\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}}\right]^T$$

So, the matrix composed of vectors characteristic of standardization forms:

$$U = \begin{bmatrix} 1 & \frac{1}{\sqrt{2}} & \cdots & [\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}} & \cdots & [\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}} \\ 0 & -\frac{1}{\sqrt{2}} & \cdots & -j[\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}} & \cdots & -n[\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}} \\ \vdots & & & \vdots & & \vdots \\ \vdots & 0 & & \vdots & & \vdots \\ \vdots & \vdots & & \vdots & & \vdots \\ \vdots & \vdots & \cdots & (-1)^i C_j^i[\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}} & \cdots & (-1)^n C_n^i[\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}} \\ \vdots & \vdots & & & & \\ \vdots & \vdots & & \vdots & & \vdots \\ \vdots & \vdots & & \vdots & & \vdots \\ 0 & 0 & \cdots & 0 & \cdots & (-1)^n[\sum_{i=0}^{n}(C_n^i)^2]^{-\frac{1}{2}} \end{bmatrix}$$

$$U_{(i+1)(j+1)} = (-1)^i C_j^i[\sum_{i=0}^{j}(C_j^i)^2]^{-\frac{1}{2}}$$

Its inverse is worked out: $U^{-1} = H =$

$$\begin{bmatrix} 1 & \cdots & (-1)^0 C_j^0[\sum_{i=0}^{0}(C_0^i)^2]^{\frac{1}{2}} & \cdots & (-1)^0 C_n^0[\sum_{i=0}^{n}(C_0^i)^2]^{\frac{1}{2}} \\ 0 & \cdots & (-1)^1 C_j^1[\sum_{i=0}^{1}(C_1^i)^2]^{\frac{1}{2}} & \cdots & (-1)^1 C_n^1[\sum_{i=0}^{1}(C_1^i)^2]^{\frac{1}{2}} \\ \vdots & & \vdots & & \vdots \\ \vdots & \cdots & (-1)^m C_j^m[\sum_{i=0}^{m}(C_m^i)^2]^{\frac{1}{2}} & \cdots & (-1)^n C_n^m[\sum_{i=0}^{m}(C_m^i)^2]^{\frac{1}{2}} \\ 0 & \cdots & (-1)^n C_j^n[\sum_{i=0}^{n}(C_n^i)^2]^{\frac{1}{2}} & \cdots & (-1)^n C_n^n[\sum_{i=0}^{n}(C_n^i)^2]^{\frac{1}{2}} \end{bmatrix}$$

$$h_{(m+1)(j+1)} = (-1)^m C_j^m[\sum_{i=0}^{m}(C_m^i)^2]^{\frac{1}{2}}$$

Also, compose the diagonal matrix D with the characteristic value of Matrix A and work out its t power:

$$D^t = \begin{bmatrix} 1 & & & & & & \\ & \frac{1}{2^t} & & & & & \\ & & \frac{1}{2^{2t}} & & & & \\ & & & \ddots & & & \\ & & & & \frac{1}{2^{mt}} & & \\ & & & & & \ddots & \\ & & & & & & \frac{1}{2^{nt}} \end{bmatrix}$$

In the formula, (m+1) is the column ordinal mark of Matrix D.

$\therefore A^t = UD^tH$: Put the values of the elements U, D^t and H into the formula and the result is:

$$A^t = \begin{bmatrix} \frac{(2^t-1)^0}{2^{0t}} & \frac{(2^t-1^1)}{2^t} & \cdots\cdots & \frac{(2^t-1)^{j-0}}{2^{jt}} & \cdots\cdots & \frac{(2^t-1)^{n-0}}{2^{nt}} \\ 0 & \frac{(2^t-1)^0}{2^t} & \cdots\cdots & C_j^i\frac{(2^t-1)^{j-1}}{2^{jt}} & \cdots\cdots & C_n^i\frac{(2^t-1)^{n-1}}{2^{nt}} \\ \vdots & 0 & & \vdots & & \vdots \\ \vdots & \vdots & & \vdots & & \vdots \\ & & \cdots\cdots & C_j^i\frac{(2^t-1)^{j-i}}{2^{jt}} & \cdots\cdots & C_n^i\frac{(2^t-1)^{n-i}}{2^{nt}} \\ \vdots & \vdots & & \vdots & & \vdots \\ \vdots & \vdots & & \vdots & & \vdots \\ 0 & 0 & \cdots\cdots & 0 & \cdots\cdots & C_n^n\frac{(2^t-1)^{n-n}}{2^{nt}} \end{bmatrix}$$

In the formula (i+1) is the row ordinal mark of Matrix A^t; i=0, 1, 2, … n; (j+1) is its column ordinal mark; j = 0, 1, 2, … n. The general formula of various A^t elements is:

$$C_j^i(2^t-1)^{j-i}/2^{jt}$$

Put A^t into Eq 1, then: ${}_4Pr_t$=

$$\begin{bmatrix} C_n^0(\frac{3\times 2^{t-1}-1}{3\times 2^{t-1}})^n \\ C_n^1(\frac{3\times 2^{t-1}-1}{3\times 2^{t-1}})^{n-1}(\frac{1}{3\times 2^{t-1}})^2 \\ C_n^2(\frac{3\times 2^{t-1}}{3\times 2^{t-1}})^{n-2}(\frac{1}{3\times 2^{t-1}})^2 \\ \vdots \\ \vdots \\ C_n^{n-1}(\frac{3\times 2^{t-1}-1}{3\times 2^{t-1}})(\frac{1}{3\times 2^{t-1}})^{n-1} \\ C_n^n(\frac{1}{3\times 2^{t-1}})^n \end{bmatrix}$$

A matrix equal to A may be set up according to the ratio between various individuals and various gametes which they produce and which carry n to zero dominant genes. Therefore, in the a generation, the probability of various gametes is:

$${}_4Pb_t = A\,Pr_t = \begin{bmatrix} C_n^0(\frac{3\times 2^t-1}{3\times 2^t})^n \\ C_n^1(\frac{3\times 2^t-1}{3\times 2^t})^{n-1}(\frac{1}{3\times 2^t}) \\ C_n^2(\frac{3\times 2^t-1}{3\times 2^t})^{n-2}(\frac{1}{3\times 2^t})^2 \\ \vdots \\ \vdots \\ C_n^{n-1}(\frac{3\times 2^t-1}{3\times 2^t})(\frac{1}{3\times 2^t})^{n-1} \\ C_n^n(\frac{1}{3\times 2^t})^n \end{bmatrix}$$

So, under multiple testcross system, the probabilities of various zygotes classified according to the number of homozygosized loci and various gametes classified according to the carried number of dominant genes are, respectively the expanded items of the following 2 binomial expressions:

$$(\frac{3\times 2^{t-1}-1}{3\times 2^{t-1}}+\frac{1}{3\times 2^{t-1}})^n=1 \text{ and}$$

$$(\frac{3\times 2^t-1}{3\times 2^t}+\frac{1}{3\times 2^t})^n=1_0$$

A comparison between system III and system IV in the progress of homozygosis: Yang Jike (1979) and Chang Hong *et al.* (1988; 1995) have proved the progress of homozygosis under system of breeding of hybrid animals with desirable phenotype in themselves, taking the ideal type generation of livestock colony as F_1 generation. Under this system, the ratios of various phenotypes classified according to the number of dominant characters are the unfolded items of the following binominal expression:

$$(\frac{t^2-1}{t^2}+\frac{1}{t^2})^n=1;$$

In the animal group of n dominant type (the so-called ideal type), the ratios of various types of genes classified according to the number of homozygosized loci are the unfolded items of the following binominal expression:

$$(\frac{t-1}{t+1}+\frac{2}{t+1})^n=1$$

Therefore, in the cattle populations of different generation, the individual probability of homozygosis of all loci is:

$${}_3Pr_{D\cdot t}=(\frac{t-1}{t})^{2n}$$

But, under the multiple testcross system, this probability is:

$${}_4Pr_{D\cdot t}=(\frac{3\times 2^{t-1}-1}{3\times 2^{t-1}})^n$$

When, n = 2, 3, 4, the multiple testcross system can, only within 5-6 generations, make dominant homozygotes of n loci take up over 95% of the cattle population. But for the former, it takes 78.48, 117.48 and 156.47 generations to each the same level. The breeding of hybrid animals with desirable phenotype in themselves is 2 generations earlier than the latter in planning start time. Based on the start point of the latter, the rate of progress of homozygosis under the 2 systems is illustrated in Fig. 1:

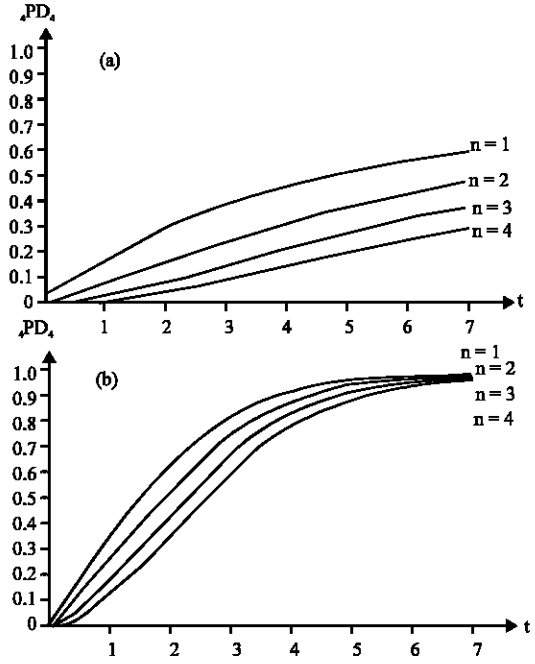

Fig. 1: The probaailities of dominant homozygote at n loci in livestock colony for different generation ($Pr_{D\cdot t}$)

- ${}_3Pr_{D\cdot t} = \varphi(t) = (\frac{t-1}{t})^{2n}$,
  breeding of hybrid animals with desirable phenotype in themselves
- ${}_4Pr_{D\cdot t} = \varphi(t) = (\frac{3\times 2^{t-1}-1}{3\times 2^{t-1}})^{n}$ multiple testcross

Simulated test: The simulated test of *drosophila melanogaster* is to test the result of the above theoretic investigation on the progress of homozygosis under the two systems of multiple testcross and breeding of hybrid animals with desirable phenotype in themselves.

MATERIALS AND METHODS

The following 4 prototypic varieties of *drosophila melanogaster:*

- Wild type, i.e. wild type in *drosophila melanogaster*, represented by ++/++ in this essay.
- Vestigial wing type, i.e. vestigial wing in *drosophila melanogaster*. It is a recessive mutation type of genetic locus with 67 Morgan of the second chromosome, represented by vg+/vg+.
- Ebony body, i.e. ebony body in *drosophila melanogaster*. It is a recessive mutation type of genetic locus with 70.7 Morgan of the third chromosome, represented by +e/+e.
- Ebony body with vestigial wing in *drosophila melanogaster*. It is the double mutation type of the above 2 loci, represented by vg e/vg e.

Methods: The wild type with stable heredity is chosen and bred through the 2 systems of breeding of hybrid animals with desirable phenotype in themselves [III] and multiple testcross [IV], with ebony body in *drosophila melanogaster* and vestigial wing in *drosophila melanogaster* as parents in hybridization. The former takes the filial generation of primary hybridization as F_1 from which inner-colony mating starts. Wild male and female *drosophela melanopasters* are retained as breeds for several generations. From its F_2 generation populations are selected some wild type female *drosphila melanogasters* to mate with wild type males from primary populations (simulate male cattle of double dominant homozygosis selected by multiple testcross). The breeding group of the IV system is set up with the filial generation as F_1 and it mates with the wild type male from the primary population for each generation. The phenotypic ratio under the 2 systems is recorded for each generation. Some wild type males are taken at random from different groups of the 2 systems to mate female ebony body with vestigial wing by testcross. The frequency of various gametes is monitored. The sampling number for generations of breeding is all 20 pairs, except for F_2 breeding animals and F_2 to F_4 testcross group of system IV whose number is 50 pairs.

The following formula is used to analyze the probability of x^2 value:

$$\beta = 1 - \int_0^{(x^2)} \frac{1}{2^{(\frac{df}{2})}[\Gamma(\frac{df}{2})]} (x^2)^{\frac{df}{2}-1} \cdot e^{-(\frac{1}{2})(x^2)} d(x^2)$$

RESULTS

Phenotypic ratio population from each generation: The total numbers of emergence of F_1, F_2, F_3 in system IV are, respectively 281, 345 and 983, all belonging to wild type. The distribution of phenotypes in system III is shown in Table 1.

From Table 1, the phenotypic ratios of each generation of in the system of breeding of hybrid animals with desirable phenotype in themselves conform to the

Table 1: Phenotypic distribution of different generations of system III

	N	±	vg/vg ± and ± e/e	vg/vg e/e	$\chi^2(\beta)$
F_2	674	391	243	40	0.86(0.6505)
F_3	274	223	48	3	0.93(0.6281)
F_4	430	394	40	2	2.77(0.2503)
F_5	371	345	26	0	0.86(0.6505)

Table 2: Phenotypic distribution of offspring of each generation from wild type male in *Drosophila melanogaster*

		N	±	vg/vg ± and ± e/e	vg/vg e/e	$\chi^2(\beta)$
I	F_2	308	138	138	32	0.16(0.9231)
	F_3	397	226	150	21	0.63(0.7298)
	F_4	359	214	134	11	5.05(0.0801)
II	F_1	406	287	110	9	0.62(0.7334)
	F_2	822	674	144	4	3.59(0.1661)
	F_3	704	634	70	0	4.84(0.0889)

Table 3: The percentage of double dominant homozygosity in populations of different generations

			Discrepancy from expectant	
		Percentage	t	β
	F_2	6.03±1.21	0.041	>0.50
	F_3	19.88±1.99	0.015	>0.50
III	F_4	20.91±2.33	0.840	>0.25
	F_1	45.81±2.76*	0.123	>0.50
IV	F_2	64.96±0.92*	0.688	>0.25
	F_3	80.11±0.73	0.757	>0.25

result of theoretic study. As for restoration of phenotypic characteristics of breed, the system IV is more efficient.

Phenotypic ratios of descendants of each generations wild type male by testcross: The phenotypic ratios of generations in the 2 systems are in agreement with the corresponding theoretic gamete frequency (Table 2). The formula for the progress of homozygosis under the 2 systems is confirmed. The 2 systems are of great discrepancy in the progress of homozygosis.

Ratios of double dominant homozygotes in populations of each generation: According to the ratio of wild types of each generation and the phenotypic distribution of their descendants from testcross, the proportion of double dominant homozygotes in the population is estimated as follows (Table 3):

Differences between corresponding generations under two systems are significant extremely.

The results are all in agreement with theoretic study. The F_1 and F_2 generations of system IV are, respectively 25.93 and 44.05% higher than the corresponding generations (F_3 and F_4) of system III in the ratio of double dominant homozygotes ($p<0.01$).

DISCUSSION

About system I and II: The thremmatological effects of animal cloning and MOET system can greatly promote the seedstock ratio of only a few or only 1 or 2 individuals in the population. In China today, the population of the fine breed yellow cattle is sharply reducing, or even on the verge of endangered and it is urgent to maintain genetic diversity in the breed. In such a situation neither of the two systems is feasible. As an auxiliary technology in promoting the homozygosis progress of Mondelian character, its application has to be based on the genotypic selection aided by testcross. Considering that no molecular genetic mark about good Mondelian character in yellow cattle is available which is mature enough for application, the donor should be determined according to testcross (or descendant test) results instead of phenotype. It is non-scientific, anti-natural and infeasible to wish to select donors according to phenotype generation after generation and to use animal cloning and MOET to replace normal reproductive methods to restore the breed features.

Difficulties possible in system IV: When n is relatively great, the probability of emergence of n dominant homozygotes is relatively low at the beginning of implementation of system IV. In such a situation, only the male cattle with maximal (suppose: amount to n-k) homozygosized loci through multiple testcross can be kept as breeds. Even so, the F_1 is still for higher than the corresponding generation (F_3) of III system in n dominant homozygotes. The ratio of the2o is:

$$[(3\times 2^{t-1}-1)(t+3)/3\times 2^{t-1}(t+1)]^{n-k}=1.3^{n-k}$$

Another difficulty at the beginning of implementation is that the number of animals receiving test is too great when n is comparatively big. This is the limit to the application of the system. With the contemporary technology, it is preferable to implement it when n ranges from 2-5, depending on the specific conditions of breeds and cattle populations.

CONCLUSION

In the endeavor to rescue the fine breed of yellow cattle, the breeding system of multiple testcross is comparatively a better method to reshape the good Mondelian breed characteristics.

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