

PREDICTION OF DIFFUSION OF HOLSTEIN GENES WITHIN
THE FRENCH FRIESIAN POPULATION

Previsiones sobre la difusion de genes Holstein en el
interior de la poblacion Pie-Noire Francesa

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INTRODUCTION

Like in most West European countries, the Holstein breed is spreading dramatically in France (tables 1 and 2). This extension is probably linked to the present economic context, in which emphasis is laid on milk capacities.

The consequence of these facts on our national milk and beef production may be evaluated by estimating the diffusion of Holstein genes at first.

A first attempt made in France some years ago (COLLEAU, 1978) showed that the French Friesian population would most likely be strongly penetrated by the Holstein genes.

The purpose of the present paper is to give the main results of a second work, taking into account the recent acceleration of the process, especially in young bulls.

CALCULATION GOALS AND PRINCIPLES.

The purpose of our calculations was to evaluate for the next 15 years (1982-1997), the degree of diffusion of Holstein genes within the French Friesian "commercial" populations directly involved in the national milk and beef production, opposite to the "selection" populations :

- young calf populations
- lactating cow populations.

When programming the calculations, versatility was required since the diffusion of Holstein genes results at any moment from two phenomena:

1-The consequences of former imports of Holstein breeding animals that could be foreseen from a model by defining simulation rules (genetic and demographic parameters, selection procedures).

2-The consequences of recent imports that escaped the model since the involved breeding animals were not born in France.

Thus, we worked iteratively from the first imports of Holstein animals (1968), applying a native selection scheme, the parameters of which are exposed in table 3. That selection enhances the diffusion of Holstein genes.

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TABLE 1 - Genetic distribution of the French Friesian bulls before testing

Year of birth	Frequencies of the genetic categories					Average frequency of Holstein genes
	0% HF	25%	50%	75%	100% HF	
68	93		2		5	6
69	92				8	8
70	85	1	3		11	13
71	73	1	9		16	21
72	63	1	11	1	25	31
73	57	3	13		27	34
74	57	1	10	1	31	37
75	51	4	17	3	26	37
76	42	4	14	8	32	46
77	31	4	19	11	35	54
78	10	2	22	9	57	75
79	5	1	22	20	51	78

TABLE 2 - Genetic distribution of the French Friesian service A.I. bulls

Year	Frequencies of the genetic categories					Average frequency of Holstein genes
	0% HF	25%	50%	75%	100% HF	
68	99,6				0,4	0,4
69	99				1	1
70	98				2	2
71	96,5				3,5	3,5
72	95				5	5
73	94		1		6	6
74	96				4	4
75	91		2		7	8
76	88		2		10	11
77	83		2		15	16
78	77	0,5	3		19	21
79	61	1	8		30	34

Table 3 - Hypotheses and parameters considered in the model

- 1 The selection criterion used is the average "valuable solid yield" (AVS), as defined by POUTOUS and al (1981) $AVS = 1/2 (FY+1,2PY)$ with FY, PY= fat yield, protein yield, respectively.

- 2 The difference pure Holstein - pure European Friesian is 25 kg AVS, with a genetic within breed standard deviation of 17 kg AVS (BONAITI and MOCQUOT, 1982 ; MOCQUOT and BONAITI, 1982).

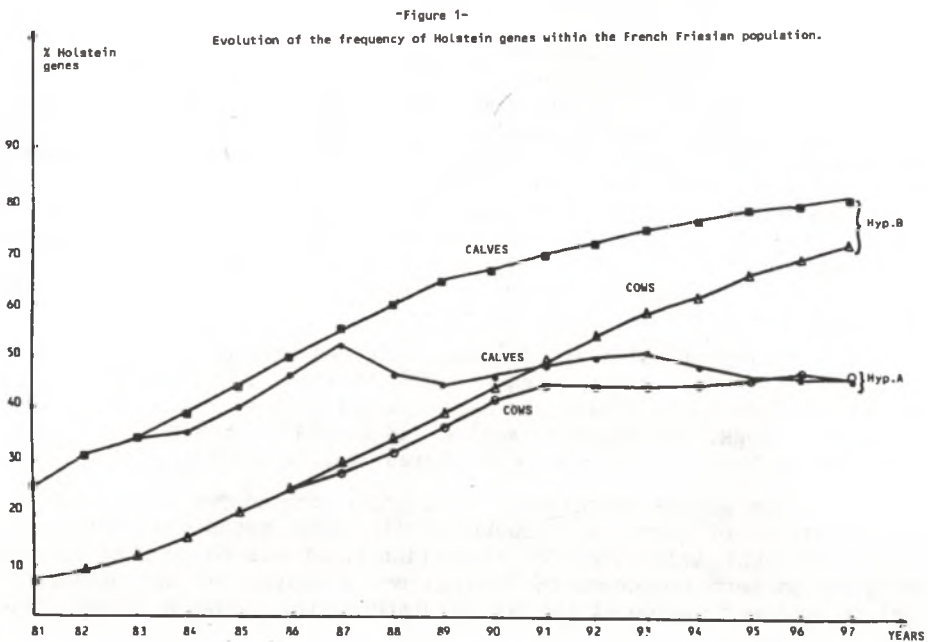
- 3 The bull sires are chosen within the upper 3% for AVS, the average accuracy being 0.85.

- 4 The bull dams are chosen within the upper 3% for AVS of cows with at least 3 lactations, the average accuracy being 0.50.

- 5 Young bulls are tested at the age of six years. 15% of all A.I. are made by these bulls

- 6 Service bulls are chosen within the upper 45% for AVS. Subsequent utilisation is supposed to be steadily 2 years and independant of genotype

- 7 Cows are supposed to be used during 8 lactations at the most (first calving at 3 years). Culling rate is equal to 25%, except after lactation 8.



The import of Holstein bulls having been steady since that date especially that of young bulls intended for testing, we should replace the predicted model values of Holstein gene frequencies by the values actually observed. The model was thus constrained during 12 consecutive years for young bulls (bulls from 1968 to 1979) and for service bulls (inseminations from 1968 to 1979), taking into account the real results concerning these groups shown in tables 1 and 2. On the contrary, the model was not constrained at all for the commercial groups (calves, milking animals) because the corresponding imports were considered as negligible.

For long term previsions, animals to be born have to be taken into account. In that respect, the young bull group plays the most decisive role. Within our study, we estimated that the final truth for that group would lie between two extremes:

1 - Hypothesis A

From 1981 on, the young bulls are bred by home-born or tested animals i.e. total stop of breeding animal or semen imports, the level of diffusion for Holstein genes being estimated as satisfactory and sufficient.

2 - Hypothesis B

The French frontiers remain open and the bulls to be tested are purebred Holstein, either home-born or imported.

BRIEF SURVEY OF THE METHODOLOGY USED

There is no place here to give a full description of calculations, but they will be given in a paper to be published in *Annales de Génétique et de Sélection Animale*.

The main traits of the calculations are the following:

1-The percentages of Holstein genes were processed as discrete variates varying from 1 to 10, corresponding to the segments 0-10%, 10-20%, ..., 90-100% respectively. The interest of that transformation is that with a reasonable loss of accuracy, it will allow us to use a matricial algebra and not too large matrixes contrary to what would have happened if all really possible genotypes obtained after some 20 years of crossbreeding were kept different. Accordingly, we developed matrixes representing the main categories of animals (females, young bulls, service bulls, bull sires, bull dams, etc...), with 10 columns and a varying number of lines, filled with within line frequencies (sums per line = 1).

2 - Mating of males and females scattered through 10 genetic groups led to 19 different genetic groups, *sensu stricto*. All "odd-sum" matings were thus considered as giving the same results as the immediately adjacent "even-sum" matings. For example, mating 3x8 (sum=11) gave the same progeny as 0.5 times mating 5x5 (sum=10) + 0.5 times mating 6x6 (sum=12).

3 - The groups submitted to selection procedures were treated as varying mixtures of normal distributions with known means and variances for the criteria under selection. The truncation point was calculated by iteration using on each component of the mixture a polynomial approximation of the distribution function of the normal distribution (ABRAMOWITZ and STEGUN, 1964).

When the total percentage of selected animals was considered as representing the selection procedure accurately enough, the conditional sub-population frequencies within the selected animals were evaluated and put into the adequate matrixes, for subsequent utilization.

RESULTS

1 - Hypothesis A : closed frontiers

In 15 years, the percentage of Holstein genes will be approximately 50%, for calves as for cows. As a matter of fact, this level will almost be obtained as soon as in 1990.

The 50% level corresponds to the irreversible consequence of all the imports already made.

2 - Hypothesis B : open frontiers and exclusive use of young purebred Holstein bulls.

The curves corresponding to that hypothesis are located above the first ones from 1984 for calves and 1988 for cows. According to that hypothesis, calves will be 80% Holstein and cows 70% Holstein in 1997. The average annual progression frequency will be 3.3% for calves and 3.8% for cows.

CONCLUSION

Despite the simplification of the model, it is obvious that the French Friesian population will be very heavily (50% and more) influenced by the Holstein genes, as soon as in 1987 for calves. That situation may develop similarly in other countries (see the communications at the DUBLIN EEC Seminar, 1981).

The short-term consequences are an abrupt acceleration of the annual genetic progress for milk production (80-100 kg per year as shown by our first approximations) and a deterioration of beef performances which have to be reduced by specific selection procedures.

SUMMARY

A genetic and demographic model is used to evaluate the frequency of the Holstein genes within the French Friesian population. That model takes into account the French selection procedures and the decisions of importing Holstein bulls.

Previsions are relatively accurate till 1987, a year when calves are 50 % Holstein on an average and lactating cows are 33 % Holstein.

At the end of the following ten years (1997), the diffusion of the Holstein genes will amount to very high values (80 % for calves and 70 % for cows) or moderate values (50 % for the two sets) according to the strategic choice made from 1981 on : keep the frontiers opened or closed to new importations.

RESUMEN

Un modelo genético demográfico ha sido utilizado para evaluar la frecuencia de los genes Holstein en la población Pie-Noire Francesa. Este modelo tiene en cuenta los sistemas de selección utilizados en Francia y la política de importación de toros Holstein.

Las previsiones son relativamente precisas hasta 1987, año en el cual los terneros serán 50 % Holstein como media y las vacas en lactación 33 % Holstein.

Al final de los 10 años siguientes (1997), la difusión de los genes Holstein puede llegar a niveles muy elevados (80 % en los terneros y 70 % en las vacas) o por el contrario relativamente moderados (50 % en las dos categorías de animales) según se efectue a partir de 1981 el cierre o la apertura de las fronteras a nuevas importaciones de genes Holstein.

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