Original article

Impact of the use of bovine somatotropin (BST) on dairy cattle selection

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Summary -- A very simple breeding scheme for milk yield was generated by a Monte-Carlo method in order to evaluate the potential impact of bovine somatotropin (BST) on genetic gains and on the discrepancies between true and estimated breeding values. The parameters were treatment rate (10%, 30%, 50%), reporting (complete or random), BST allocation system (random, best or worst cows), data correction system (none, conventional BLUP or bivariate BLUP) and some dispersion parameters of the additional yield provided by BST.

Given that there were no herd effects and no embryo transfer, the range of the decrease for genetic gains was 1-10%, not fully explained by the decrease in selection accuracy, and was relatively well balanced between the male and female gene transmission paths. The perception of this situation is difficult especially when BST is allocated to the best cows because very large biases in the evaluation may occur (up to 30% of the true selection differentials). These biases occur even when reporting is complete and when a conventional BLUP is implemented. This problem disappears when a multi-trait BLUP is applied after completely discarding the treated parts of lactation. In this case, losses of genetic gains are relatively moderate as well.

Possible herd effects were ignored in the simulation process to give the opportunity of correct calculations for selection accuracies. This artificial prerequisite should be removed in further studies.

cattle selection − milk yield − bovine somatotropin − genetic gain

Résumé − Impact de l'utilisation de la somatotropine bovine (BST) sur les programmes bovins de sélection laitière. *On a simulé de manière aléatoire le fonctionnement d'un programme très simple de sélection laitière pour évaluer l'impact de la BST sur le progrès génétique et sur les écarts entre valeurs génétiques vraies et estimées. Les paramètres étaient le taux de traitement (10%, 30%, 50%), le taux de déclaration (total ou aléatoire), le système de choix des vaches traitées (au hasard, bonnes ou mauvaises vaches), le type de correction des données (aucune, BLUP classique ou BLUP bivariate) et certains paramètres de dispersion concernant le gain de production permis par la BST.*

Sachant qu'il n'y avait ni effet troupeau ni transfert embryonnaire, le taux de diminution du progrès génétique se situe dans la zone 1-10%, ne s'explique pas totalement par la réduction de précision de la sélection et se répartit assez bien entre les voies mâles et femelles de transmission des gènes. La perception de cette situation est obscurcie, en particulier si la BST est utilisée sur les meilleures vaches parce que des biais très importants dans l'évaluation des reproducteurs peuvent survenir (jusqu'à 30% des différentielles de sélection réelles). Ces biais ne disparaissent pas après correction selon un BLUP classique dans la situation favorable où toutes les vaches traitées sont correctement déclarées.

L'utilisation d'un BLUP *multicaractère sur des lactations entières ou amputées de leur partie obtenue sous traitement permet de faire disparaître cette nuisance. Par ailleurs, dans cette situation, les réductions de progrès génétique sont relativement modiques.*

Les éventuels effets troupeau ont été ignorés dans le processus de simulation, de manière à faciliter le calcul exact de la précision des indices de sélection. Cette condition artificielle devrait être levée dans les études ultérieures.

bovins – sélection – production laitière – somatotropine bovine – progrès génétique

I. INTRODUCTION

Growth hormone obtained from genetic engineering induces large changes of milk yield in cattle (see the review by Chilliard, 1988a, b). It might therefore be integrated into the modern production techniques used for dairy cattle. The new questions asked to breeders would be the consequences of a relatively large uncertainty about the statistical and biological parameters concerning the response to the hormone. Additional challenges would be generated in the case of possible ignorance of the real status of the cows, treated or not treated (poor reporting or, at worst, cheating).

Two main questions, which are distinct although partially overlapping, arise from an operational viewpoint:

1) What is the reduction in the annual genetic gains in comparison with the corresponding value in an identical BST-free breeding scheme?

2) What are the discrepancies between the real selection differentials and the apparent ones, as seen from the breeding value estimates of elite animals?

Deterministic modelling of these questions is not an easy task, especially in the situation where BST is not randomly allocated. This is the reason why the first known numerical studies have resorted to Monte-Carlo methods (Burnside and Meyer, 1988; Frangione and Cady, 1988; Simianer and Wollny, 1989).

Conversely, this has strongly limited the scope to very simplified breeding schemes, in attempts to mimic the main aspects of the usual complex schemes, on relatively small numbers of animals to save computation time.

In the present paper, this type of approach is applied to embryo transfer-free schemes, as in the preceding studies. The objective is to give clear answers to the above questions. In addition, the source of the potential losses will be examined in reference to standard selection theory. The potential of more adequate evaluation procedures such as multi-trait BLUP will be tested too.

II. MATERIEL AND METHODS

A. Breeding scheme

Unrelated sires (100) were progeny tested with 50 daughters each, related only through their sires. The top 25 and 3 sires were considered as cow sires and bull sires respectively. The best 5% of the daughters were considered as potential bull dams, which represent near the maximum selection pressure possible without embryo transfer (ET). It assumes only 250 dams to produce 100 young bulls.

B. Constants

The additional yield provided by BST amounts to 1 000 kg on average, with a phenotypic standard deviation of 200 kg. This roughly corresponds to the order of magnitude of the results obtained on cows treated for 8 months after a 2-month BST-free period, in order not to alter dramatically the cow's energetic balance, as recommended by nutritionists.

The genetic and phenotypic parameters concerning the 2-month part lactation and the whole lactation were drawn from the detailed results given by Danell (1982). This lead to h^2 values of 0.18 and 0.28 respectively, with genetic and phenotypic correlations of 0.85 and 0.77. Wilmink (1987) gave very similar results. It should be kept in mind that the average effect of BST is equivalent to 2 genetic standard deviations for the full lactation.

C. Parameters

1) Genetic situation

S_1: additional yield due to BST is not heritable and independent of preceding yield;

S_2: additional yield is heritable ($h^2 = 0.30$) and negatively correlated to the preceding yield ($r_G = r_E = -0.5$);

S_3: additional yield is heritable ($h^2 = 0.30$) and independent of preceding yield;

S_4: additional yield is heritable ($h^2 = 0.30$) and positively correlated to the preceding yield ($r_G = r_E = 0.5$).

These situations were chosen because nothing is known about the genetic parameters of additional yield. Contradictory information from small samples is given on phenotypic parameters. The lack of free access to data from BST studies has precluded thorough analysis.

On the other hand, the observation that BST brings an extra yield for every treated cow excludes from the parameter space, situations where genetic and phenotypic correlations between the 2 total yields (with and without BST) are too low. Considering for instance that $r_P = r_G = 0.8$, as in a previous personal study, implies that in some cases extra yield can be negative (never observed when comparing daily pre- and post-injection yields). All the correlations r_G or r_E resulting from our 4 situations are above 0.96.

2) Treatment rates: 10%, 30%, 50%

3) Reporting rates: 50%, 100%. When reporting is partial, cheating is not supposed to occur, i.e. treated cows are reported at random.

4) Treatment allocation: at random, on the best or worst cows, based on their phenotypic 2 month partial yield.

5) Methods of analysis: In the first analysis (correction 1), the model used included an additive effect for treatment, a sire effect and a cow within sire effect. As it will

be seen, this simple model is not robust to a non-random allocation of BST and, as suggested by Ducrocq and Foulley (personal communication), a multi-trait BLUP evaluation system could be used by taking into account the BST-free lactation parts, which would allow a better evaluation of fixed effects. A second analysis (correction 2), *i.e.* a bivariate BLUP, is envisioned as extreme implementation of this idea where treatment effect is ignored but where treated parts of lactation are deliberately excluded. In this way, the unknown dispersion parameters concerning the effect of BST would be certain not to interfere with the evaluation (at least when BST reporting is complete).

D. Obtaining BLUP evaluations

To save computation time, advantage was taken of the block structure of the data. By algebraically manipulating $(\alpha I + \beta J)$ - type matrices and their inverses, it was therefore possible to solve directly the linear system and to derive the random variance–covariance errors for the estimates, given that the model is true. The general linear system can be found in Henderson (1975), Foulley *et al.* (1982), Schaeffer (1984) for instance. The detailed list of the derivations used for our case is rather lengthy (especially for bivariate BLUP) and not essential to an understanding of the results. These are the reasons why it will not be given here. Obtaining the accuracies of the estimates without any approximation was felt to be important in order to analyse the phenomena as deeply as possible.

   An animal model was solved for the females to get estimates for bull dams and from these results, the solutions of a sire model were obtained (to get estimates for cow and bull sires), because it can be shown that with our initial assumptions, the estimate s_i for a sire i is equal to

$$2 \sum_{j=1}^{n_i} \widehat{a}_{ij}/(n_i + 3)$$

where $\widehat{a}_{ij}$ is the estimate for the jth daughter.

   In this sequence of operations, a direct inversion is needed for the incidence matrix of fixed effects after absorption of the animal effects. Herd effects were excluded to save computation time, since 300–500 herds would have been needed. The consequences of this decision will be discussed.

E. Comparisons to reference scheme (see IIIA)

Generally speaking, all the results are expressed as a percent of the reference scheme. Approximate standard errors for this ratio can be obtained first by linearizing the ratio and second by using the observed between-replicate variances for the reference and BST schemes. Given these last values, a relatively high number of replicates (100) was considered necessary.

III. RESULTS

A. Reference scheme

The results obtained from 300 replicates are shown in Table I. They give for each of the 3 significant gene transmission paths, the true selection differentials, the apparent selection differentials (from BLUP evaluation), the true accuracies ($r_{G\widehat{G}}$) and the calculated accuracies. There is a very good agreement between observed and calculated parameters. It can also be verified that these parameters do not correspond to those obtained in an infinite population of unrelated animals.

Table I. Efficiency of the reference scheme (300 replicates).

	Cow-sire path	Bull-sire path	Bull-dam path
Observed [1] selection differentials	1.11	1.95	1.27
Calculated selection differentials			
– finite population	1.11	1.95	1.26
– infinite population	1.13	2.02	1.28
Observed [2] accuracies	0.89	0.89	0.63
Calculated accuracies			
– finite population	0.89	0.89	0.62
– infinite population	0.89	0.89	0.62

[1] In genetic standard deviation units for the total untreated lactation.
[2] Correlation coefficient between G and $\widehat{G}$.

B. Cumulative selection differentials

The asymptotic yearly genetic gains are proportional to the sum of the 3 selection differentials on the cow-sire, bull-sire and bull-dam paths when the cow-dam path is neglected (Rendel and Robertson, 1950). The decrease of that sum, expressed as a percent of the corresponding value in the reference scheme, is shown in Table II. Most values are in the range 1–10%. For accurate comparisons, it should be kept in mind that there is some fuzziness due to random errors (standard error of about 1.2%).

When no data correction is applied, the total range for losses is 0–8%. When correction 1 is applied, the situation is improved only if reporting is complete and

Table II. Decrease of the selection differentials (in % of the reference selection scheme).[a]

BST Allocation	*Correction system*	*% Reporting*	*Genetic situation and treatment rate*											
			S_1			S_2			S_3			S_4		
			10%	*30%*	*50%*	*10%*	*30%*	*50%*	*10%*	*30%*	*50%*	*10%*	*30%*	*50%*
	None	0	4	5	6	5	7	7	3	5	8	5	4	8
At random	n°1	50	2	4	5	4	6	5	2	4	7	4	3	6
	n°2	50	3	7	9	5	8	10	3	7	11	5	7	11
	n°1	100	2	1	2	3	3	2	0	1	3	2	1	3
	n°2	100	2	2	5	3	4	5	1	2	6	3	2	6
	None	0	4	3	4	7	6	4	4	4	6	7	3	5
On best cows	n°1	50	6	7	8	9	10	8	6	8	9	9	8	8
	n°2	50	4	6	7	6	8	7	4	7	9	7	7	8
	n°1	100	7	10	9	8	12	10	6	10	11	8	8	9
	n°2	100	3	5	8	4	7	8	2	4	10	4	5	9
	None	0	2	3	6	4	5	7	0	3	7	3	2	7
On worst cows	n°1	50	2	3	7	4	6	7	1	4	8	3	3	8
	n°2	50	2	4	11	4	8	13	1	5	11	2	3	11
	n°1	100	2	5	10	4	7	9	1	5	11	4	5	11
	n°2	100	0	1	3	2	2	2	0	0	3	2	0	3

[a] Standard deviations are around 1.2%.

BST allocated randomly. With non-random allocation fo BST, its effect is poorly estimated and this leads to an additional error for evaluating breeding values. For instance, in the S1 situation, BST used on the 30% best cows with total reporting, the estimate of the hormone effect is not 1 000 kg but 1 200 kg. When correction 2 is applied, the results are better than in the no-correction situation, except when the best cows are treated with a high treatment rate. The source of these losses is obvious, since for many animals the old variable is replaced by a less heritable one and imperfectly correlated with it.

Comparison between the situations S_1 and S_3 shows that the value of h^2 for additional yield has no detectable effect on the losses, a probable consequence of the fact that the genetic standard deviation for this yield cannot be very high in comparison with the parameters for full lactations. In contrast, comparison between situations S_2, S_3 and S_4 shows that the value of the correlations between additional yield and "BST-free" yield has a perceptible influence. The smallest losses are obtained when the correlation is null. Greater losses are incurred with positive correlations but the worst situation is obtained when the worst cows respond the best to hormone and *vice versa.* Therefore, good information on the values for the correlations involved would be useful.

The most detrimental situation of BST allocation is the system when BST is provided to the best cows, except for high treatment rates (50%) where it is the contrary.

C. Discrepancies between real and apparent sum of selection differentials

A general survey of Table III shows that overestimation or underestimation of the cumulated selection differentials (i.e. of the potential genetic gain) can exist. The total range goes from −30 to +30%.

Table III. Biases affecting the apparent selection differentials in % of the true selection differentials.[a]

BST allocation	Correction system	% reporting	S_1			S_2			S_3			S_4		
			10%	30%	50%	10%	30%	50%	10%	30%	50%	10%	30%	50%
	None	0	+4	+ 9	+ 9	+3	+6	+ 4	+5	+ 8	+10	+6	+11	+15
At	n°1	50	+2	+ 6	+ 7	+1	+4	+ 2	+3	+ 5	+ 8	+4	+ 9	+13
random	n°2	50	+5	+11	+14	+4	+8	+10	+5	+10	+14	+6	+13	+18
	n°1	100	−1	0	+1	−1	−2	−5	0	0	+ 2	−1	+ 3	+ 4
	n°2	100	−1	0	0	0	+1	0	+1	−1	− 1	0	− 1	− 1
	None	0	+20	+27	+28	+18	+25	+23	+21	+27	+28	+25	+31	+30
On best	n°1	50	+ 9	+16	+20	+7	+15	+16	+10	+16	+21	+13	+20	+23
cows	n°2	50	+16	+26	+30	+13	+24	+26	+17	+26	+32	+20	+30	+33
	n°1	100	−18	−30	−33	−19	−32	−39	−18	−31	−31	−18	−28	−25
	n°2	100	0	−1	0	1	1	0	0	−3	0	0	0	0
	None	0	−12	−25	−31	−12	−29	−37	−11	−27	−31	−8	−22	−23
On worst	n°1	50	−14	−27	−31	−13	−30	−38	−13	−28	−31	−11	−25	−25
cows	n°2	50	− 6	−11	−13	− 5	−12	−16	− 5	−13	−15	− 4	−11	−10
	n°1	100	−16	−30	−32	−14	−31	−39	−15	−30	−31	−14	−28	−26
	n°2	100	− 1	0	0	0	1	0	0	− 2	0	0	− 1	0

[a] Differentials summed over the 3 transmission paths.

With no data modification, a noticeable overestimation of the selection differentials occurs, except when poor cows are treated, which leads to an underestimation. This would bring some perturbation into the breeding scheme. For instance, in the situation S_1 (30% treated at random), it is found in Table II that genetic gain is decreased by 5%. When taking into account the corresponding figure in Table III, an AI organization would have every reason to believe that genetic gain is *increased* by 4%. This type of comparison is even more dramatic when BST is not allocated at random. With no correction, S_1 (30% on best cows), genetic gain is decreased by 3%, whereas it is believed that it should increase by 24%.

As expected, partial reporting and correcting does not help the situation. When reporting is exhaustive, it can be observed that correction 1 leads to strong underestimations except when BST is randomly allocated: if good cows are treated, they are overcorrected and if poor cows are treated, they are undercorrected, both cases leading to an apparent shrinkage of the genetic variation range. Correction 2 leads to an almost perfect adequacy of the estimate genetic gains. This is not surprising and can be considered a check of the soundness of the calculations. The most important point is that this unbiased type of estimation is relatively unexpensive in terms of real genetic gains, as seen from Table II. Therefore multi-trait BLUP, with a drop of the treated parts of lactation, is by far the best solution among the possibilities investigated here. Better solutions can certainly be obtained if they are of the multi-trait-type, after a REML step for calculating the unknown variances and covariances on treated parts.

Table IV shows for the S_1 example that biases of selection differentials are only very weakly related to biases of accuracies. Once again, there is a very good agreement between true and predicted accuracies for the type 2 correction with complete recording: variation around 0 is small and of random nature.

Table IV. Overestimation of the apparent accuracies in % of the true accuracies (situation S_1).

BST allocation	Correction system	% reporting	Males			Females		
			Treatment rate			Treatment rate		
			10%	*30%*	*50%*	*10%*	*30%*	*50%*
	None	0	1.2	2.7	3.8	3.2	8.0	9.8
At	$n^\circ 1$	50	0.7	1.6	2.7	1.7	5.1	6.9
random	$n^\circ 2$	50	0.9	2.6	4.8	3.1	8.8	12.3
	$n^\circ 1$	100	0.1	−0.1	0.5	0.1	0.9	1.2
	$n^\circ 2$	100	−0.1	−0.3	0	−0.1	0.1	−0.1
	None	0	1.4	2.0	3.0	3.2	5.8	6.5
On best	$n^\circ 1$	50	1.7	3.0	4.0	4.7	9.3	9.9
cows	$n^\circ 2$	50	0.7	1.4	3.1	2.3	5.2	6.3
	$n^\circ 1$	100	2.8	6.7	8.2	5.7	11.3	14.9
	$n^\circ 2$	100	0	−0.3	0.1	−0.1	0.2	0.1
	None	0	0.7	3.0	4.6	1.7	5.9	8.2
On worst	$n^\circ 1$	50	1.3	4.3	5.7	3.4	8.3	11.0
cows	$n^\circ 2$	50	1.0	4.1	9.0	3.4	11.7	20.0
	$n^\circ 1$	100	2.4	6.4	8.3	5.6	11.2	14.9
	$n^\circ 2$	100	0	−0.2	0.3	−0.1	0.1	0.2

D. Examination of the origin of the losses for situation S_1

Inspection of all situations is not given: this would lead to a large amount of figures. Situation S_1 is chosen and exemplifies very well the general pattern of results obtained. From the comparison between Table II, Table V (accuracies of selection) and Table VI (selection differentials), it is obvious that the reduction of genetic gains cannot be totally explained by a reduction of accuracy. This is the consequence of mixing different distributions of predicted breeding values for total milk yield (different population expectations and within population variances). This situation is encountered even for the 100% recording correction 2 situation. It should remembered that the conventional way of predicting selection differential (selection intensity × selection accuracy × genetic standard deviation) is only correct if there is 1 population and if linearity of regression and homoskedasticity of error variances hold. None of these 3 conditions is met in a BST situation. The impact of BST is not a mere reduction of heritability.

Table V. Decrease of the accuracies of selection ($r_{G\widehat{G}}$) in % of the corresponding values in the reference scheme (situation S_1).[a]

BST allocation	Correction system	% reporting	Males			Females		
			Treatment rate			Treatment rate		
			10%	30%	50%	10%	30%	50%
	None	0	1.2	2.6	3.7	3.1	7.4	8.9
At	n°1	50	0.7	1.6	2.6	1.7	4.9	6.5
random	n°2	50	0.8	2.9	5.4	2.2	8.8	13.1
	n°1	100	0.1	0	0.5	0.1	0.9	1.2
	n°2	100	0.1	0.9	2.9	0	3.4	6.8
	None	0	1.4	2.0	2.9	3.1	5.5	6.1
On best	n°1	50	1.7	2.9	3.9	4.5	8.5	9.0
cows	n°2	50	0.6	1.8	3.9	1.5	5.7	8.2
	n°1	100	2.7	6.3	7.6	5.4	11.2	13.0
	n°2	100	0.2	1.0	3.0	0	3.5	7.0
	None	0	0.7	2.9	4.4	0.7	5.6	7.6
On worst	n°1	50	1.3	4.1	5.4	1.3	7.6	9.3
cows	n°2	50	0.9	4.3	9.1	0.9	11.2	18.7
	n°1	100	2.3	6.0	7.7	2.3	10.8	13.0
	n°2	100	0.2	1.1	3.2	0.2	3.4	7.1

[a] Random standard deviations are around 0.3%.

As might be anticipated, the bull-dam path is the most affected in terms of accuracy and in terms of selection differential. The sire paths are much less affected but they act twice in the creation of genetic gains. This explains why 40-50% of

Table VI. Decrease of the selection differentials in % of the corresponding values in the reference scheme (situation S_1).

Allocation	Correction system	% reporting	Cow sires			Bull sires			Bull dams		
			Treatment rate			Treatment rate			Treatment rate		
			10%	30%	50%	10%	30%	50%	10%	30%	50%
	None	0	1.1	4.0	6.2	4.0	2.5	3.4	6.7	9.1	8.6
At	n°1	50	0.7	3.5	5.5	1.9	2.3	2.1	4.5	7.3	8.1
random	n°2	50	0.9	4.9	7.5	3.0	2.8	5.5	7.2	14.8	7.2
	n°1	100	0.2	1.2	3.4	3.1	0	0.8	1.3	1.0	1.1
	n°2	100	0.2	2.3	5.8	2.1	1.0	3.1	0.8	3.4	6.4
	None	0	1.5	3.3	6.0	3.5	2.1	3.7	9.7	5.0	3.6
On best	n°1	50	1.9	4.5	7.1	5.6	3.6	6.0	15.4	16.3	12.9
cows	n°2	50	1.1	3.2	7.4	3.9	3.0	5.0	11.1	12.8	11.5
	n°1	100	3.2	8.0	9.9	7.3	9.4	7.6	11.0	13.0	10.3
	n°2	100	0.6	2.6	5.7	3.0	3.7	5.0	5.0	10.1	14.2
	None	0	0.1	4.9	6.7	2.5	1.0	5.6	1.5	2.7	6.3
On worst	n°1	50	0.7	5.7	7.8	2.5	1.9	6.6	1.8	1.9	8.1
cows	n°2	50	0	5.7	11.1	2.8	1.6	7.3	1.0	1.6	17.6
	n°1	100	1.4	7.9	10.6	3.0	2.8	8.9	2.4	2.8	11.8
	n°2	100	0	2.7	4.9	1.2	1.0	3.2	0	1.0	0.7

[a] Random standard errors are around 1.4% for cow sires, 1.9% for bull sires and 0.8% for bull dams.

the reduction of genetic gain comes from the male paths, as shown by a detailed examination of the figures. The impact of BST on breeding schemes cannot either be oversimplified as a process that weakens the efficiency of the bull-dam path.

E. Treatment rates within the elite populations

Results are shown only for situation S_1 but they give a good idea of the other situations (Table VII). From the random BST treatment, it appears that the probability for a treated cow to be considered as a bull dam is considerably increased (by 2 or 3). For correction 2 and total reporting, the probability is decreased, as might be anticipated since the standard deviation of the breeding values estimates is smaller for the treated cows. As to the allocation to best cows, all bull dams are treated and then a doubt comes into mind: are these cows considered as good because they were treated or is it the contrary: were they treated because they are really good? From the multiple trait results, we known that in this situation a large fraction of the treated animals (41/87, 71/98, 87/100) would have great chances to be chosen as bull dams anyhow. However, we are in the artificial situation where we know the breeding value of the animals: in practice, a heavy doubt would persist.

Table VII. Percentage of treated cows within the progeny of the selected bulls and within the selected cows' population (situation S_1).

Allocation	Correction system	% reporting	Daughters of cow sires			Daughters of bull sires			Bull dams		
			Treatment rate			Treatment rate			Treatment rate		
			10%	30%	50%	10%	30%	50%	10%	30%	50%
	None	0	11	32	52	12	33	54	33	68	85
At	$n^{o}1$	50	10	31	52	11	33	52	23	56	78
random	$n^{o}2$	50	11	31	52	11	33	53	29	65	84
	$n^{o}1$	100	10	30	50	10	30	50	11	31	51
	$n^{o}2$	100	10	30	50	10	30	50	6	19	36
	None	0	16	41	42	22	51	71	87	98	100
On best	$n^{o}1$	50	15	40	43	20	48	69	67	96	99
cows	$n^{o}2$	50	16	41	43	21	50	71	72	96	99
	$n^{o}1$	100	14	36	44	16	41	63	9	36	64
	$n^{o}2$	100	15	40	39	20	48	69	41	71	87
	None	0	6	23	52	5	18	36	1	8	28
On worst	$n^{o}1$	50	6	23	52	5	18	37	1	11	32
cows	$n^{o}2$	50	6	23	52	4	17	36	3	20	44
	$n^{o}1$	100	7	24	50	5	19	38	2	15	39
	$n^{o}2$	100	6	21	50	4	16	30	0	0	1

Hence the psychological interest of excluding treated parts of lactation for data processing.

IV. DISCUSSION

A. Biases of this study

Here, experimental conditions are rather mild ones to evaluate the impact of BST.

– Due to operational considerations, the between-herd variability was dropped, although it is well known that a between-herd variability exists. This variability would be very likely increased by use of BST, since the specialists generally agree in saying that additional yield is all the more substantial as the feeding level is good (probably BST × herd interaction). Furthermore, there is no clear reason why every farmer would apply strictly the same system for choosing the cows to be treated. Finally, if non-reporting and cheating cannot be eliminated, this implies, for human reasons, that there would be a between-herd variance for these variables. All these reasons can bring substantial additional errors to the situation studied here.

– Embryo transfer situations were not studied, despite their growing influence in practical dairy breeding schemes. Given that female gene transmission paths have more importance, then it can be anticipated that the losses would be greater.

B. *Comparison with previous studies*

Simianer and Wollny (1989) studied in their alternative IV a situation similar to our situation S_1: the additional yield ($\mu = 1\,000$ kg, $s_p = 250$ kg) was not heritable and did not depend on anything. They nevertheless supposed an additive herd effect. They found also that a type 1 correction decreases the accuracy of selection except when BST is allocated at random or almost. In the most favourable case (total reporting, BST allocated at random), they found a decrease of 10% for the genetic gain when 20% of the animals are treated. This is much more than the value obtained here for this case (around 2%).

Burnside and Meyer (1988) concentrated only on sire evaluation problems, assuming a multiplicative effect of BST and a between-herd variability, and stretched the range of genetic situations to as far as 0.6 for the phenotypic or genetic correlation between yields with and without BST. In these circumstances, accuracy is badly decreased. For a more likely situation ($r_G = 1$, $r_p = 0.8$), the accuracy is not greatly changed but noticeable biases are induced: in comparison with the reference situation, the mean absolute difference between the true breeding value and its estimate increases by 25% when the best 2/3 cows in 2/3 of the herds are treated. This implies that the mean value of elite sire estimates would be biased as well.

CONCLUSION

The present study cannot be considered as exhaustive on the topic. However, it is clear that the possible problems in dairy breeding schemes brought about by BST administration should not be underestimated. Unfortunately, simple ideas that could justify comfortable solutions, are not at all supported by the present results, as confirmed by the preceding studies when a meaningful comparison was possible.

Losses of genetic gains are not proportional to losses of accuracy, which implies, for instance, that only increasing the number of daughters per bull would not be sufficient to eliminate these losses. The losses are almost equally balanced between female and male paths, which implies that attention should be given to each path: contracting herds, for instance, for bull sampling would therefore be a partial solution. Finally, even considering only genetic gains is not sufficient since in some situation genetic gains can be kept almost intact whereas the sire and dam evaluations are significantly biased, a fact likely to introduce mistrust from the farmers towards the breeders.

The solution proposed here, i.e. to exclude the treated parts of lactation for breeding purposes and to use a multi-trait BLUP, is only satisfactory if reporting is correct. Furthermore, it would complicate the calculations.

The use of BST on dairy farms, and possibly other new tools coming from biotechnology research, probably means that dairy breeding schemes will be deeply

modified towards contracted and artificial systems. This might result in an increased cost of AI.

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