

SIMULATIONS ON COOPERATIVE BREEDING BETWEEN NORDIC RED DAIRY CATTLE POPULATIONS WITH DIVERSE OBJECTIVES

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Abstract. Small or limited population sizes of four Nordic red and red-and-white dairy cattle breeds restrict the rate of genetic improvement and make them less competitive as compared to the Holstein-Friesian populations. A simulation study was undertaken in order to evaluate opportunities for improvement of the competitiveness through cooperative breeding plans. A deterministic model based on the gene flow method was used. Progeny testing schemes were evaluated on the basis of genetic gain for the four populations of different sizes. Each breed was assumed to adopt three breeding objectives, i.e. milk yield, calving performance and mastitis resistance (MR). Three alternative economic weights for MR (500, 1410 and 2000 per phenotypic standard deviation) were used to differentiate slightly the populations. The schemes with the highest gains were used to evaluate the effect of cooperation on bull sire selection among all progeny tested bulls in the populations. It was found that the population with the lowest weight on MR obtained the lowest benefit from the cooperation whereas the three others obtained similar genetic progress, indicating that cooperation should be regarded as the first step towards uniting populations into one breeding unit.

Keywords: Geneflow, deterministic simulation, multitrait evaluation.

ŠIAURĖS EUROPOS ŽALŪJŲ PIENINIŲ GALVIJŲ POPULIACIJŲ KOOPERUOTO VEISIMO MODELIAVIMAS SIEKIANT ĮVAIRIŲ TIKSLŲ

Santrauka. Keturių Šiaurės Europos žaliųjų ir žalmargių galvių veislių populiacijos yra nedidelės arba ribotos, todėl nėra sąlygų jas genetiškai tobulinti ir padidinti jų sugebėjimą konkuruoti taip, kaip kitos veislės, pvz., Holšteino fryzai. Galvių populiacijų kooperuoto veisimo modeliavimo tikslas buvo įvertinti, ar galima naudojantis kooperuoto veisimo planu pagerinti sugebėjimą konkuruoti. Taikytas determinavimo modelis, pagrįstas genų srauto metodu. Palikuonių tyrimo schemas vertintos pagal genų padidėjimą keturių skirtingų dydžių populiacijose. Numatyta, kad bus atsižvelgiama į tris kiekvienos veislės rodiklius: pieno kiekio, veršiamosios eigos ir atsparumo mastitui (AM). Trys alternatyvios ekonominės atsparumo mastitui reikšmės (500, 1410 ir 2000 fenotipiniam standartiniam nuokrypiui) naudotos tam, kad būtų galima šiek tiek diferencijuoti populiacijas. Schemos, pasižymėjusios didžiausiu genų padidėjimu, naudotos kooperavimo efekto bulių tėvams apskaičiuoti ir iš populiacijos atrinkti bulius, įvertintus pagal visus palikuonis. Nustatyta, kad populiacijoje, kur atsparumas mastitui mažesnis, mažiausia buvo ir kooperavimo nauda. Trijų populiacijų genetinė raida panaši. Vadinasi, kooperavimo metodas galėtų būti pirmasis žingsnis sujungiant populiacijas į vieną veisimo vienetą.

Raktažodžiai: genų srautas, determinavimo modelis, daugybinis požymių įvertinimas.

Introduction. During the recent decades the Holstein cattle breed has become more and more dominant in the dairy production in areas of temperate climate. As a consequence, the population size of many regional and national dairy breeds, such as the Red Nordic dairy cattle populations, has decreased. A small population size worsens the competitiveness of the minor breeds (Christensen, 1995; Christensen & Pedersen, 1997) and stresses the need for efficient breeding schemes for these breeds. Another way to overcome the problem of a limited population size is by cooperation in terms of common breeding value estimation and bull selection across populations. The extent the populations will benefit from cooperation will probably depend on the uniformity of breeding goals. It is the objective of this study to evaluate perspectives of cooperation between

populations of different sizes, having slightly diverse breeding goals.

Materials and methods. The sizes of four populations were set to 50.000 (D), 180.000 (S), 200.000 (F) and 280.000 (N), in order to mimic the red dairy cattle populations in Denmark, Sweden, Finland and Norway.

The breeding objectives included the three traits: yield (Y), calving performance (CP) and mastitis resistance (MR). Heritabilities used for yield, calving performance and mastitis resistance were 0.28, 0.11 and 0.04, respectively, and correlations were assumed to be zero except for $r_{P(Y,MR)} = 0.03$, $r_{A(Y,MR)} = -0.35$ and $r_{A(CP,MR)} = 0.20$ (Sørensen, 1999). The economic weights per σ_P were assumed to be 1,000 and 330 for yield and calving performance, respectively. For MR three alternatives were assumed, i.e. 500 for population F, 1410 for D and S and

2000 for N. This leads to three sets of slightly diverse breeding goals.

The breeding schemes studied were progeny testing schemes without and with cooperation between the four dairy cattle populations. The cooperation was at the bull sire level where each population selected sires with respect to their own objective among all progeny tested bulls in the four populations. The distribution of cows through lactation 1 to 6 was assumed to be 38%, 29%, 18%, 8%, 4% and 3%, respectively, in all populations. The number of test bulls was found as $N_{TB} = 0.38 \times N_P \times p / N_d$, with proportion of first lactation cows of 0.38; N_P population size; p test capacity (proportion of N_P) and N_d daughter group size. Six proven bulls were selected in the three smallest populations (D, S and F), while 10 proven bulls were selected in the largest population (N). All populations used six bull sires. Thus, without cooperation proven bulls were also bull sires in the three smallest populations. All reproductive females were potential bull dams and the number of selected bull dams was assumed to be $4 \times N_{TB}$.

Index information sources were cows 1st lactation yield, progeny group of young test bulls (variable in size) and 1,000 daughters of proven bulls. All daughters gave information on yield and calving performance, where as only 70% gave information on mastitis resistance (Lindhé, 2000). Cow indexes included own and dam performance as well as sire and maternal grandsire progeny information. Bull indexes included dam performance and own, sire and maternal grandsire progeny information. Indexes were updated as soon as information became available.

A deterministic simulation model based on the gene flow method (Hill, 1974) and the selection index theory (Hazel, 1943) was developed and used to evaluate the progeny testing schemes. Genetic progress is modelled by splitting the female and male population into eight and seven age classes of one year, respectively, each age class having its own distribution. Animals within an age class have different trait distributions depending on types of the dam (cow or potential bull dam) and sire (young bull, proven bull or bull sire). Age classes are split into subclasses according to the pedigree, i.e. by the type of the sire, dam and maternal grandsire, and each subclass is represented by a fixed multivariate trait distribution and an updated index distribution. Cows had offspring in their

last six age classes. Test and proven bulls had offspring in their third and seventh age class, respectively.

Selection of bull dams, proven bulls and bull sires was based on the total merit index (TMI) and optimised through all relevant subclasses using the algorithm of Ducrocq & Quaas (1988), which together with the above defined subclasses makes the selection step a close mimic of selection based on BLUP estimated EBVs. For more detailed description of the model see Jørgensen & Sørensen (2002b).

For each population a scheme was outlined and alternative breeding plans were simulated by varying test capacity (p) in steps of 5% and progeny group sizes of test bulls (N_d) in steps of 10 daughters (Jørgensen & Sørensen, 2002a). For each scheme the plan with the highest annual genetic gain in terms of TMI was considered the optimum one. The simulations were initiated with identical multivariate trait distributions for all populations. All plans were simulated without discounting for a period of 100 years, which resulted in an approximate steady phase of gain. Thus, the annual gains presented in Table 1 and 4 have been averages for the last 10 years. Benefit of cooperation is presented as years of separate selection needed to obtain a cumulated response equal to a genetic lag between the two strategies.

The research results. Separate breeding in the four populations resulted in the optimum plan for each progeny testing scheme given in table 1. Test capacity varied from 45% to 55% of N_P for individual populations and number of daughters varied from 40 to 90. The population D and S selected for the same breeding objective and the difference in their breeding plans and annual responses was due to a different population size. Population F, having the lowest economic weight on mastitis resistance, obtained the highest annual response in yield and the lowest annual responses in calving performance and mastitis resistance. Population N, having the highest economic weight on mastitis resistance, was the only population obtaining a desirable positive annual response in this trait. Population N with the lowest relative economic weight on yield obtained an annual gain in yield similar to that of population D. The gain in TMI can not be compared throughout alternative sets of objectives due to deviating economic weights for mastitis resistance.

Table 1. Optimised plans without cooperation (Mod. e. Jørgensen and Sørensen, 2002a)

Population	Objective ¹	p ²	N _d ³	Annual response ⁴			
				TMI	Y, 10×σ _p	CP, 10×σ _p	MR, 10×σ _p
F	L-MR	45	50	138	1.39	0.17	-0.12
D	I-MR	55	40	116	1.11	0.20	-0.01
S	I-MR	50	60	132	1.25	0.23	-0.01
N	H-MR	55	90	138	1.12	0.27	0.08

¹: L-MR: low economic weight of mastitis resistance;
I-MR: intermediate economic weight of mastitis resistance;
H-MR: high economic weight of mastitis resistance.

²: p = test capacity in percent of population size. ³: N_d = number of daughters in the test group.

⁴: TMI = total merit index; Y = yield; CP = calving performance; MR = mastitis resistance.

In cooperation schemes the exchange of bull sires was observed differ among populations and change during the time. Table 2 shows that in the year one the distribution of bull sires was proportional to the size of the four populations. As time went on population F, S and N selected an increasing proportion of the bull sires from their own population. This trend was very clear for

population F, which almost did not participate in the cooperation in the year 100. Due to the identical breeding objective the distributions of bull sire population of origin were the same for population D and S. The difference in population size between D and S was the reason why D selected an increasing proportion of bull sires from S.

Table 2. **Relative distribution of bull sires according to the origin within population during the time (percentage)**

Year	1			25			50			100		
Population	F	D/S	N	F	D/S	N	F	D/S	N	F	D/S	N
Origin: F	27	27	26	53	17	5	73	11	1	95	2	0
D	9	8	8	5	5	4	3	6	3	0	6	3
S	26	26	25	27	33	27	19	39	26	4	45	26
N	38	39	41	15	45	64	5	44	70	1	47	71

An alternative way to investigate the exchange of bull sires is to study the proportion of genes from the cooperating populations present in each population, which reflects the cooperation history (Table 3). It was found that the genetic composition of the four populations was

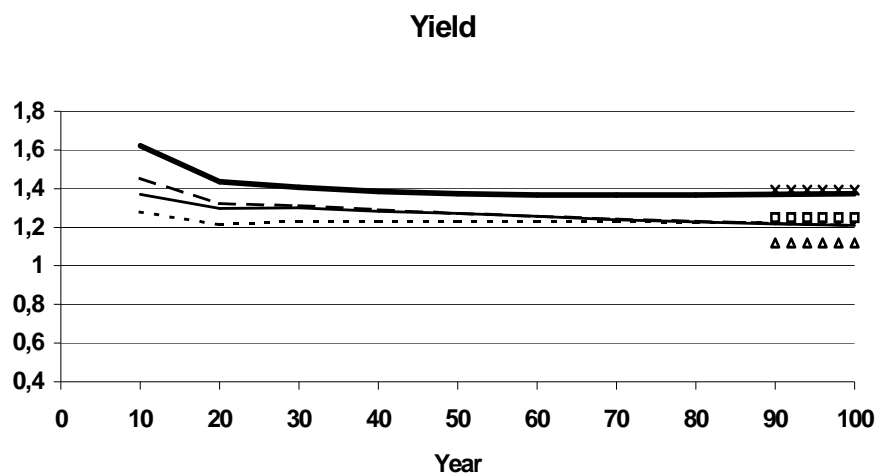
changing until the year 50, after which the genetic compositions were rather stable; e.g. in the year 100 population F and N contributed to population F with 30% and 37% of the genes, respectively.

Table 3. **Genetic composition of populations during the time (percentage)**

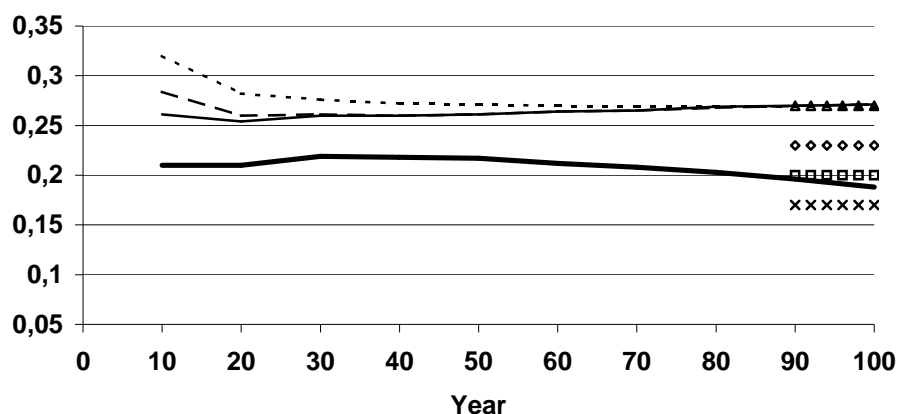
Year	25				50				100			
Population	F	D	S	N	F	D	S	N	F	D	S	N
Genes from: F	43	21	20	18	33	23	22	20	30	22	22	22
D	6	19	6	6	7	8	7	6	6	6	6	6
S	22	24	39	22	26	27	29	27	27	28	28	27
N	29	36	35	54	34	42	42	47	37	44	44	45

The last 10 year responses from the separate schemes and smoothed curves from the cooperative schemes show that F, as expected, had the highest response for yield and lowest response for the other traits (Figure 1). The responses for population D, S and N became increasingly identical during the time. The gain in calving performance in the year 100 was almost equal to that in the separate scheme of population N, where as the gains in yield and

mastitis resistance were between the responses obtained in the separate schemes of N and the populations D and S. The responses of population F followed a different pattern by initially approximating the other populations and then by moving towards the separate scheme of F. This picture for mastitis resistance is the most obvious seen in Figure 1.



Calving performance



Mastitis resistance

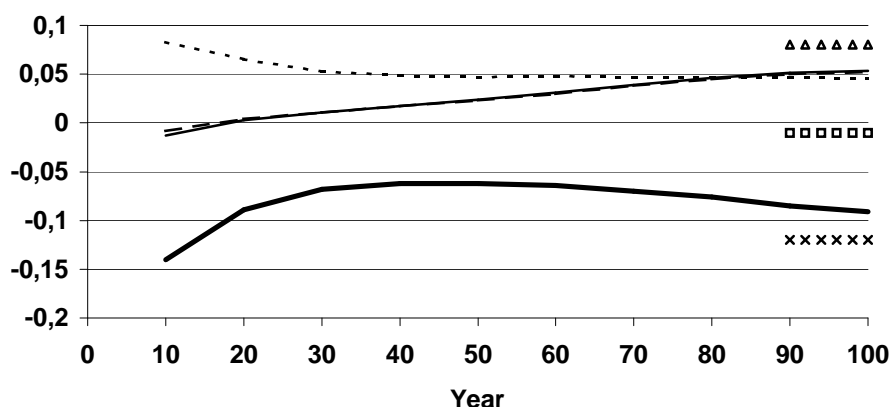


Figure 1. Annual trait responses, in σ_p units, during the time in separate and cooperative schemes

(Separate schemes: F = $\times\times$; D = $\square\square$; S = $\diamond\diamond$; N = $\triangle\triangle$.)

Cooperative schemes: F = bold line; D = line; S = punctured line; N = dotted line)

Although population D and S differed from N in the breeding objective, they obtained similar annual responses for all traits in the year 100 and thus, in TMI (Table 4). Population F, with low weight of mastitis

resistance, achieved a larger gain of yield and lower gains of calving performance and mastitis resistance than the other populations.

Table 4. Annual response in optimised plans with cooperation¹

Population	Breeding objective			Trait		
	L-MR	I-MR	H-MR	Y, $10\times\sigma_p$	CP, $10\times\sigma_p$	MR, $10\times\sigma_p$
F	139	131	125	1.37	0.19	-0.09
D & S	133	137	140	1.21	0.27	0.05
N	133	137	140	1.22	0.27	0.05

¹) Notation as in Table 1.

The differences of the 1st parity cows between separate and cooperative schemes at a given time divided by the annual gain in separate schemes are approximately equivalent to the genetic lag in the years between the two strategies, i.e. with respect to yield and calving

performance all populations benefited from cooperation (Table 5). However, in some cases as for F difference in yield decreased after year 25 or 50. In population N the calving performance in the year 100 was practically similar for the two strategies. With respect to mastitis

resistance populations F, D and S benefited from cooperation, while N did not. The large genetic lags obtained for D and S are due to different sign of responses

under the two strategies. During the time period of the study the overall effect of cooperation in the term of TMI was positive for all populations.

Table 5. Benefit of cooperation expressed in years of separate selection

Population	F			D			S			N		
Year	25	50	100	25	50	100	25	50	100	25	50	100
TMI	1.3	1.9	2.7	4.6	9.5	16.9	1.8	3.3	5.2	1.0	1.7	2.7
Y	6.9	4.0	1.6	4.0	7.7	12.0	1.6	2.3	2.1	1.9	4.3	7.9
CP	4.4	6.4	2.5	6.4	14.1	27.3	2.5	5.2	10.6	0.8	0.6	0.1
MR	4.8	24.6	34.0	24.6	85.4	243.0	34.0	146.0	486.0	-4.6	-14.9	-31.3

Discussion and conclusions. Non-steady state results from gene flow models are sensitive to the nature at the initiation of simulations. In the presented simulation populations were initiated with identical multivariate trait distributions. This is a rather unrealistic situation, but on the other hand, it is reasonable to assume that cooperating populations are uniform with respect to the organisation, registration protocols, breeding evaluation procedures, breeding objectives, management systems and production levels.

The general idea behind cooperation is to overcome some of the negative effect of limited population size on selection differential and intensity (Burrows, 1971). In the first 25 years annual TMI-gain with cooperation was approximately 20%, 7%, 5% and 4% higher than for a separate breeding in population D, S, F and N, respectively. This superiority decreased gradually until the year 100 where the corresponding figures were approximately 19%, 5%, 0% and 2%. The benefit of the cooperation decreased with increasing population size.

For population F the economic weight of mastitis resistance was too low to overcome the effect of a negative genetic correlation with yield. As a consequence, the participation of F in the cooperation decreased during the time. Thus, the benefit of cooperation depends on the diversity of the breeding objectives involved and the genetic correlation between the traits. Another consequence of cooperation was that the realised genetic responses did not reflect directly any of the defined breeding objectives.

Nielsen et al. (2001) and Sørensen et al. (2002) used a stochastic simulation to study the effect of cooperation between two populations similar to population D and S in the present study. Both studies investigated the effect of sets of breeding objectives with two traits and different breeding schemes. The study of Jørgensen & Sørensen (2002a) was similar to the present study, except that the breeding schemes were optimised according to a simple economic assessment. The results from these investigations are in general agreement with the present study.

Dairy cattle breeding organisations are normally operating with a planning period of no more than 50 years. This study shows that with this time horizon populations of limited size will benefit from cooperation.

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