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Partial Restricted Selection Indexes to Fix the Length of Days Open in High – Yielding Dairy Cows

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ABSTRACT

The main goal of the current work is to break the undesirable genetic linkage between milk yield (MY) and length of days open (DO) by using partial restricted selection indexes. Eight unrestricted selection indexes to increase MY and decrease the number of DO and the number of services per conception (NSC) were constructed. The sources of information were various combinations of yields of milk, fat (FY), and protein (PY) beside DO and NSC. Required phenotypic and genetic parameters were estimated from 2538 lactation records of 846 Holstein cows, offspring of 98 sires, and 588 dams, adopting a multi-trait animal model with repeated records. Positive genetic correlations (0.33 to 0.99) were obtained among productive traits. Lactation curve traits were lowly genetically inter-correlated (-0.16 to +0.24). Genetically, MY was more related to DO (0.85) than the NSC (0.58). Selection for aggregate genotype involving MY, DO and NSC would develop Holstein cows with abundant MY (643.5 to 994.8kg) and longer DO (11.3 to 21.3 days) and higher NSC (0.15 to 0.37 service). Due to the collapse of selection accuracy, complete restriction of full index failed to break the unfavorable genetic associations between MY and DO. Meanwhile, it is possible to alleviate the rate of deterioration in reproduction in high lactating Holstein cows using the partial restricted indexes in the case of accepting the barter between the gains from increasing MY by the loss from prolonging DO.

Key words: High yielding dairy cows; Productive traits; Lactation curve traits; Reproductive traits; Selection indexes; Expected gain

INTRODUCTION

The main criticisms of modern high lactating Holstein cows are their lengthening of day's open, increasing number of services per conception, lengthy calving intervals, and consequently low calf-crop per cow. This occurs due to these traits have strong negative genetic correlations with fat, protein, and milk yields (Zavadilová and Zink 2013; Salem and Hammoud 2016a; Abosaq et al. 2017; Frioni et al. 2017; Habib et al. 2020; Zahed et al. 2020; Shemeis and Gouda 2021; Worku and Aylew 2021). Extending the breeding objective in Holstein cows to include reproductive performance traits beside the yield traits was introduced as a strategy to overcome this problem by several authors (Miglior et al. 2005; Faid-allah 2015; Sanad 2016; Abosaq et al. 2017). Applying this strategy did not help so much due to the higher attention paid to the yield traits. Other authors (Ghiasi et al. 2013; Gouda et al. 2017; Shemeis and Gouda 2021) recommended applying restricted selection indexes to break the unfavourable genetic correlations causing this problem. This action also failed because imposing the complete restrictions resulted in zero genetic changes in reproductive traits, resulting in huge reduction in selection accuracy to unacceptable values.

The present study aimed to i) calculate of phenotypic and genetic parameters for the attributes that describe the productive and reproductive performance and lactation curve, ii) construct unrestricted selection indexes to quantify the expected harm facing reproduction when selection for aggregate genotype involving MY, DO and NSC is applied, iii) test if the restriction to zero genetic changes in DO of the most accurate index could break the unfavorable correlations, and vi) construct partial restricted selection indexes to use when trading-off the gain from reducing the loss from long DO with apart from the gain in milk yield is acceptable.

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MATERIALS AND METHODS

The current study used data collected from a commercial dairy herd described by Habib et al. (2020) in which a total of 2538 records of 846 Holstein cows, offspring of 98 sires and 588 dams, were collected over 24 years from 1994 to 2017, and used in estimation of the parameters required for this study.

Management

Cows were fed on total mixed ration (TMR), kept, and reared under natural environmental conditions. To reduce the heat stress during the hot climate, a cool spraying system was supplied. The composition of the TMR used and plan of feeding were described in detail by Habib et al. (2020). The Heifers were artificially inseminated at 375kg body weight. After calving, three times a day machine milking was applied, and the calves were artificially suckled till weaning at 3-month of age.

Traits considered

305-yields of milk (MY), fat (FY), Protein (PY), fat: protein ratio (F/P), peak-kg (P1), peak-day (P2), persistency (Pr), number of days open (DO) and Number of services per conception (NSC) of the Holstein Friesian cows involved in the present study.

Statistical analysis

Repeated records multi-trait animal model was applied to calculate the phenotypic and genetic parameters through VCE-6 software program (Groeneveld et al. 2008) adopting the following model:

$$\mathbf{y= Xb + Za + Wp + e}$$

Where:

y = the observations vector of the studied traits,
b = the fixed effects vector (grand mean, parity; 3 levels, year of calving; 24 levels and season of calving; 4 levels)
a = the random additive genetic direct effects vector,
p = the permanent environmental effects vector
X, Z and W = known incidence matrices relating observations to the respective fixed, random, and permanent environmental effects with Z augmented with columns of zeros for animals with or without records, and
e = the random residual effects vector.

It was assumed that permanent environmental, random, and residual effects are distributed independently with zero mean and variance $\sigma^2_{P,}$, σ^2_a, and σ^2_e, respectively. Therefore: var(a)= $A\sigma^2_a$; var(p)= $I\sigma^2_P$; var(e)= $I\sigma^2_e$.

Definition of the aggregate genotype

Maximizing net profit of the dairy producers through the selection for higher MY, shorter DO and lower NSC, was the breeding goal of the present work. The aggregate genotype (T) was defined as:

$$\mathbf{T = v_1 g_{MY} + v_2 g_{DO} + v_3 g_{NSC}}$$

Where:

g_{MY} = the additive genetic value for milk yield (MY),
g_{DO} = the additive genetic value for days open (DO),
g_{NSC} = the additive genetic value for number of services per conception (NSC), and
v_1, v_2 and v_3 = the relative economic weights for MY, DO and NSC, respectively.

Definition of net income

Assuming constancy of costs of production, the net profit for each cow was computed in terms of revenue of accumulative MY over the first three lactations multiplied by 10 Egyptian Pounds (EGP)/kg milk + the value of the cow as a source of beef (60000 EGP/cow aged 4years – 1000 EGP/month higher than 4-year). Several combinations of the studied traits have been separately investigated. The highest coefficient of determination ($R^{2=}$ 0.88) of the net profit was obtained when MY, DO and NSC were involved in the multiple regression equation.

Estimation of economic values

The estimated economic values of MY, DO and NSC calculated by regressing the net on these three traits were 15.01, -21.20 and -26.50, respectively. The following general linear model of SAS (2011) was used in this estimation:

$$Y_{ijk} = \mu + R_i + S_j + b_1x_{1(ijK)} + b_2x_{2(ijK)} + b_3x_{3(ijK)} + e_{ijK}$$

Where:

Y_{ijk} = Net profit value of the kth cow in the ith calving year and jth calving season.
μ = grand mean
R_i = Fixed effect of the ith calving year (24-level);
S_j = Fixed effects of the jth calving season (4-level);
x_1, x_2 and x_3 = Milk yield, number of days open and number of services per conception of the kth cow in the ith calving year and jth calving season, expressed as a deviation from the corresponding means;
b_1, b_2 and b_3 = Partial regression coefficients of Y on x_1, x_2, and x_3, respectively.
e_{ijk} = Random residual effect associates with observation.

Selection indices

Various combinations of MY, FY, PY, DO and NSC were used to construct eighteen selection indices (Cunningham et al. 1970) categorized according to three strategies as followed:

I. Unrestricted indices including full index, reduced indices, and single trait indices.

II. Complete restricted index (the full index after imposing a complete restriction to the genetic change in DO=0) and

III. Partial restricted indices (the full index after imposing a partial restriction of 90 to 10% by 10 intervals to the genetic change in DO).

RESULTS AND DISCUSSION

Performance levels

Table 1 represents means, coefficients of variation and heritability estimates for productive (MY, FY, PY and F/P), lactation curve (P_1, P_2 and Pr) and reproductive (DO and NSC) traits across the three lactations.

The present level of MY (8337.73kg, Table 1) and those of 8315kg (Salem and Hammoud 2016b) and 8805 (Samoul 2015) and 8550 (Rushdi et al. 2014) were lower than the value of 10369kg found by Radwan and Abo-Elfadl (2016). Faid-Allah (2015) gave much lower value (6384.95kg) for this trait. The value of 268.89kg for FY in present work (Table 1) was higher than the two values of 246.73 and 227kg reported under the Iranian conditions, respectively by Salimi et al. (2017) and Behzadi et al. (2013), and much higher than the value of 187.3kg reported by Frioni et al. (2017) under Uruguay conditions.

Table 1: Mean±SE, coefficients of variation (CV%) and heritability estimates (h^2±SE) for productive, lactation curve and reproductive traits considered

Traits	Mean	CV%	h^2±SE
Milk yield (kg)	8337.73±47.9	28.95	0.36±0.02
Fat yield (kg)	268.89±2.11	39.44	0.30±0.02
Protein Yield (kg)	221.93±1.72	39.08	0.23±0.03
Fat: Protein	1.24±0.005	20.73	0.01±0.01
Peak (kg)	42.90±0.18	21.59	0.07±0.02
Peak (day)	75.43±1.03	68.71	0.04±0.01
Persistency	0.66±0.005	38.64	0.08±0.01
Days open (day)	166.49±2.44	73.85	0.03±0.01
Number of services per conception (service)	2.99±0.04	70.57	0.08±0.02

Protein yield in present study (221.93kg) was comparable to the value of 233.5kg recorded by Salimi et al. (2017), but much higher than the value of 182.8kg recorded by Frioni et al. (2017).

Regarding the reproductive traits, DO averaged 166.49 days in present study (Table 1), it was found to be much higher than the value of 113.1 days recorded by Radwan and Abo-Elfadl (2016) and lower than the value of 219.5 found by Salem and Hammoud (2016b). NSC averaged 2.99 services in the current study (Table 1). This value was lower than that of Samoul (2015), who reported 3.5 services on the same breed, and higher than the value of 1.9 recorded by Salem and Hammoud (2016a). The differences in herd type, number of lactations involved in the analysis and correction for environmental conditions are the probable main causes of variations in the levels of performance in the current work and those reported in literatures.

Variability

Coefficient of variation for the traits considered are shown in Table 1. It appears that DO and NSC (indicators level of reproduction level) are more variable (CV=70.57 and 73.85% for NSC and DO, respectively) than the lactation curve traits (CV=21.59 to 68.71%) and the productive traits (CV=20.73 to 39.44%). These results reveal the effect of environmental circumstances on reproductive performance.

Heritability estimates

The heritability estimates are given in Table 1 for productive, curve lactation and reproductive traits. The h^2 estimate of MY obtained in present study using the repeated records multi-trait animal model was moderate (0.36, Table 1). The present estimate value was similar to the estimates of 0.35, 0.33, 0.33, and 0.34 recorded by Sahin et al. (2012), Abosaq et al. (2017), Öztürk et al. (2021), and Lu et al. (2022), respectively. However, these values fitted out the reported estimates range of 0.17 to 0.30 using the single-trait animal model with repeated records (Pritchard et al. 2013; Chegini et al. 2018; Worku and Aylew 2021) and the reported values of 0.23 to 0.29 estimated using the single-trait animal model (Salem and Hammoud 2016a; Sanad and Hassanana 2017; Tohidi and Nazari 2023).

The present h^2- estimate for FY (0.30) in Table 1 and that of 0.27 estimated by Lu et al. (2022) were higher than the estimates 0.21 to 0.25 obtained with similar model (Carthy et al. 2016; Frioni et al. 2017; Shemeis and Gouda 2021; Jayawardana et al. 2023) and the value of 0.11 to 0.22 estimated via the single trait animal model (Stanojević et al. 2013; Albarrán-Portillo and Pollott 2013; Tohidi and Nazari 2023).

Protein yield was moderate heritable (0.23, Table 1; 0.21, Frioni et al. 2017; Jayawardana et al. 2023). Slightly higher values (0.28, 0.26 and 0.25) were estimated by Lu et al. (2022), Shemeis and Gouda (2021) and Carthy et al. (2016), respectively.

The h^2-value for fat to protein ratio estimated in the present study using the repeated records multi-trait animal model was negligible (0.01). This estimate was lower than the value of 0.16 reported in literature with similar model (Carthy et al. 2016; Chegini et al. 2018).

The traits of lactation curve were found to be low heritable (0.04 to 0.08). Whereas the h^2 estimate of peak-day (0.04) fitted within the range 0.03 to 0.13 recorded in literature (Muir et al. 2004; Albarrán-portillo and Pollott 2013; Wasike et al. 2014; Pangmao et al. 2022). However, the h^2 estimate of peak-kg (0.07) fitted out the range 0.16 to 0.27 reported in the literature (Albarrán-portillo and Pollott 2013; Wasike et al. 2014; Salem and Hammoud 2016b; Abosaq et al. 2017; Pangmao et al. 2022). The persistency trait was 8% heritable (Table 1). However, various heritability estimates were found for this trait in literature (0.18, Muir et al. 2004; 0.05, López-Ordaz et al. 2009; 0.15, Albarrán-portillo and Pollott 2013; 0.17, Wasike et al. 2014; and 0.03, Pangmao et al. 2022). Differences used in calculation of persistency is the main contributor to these differences.

The present h^2 value of 0.03 obtained for DO fitted within the range of 0.03 to 0.14 found in the literature (Salem and Hammoud 2016b; Ben Zaabza et al. 2016; Farrag et al. 2020; Zahed et al. 2020; Worku and Aylew 2021; Shemeis and Gouda 2021).

The current heritability estimate for NSC (0.08) was comparable to the low reported estimates (0.01 to 0.12) estimated by several authors (Salem and Hammoud 2016b; Farrag et al. 2020; Öztürk et al. 2021; Shemeis and Gouda 2021; Estrada-León et al. 2023).

The low h^2-value for the traits describes the lactation curve and the reproductive performance of Holstein cows illustrated that improving feeding, health, and reproductive management as non-genetic factors is ideal way to achieve these traits.

Correlations

Table 2 presents the phenotypic and genetic relationships among the traits involved in the present work.

Correlation among productive traits

In agreement with the studies of Shemeis and Gouda (2021), Chegini et al. (2018), Frioni et al. (2017), Zavadilová and Zink (2013) and Amini et al. (2011), the present study (Table 2) showed strong inter genetic (0.59 to 0.99) and phenotypic correlations (0.70 to 0.87) among MY, FY, PY. These correlations suggest that genetic improvement for any trait would entail corresponding improvement in other traits. Genetically, fat to protein ratio was highly correlated positively with MY, FY and PY (0.33, 0.75 and 0.69, respectively). Chegini et al. (2018) reported that the F/P was genetically correlated negatively with each of MY (-0.31) and PY (-0.46) and positively with FY (0.22).

Correlations among lactation curve traits

Except for the r_p between peak-kg and persistency (-0.56), lactation curve traits are lowly correlated genetically and phenotypically. The r_G of -0.16 between peak-kg and peak-day in the present study was lower than the value of (-0.28) obtained by Wasike et al. (2014). The very low negative genetic relationship between peak-kg and persistency (-0.05) is agreed with the value of -0.09 reported by Wasike et al. (2014). Peak-day and persistency were positively genetically correlated (0.24, Table 2; 0.54, Muir et al. 2004; 0.98, Wasike et al. 2014). Peak-kg had negligible phenotypic associations with peak-day (0.03, Table 2; -0.16, Wasike et al. 2014). The phenotypic correlation illustrated in present work between peak-day and persistency (-0.56) is differ in the direction and magnitude than the values 0.36 and 0.75 that obtained by Muir et al. (2004) and Wasike et al. (2014), respectively.

Correlation among reproductive traits

A moderate genetic correlation (r_G=0.36, Table 2; 0.34, Radwan et al. 2015) was found between DO and NSC. These correlations were much lower than the estimates of 0.49 to 0.99 found in the literatures (Ghiasi et al. 2011; Zambrano and Echeverri 2014; Yamazaki et al. 2014; Guo et al. 2014; Farrag et al. 2020; Zahed et al. 2020; Shemeis and Gouda 2021).

Correlation between productive and reproductive traits

Unfavorable relationships were noticed between MY and reproductive performance expressed as numbers of DO and NSC (r_G=0.85 and 0.43, respectively). The same genetic trend (0.26 to 0.99) has been recorded by several authors (Zavadilová and Zink 2013; Salem and Hammoud 2016a; Frioni et al. 2017; Abosaq et al. 2017; Zahed et al. 2020; Shemeis and Gouda 2021; Worku and Aylew 2021).

Genetically, NSC and DO are lowly correlated positively with FY (0.20 and 0.12, respectively) and PY (0.14 to 0.12, respectively) and moderately with F/P (0.48 and 0.26, respectively). The unfavorable genetic association between productive and reproductive traits in both magnitude and direction, reveal that any effort for improving yield traits genetically, would lead to negative effect on the reproduction high-yielding cows represented by longer DO and higher NSC.

Indexes

Unrestricted selection indices (alternative I)

Eight unrestricted selection indices were constructed using the above mentioned estimated genetic, phenotypic and economic parameters presented in Table 1 and 2. This alternative involved the all traits index (full index, I_1), 4 reduced indices (I_2, I_3, I_4 and I_6) and 3 single trait indexes (I_5, I_7 and I_8).

Weighing factors and value of sources of information

Table 3 showed the weighing factors (b-values), value of each trait as a source of information, indexes standard deviation (σ_I), selection accuracy (r_{TI}) and proportionate efficiency (RE) of all indexes relative to the intact index.

For the multi-trait indexes, the b-values were positive for MY, DO and NSC, and negative for FY and PY. The MY, DO and NSC are the most valuable sources of information in the full index (62.6, 23.5 and 23.8%, respectively). In the best reduced index (I_2) including the most valuable traits, MY remained the most valuable trait (74.8%) followed by DO (12.6%) then the NSC (11.6%). Omitting NSC and DO, separately, from I_2 to form I_3 and I_4, respectively increased the value of MY as a source of information to reach 75.7 and 81.1%, respectively.

Accuracy of indices

The accuracy of selection for the eight indices is presented in Table 3. The highest selection accuracy ($r_{TI=}$ 0.92) was recorded using the intact index (I_1). Due to its great contribution in the aggregate genotype, selection based on MY (the best single trait index, I_5) or MY and NSC (I_4) or MY and DO (I_3) is expected to give comparable accuracy of selection (0.60, 0.64 and 0.65, respectively). Combining the three most valuable sources of information into one index (I_2) is expected to be as 80.4% accurate as the full index.

Expected response from selection based on the unrestricted indices

The expected genetic changes in individual traits expressed absolute units of measurements and as percentage from the original means for the most accurate five unrestricted indices are given in Table 4.

Applying the first alternative of selection based on the most accurate unrestricted indices would be expected to enhance the production of Holstein cows in terms of MY (+643.5 to 994.82kg), FY (+12.09 to 25.92kg) and PY (+9.29 to 18.96kg). This improvement in yield-traits would be coupled with deterioration in the reproduction in terms of longer number of DO (+11.3 to 21.3 day) and higher NSC (+0.15 to 0.37 service).

Table 2: Genetic (above diagonal) and phenotypic (below diagonal) correlation among productive, lactation curve and reproductive traits

	MY	FY	PY	F/P	P1	P2	Pr	DO	NSC
MY	…	0.59	0.61	0.33	0.52	0.14	0.84	0.85	0.43
FY	0.70	…	0.99	0.75	0.71	-0.44	0.18	0.12	0.20
PY	0.71	0.87	…	0.69	0.74	-0.38	0.21	0.12	0.14
F:P	-0.01	0.18	-0.26	…	0.21	-0.72	-0.08	0.21	0.58
P1	0.18	0.17	0.16	0.02	…	-0.16	-0.05	0.27	0.13
P2	-0.01	-0.08	-0.07	-0.02	0.03	…	0.24	0.41	0.57
Pr	0.81	0.29	0.30	-0.02	-0.56	-0.05	…	0.50	0.52
DO	0.60	0.24	0.26	-0.02	0.02	0.01	0.02	…	0.35
NSC	-0.18	0.14	0.12	0.03	-0.04	-0.06	-0.07	0.17	…

MY=milk yield in 305-day, FY=fat yield in 305-day, PY= protein yield in 305-day, F/P=fat to protein ratio, P1=peak-kg, P2=peak-day, Pr=persistency, DO=days open, NSC=number of services per conception.

Table 3: Weighing factors (b-value), value of each trait as source of information (in parentheses), standard deviation of the index (σ_I), accuracy of selection (r_{TI}) and relative efficiency (RE) of the indices considered

Index	b-value for each source of information[a]:					σ_I	r_{TI}	RE%[b]
	MY	FY	PY	DO	NSC			
I_1(Full)	18.15 (62.61)	-76.33 (2.85)	-111.92 (4.31)	-125.23 (23.48)	197.51 (23.85)	14470.17	0.92	100
I_2	8.38 (74.86)	…	…	-63.67 (12.56)	924.82 (11.61)	11551.53	0.74	80.43
I_3	6.94 (75.67)	…	…	-42.01 (7.79)	…	10210.66	0.65	70.65
I_4	5.65 (81.14)	…	…	…	853.82 (6.79)	10101.15	0.64	69.57
I_5	5.28 (100)	…	…	…	…	9415.01	0.60	65.22
I_6	…	…	…	18.92 (34.41)	760.90 (14.47)	2904.25	0.19	20.65
I_7	…	…	…	21.13 (100)	…	2484.03	0.16	17.39
I_8	…	…	…	…	949.25 (100)	1904.89	0.12	13.04

[a]: MY= milk yield in 305-day, FY= fat yield in 305-day, PY= protein yield in 305-day, DO=days open, NSC=number of services per conception; [b]: relative to the full index (I_1)= 100.

Table 4: Expected genetic changes in productive, lactation curve and reproductive traits (intensity of selection= 1.0)

Index	Traits involved*	Productive Traits				Lactation curve Traits			Reproductive traits	
		MY	FY	PY	F/P	P1	P2	Pr	DO	NSC
I_1	Full index	994.82	12.09	9.29	-0.81	0.72	5.7	0.07	21.30	0.37
	%	11.93	4.50	4.19	-65.32	1.68	7.56	10.61	12.79	12.37
I_2	MY, DO, NSC	788.45	25.92	18.96	-0.51	1.04	1.87	0.05	13.04	0.25
	%	9.46	9.64	8.54	-40.88	2.42	2.48	7.21	7.83	8.26
I_3	MY, DO	697.03	22.93	17.11	-0.38	0.93	0.97	0.04	11.68	0.16
	%	8.36	8.53	7.71	-30.55	2.17	1.29	6.12	7.01	5.34
I_4	MY, NSC	690.39	20.53	15.03	0.01	0.80	1.47	0.04	12.08	0.21
	%	8.28	7.64	6.77	0.62	1.87	1.94	6.03	7.26	6.87
I_5	MY	643.5	19.42	14.47	0.01	0.77	0.85	0.04	11.30	0.15
	%	7.72	7.22	6.52	0.48	1.79	1.13	5.45	6.79	4.90

*: MY= milk yield in 305-day, FY= fat yield in 305-day, PY= protein yield in 305-day, F/P=fat to protein ratio, P_1=peak-kg, P_2=peak-day, Pr= persistency, DO=days open, NSC=number of services per conception; %: Expected genetic changes expressed as a percentage of the original means

Table 5: Expected reduction in accuracy of selection, index standard deviation and the rate of improvement in individual traits due to complete restriction.

Item	Full index	
	Unrestricted (I_1)	Restricted (I_{1100})
r_{TI}	0.92	0.28
σ_I	14470.2	4434.3
Δgi in:		
- Productive traits		
MY	11.93	3.54
FY	4.50	11.37
PY	4.19	9.85
F/P	-65.32	-16.13
- Lactation curve traits		
P1	1.68	2.33
P2	7.56	-3.46
Pr	10.61	0.73
- Reproductive traits		
DO	12.79	0.00
NSC	12.37	1.60

r_{TI}=accuracy of selection, σ_I=standard deviation of the index, Δgi=Expected genetic changes Expressed as a percentage of the original means, MY= milk yield in 305-day, FY= fat yield in 305-day, PY= protein yield in 305-day, F/P=fat to protein ratio, P_1=peak-kg, P_2=peak-day, Pr=persistency, Do=days open, NSC=number of services per conception.

Reproductively, selection using the best reduced index (I_2) is expected to be preferable than that based on the full index, as each round of selection with intensity equal to 1.0 based on I_2 would limit the unfavorable increase in DO and NSC by 4.96 and 4.11%, respectively. This benefit will cost the breeder 2.47% losses in the gain expected in MY.

The ominous genetic changes expected from selection based on any of the unrestricted selection indexes (I_1 to I_8) on reproductive attributes in terms of extending DO and increasing NSC would reduce the net income of the dairy producer through increasing the veterinary expense and breeding costs and reducing the calf-crop. This forces the breeder to use the restricted selection indexes to stop or at least to limit these adverse effects via using the complete or partial restricted indexes.

Complete restricted index (alternative II)

Single complete restriction with zero genetic change in DO was imposed to the full index (I_{1100}). Costs of these restrictions in terms of reduction in accuracy of selection and in the expected gain in the individual characters involved in the true breeding value are presented in Table 5.

Comparing the full index (I_1) with its completely restricted form (I_{1100}) indicate that limiting the genetic changes in DO to zero would be associated with unacceptable massive drop in accuracy of selection (r_{TI}= 0.28 only) and in the rate of gain in MY from 11.93 to 3.54%. This is due to the presence of DO in the aggregate genotype and their strong positive genetic relationships (r_G= 0.85, Table 2) with MY (the most economical contributor in the aggregate genotype). This strategy of selection is expected to increase the FY from 4.5 to 11.37% and PY from 4.19 to 9.85%.

Partial restricted indexes (alternative III)

This alternative depends on the discharge between the loss from a decrease in MY and the gain from halting the prolongation in DO. To fix the expected genetic change in number of days open at levels of 90 to 10 % by 10 intervals, nine partial restricted selectin indexes were developed from

Table 6: Expected reduction in accuracy of selection and the rate of improvement in individual traits

	Full index	Partial restricted Indexes								
Item	I_1	I_{190}	I_{180}	I_{170}	I_{160}	I_{150}	I_{140}	I_{130}	I_{120}	I_{110}
r_{TI}	0.92	0.67	0.65	0.63	0.61	0.58	0.55	0.51	0.46	0.39
Restriction rate	-	10	20	30	40	50	60	70	80	90
Δgi in:										
Productive traits										
MY	11.93	8.60	8.38	8.12	7.82	7.47	7.05	6.52	5.85	4.94
FY	4.50	5.48	5.58	5.71	5.86	6.07	6.35	6.75	7.38	8.52
PY	4.19	4.94	5.02	5.12	5.25	5.42	5.65	5.97	6.49	7.44
F/P	-65.32	-46.19	-44.91	-43.43	-41.94	-39.52	-37.10	-33.87	-29.84	-25.00
Lactation curve traits										
P_1	1.68	1.61	1.61	1.62	1.61	1.63	1.66	1.70	1.77	1.91
P_2	7.56	4.24	3.99	3.70	3.35	2.93	2.41	1.72	0.80	-0.64
Pr	10.61	7.53	7.27	6.97	6.62	6.20	5.68	5.03	4.17	2.91
Reproductive traits										
DO	12.79	8.39	8.08	7.72	7.30	6.79	6.16	5.37	4.31	2.77
NSC	12.37	8.47	8.20	7.89	7.36	7.02	6.69	6.02	5.02	3.68

r_{TI}= accuracy of selection, Δgi=Expected genetic changes Expressed as a percentage of the original means, MY= milk yield in 305-day, FY= fat yield in 305-day, PY= protein yield in 305-day, F/P=fat to protein ratio, P_1= peak-kg, P_2= peak-day, Pr= persistency, DO=days open, NSC=number of services per conception.

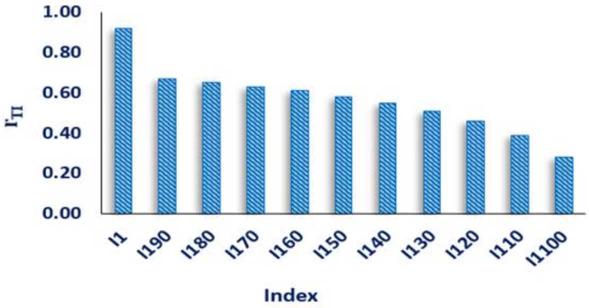

Fig. 1: Effect of complete and partial restriction of days open (DO) on accuracy of selection (r_{TI}).

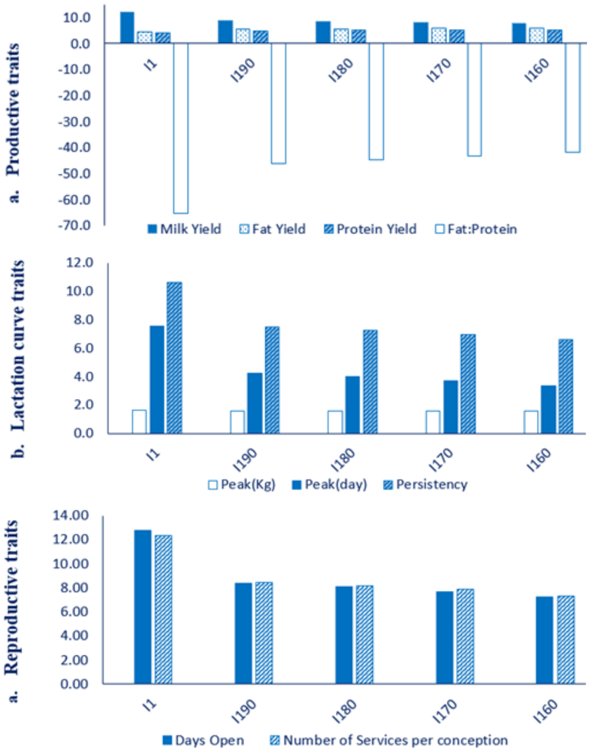

Fig. 2: Expected genetic changes in individual traits per each round of selection based on unrestricted and partial restricted indices (Expressed as a percentage of the original means).

the full index. The costs of this partial restriction in terms of loss in selection accuracy and in the expected genetic enhancement in individual traits are shown in Table 6 and Fig. 1 and 2.

Comparing the nine partially restricted indices with their completely restricted form (I_{1100}) indicates the possibility of limiting the giant reduction in accuracy of selection (Fig. 1). In the context of apprehension about the severe decline in accuracy of selection when using a high degree of restriction (90-50%), it could consider that I_{160} is the threshold at which the degree of restriction can be accepted r_{TI}=0.61 (accepting 60% of the increase in DO). Accuracy of selection is 0.61 to 0.67 for I_{190} to I_{160}, respectively, in lieu of 0.28 for the completely restricted form (I_{1100}). These tactics allow the breeder to gain 652.4 to 717.4kg in milk yield (7.8 to 8.6%) in turn of 12.15 to 13.97day increase in DO (7.3 to 8.4%).

Comparing the partial restricted indices with their unrestricted form (I_1) (Table 6 and Fig. 2) indicates the possibilities of achieving considerable improvement in the original mean of FY (5.48 to 5.86%) and PY (4.94 to 5.25%) with fixing the NSC to 7.36 to 8.47% vs 12.37% in case of using the unrestricted form (I_1).

Conclusion

It could be concluded that selection for aggregate genotype involving MY, DO and NSC is expected to develop Holstein cows characterized by abundant MY and worth reproduction in terms of longer DO and higher NSC.

It is not possible to break the unfavorable genetic associations between the most economical productive (MY) and reproductive (DO and NSC) traits using the complete restricted indexes. Meanwhile, it is possible to alleviate the rate of deterioration in reproduction in high lactating Holstein cows using the partial restricted indexes in case of accepting the barter between the gain from increasing of MY by the losing from prolonging the DO.

Author's contribution

AAH, GFG, ARS and MME suggested the research concept and plan. AAH edited, analyzed the data, constructed the selection indices and prepared the first draft. All authors participated in editing, critical reviewing, and approving the present version of the manuscript.

Ethics approval

This manuscript does not require IRB/IACUC approval because there are no human and animal participants.

Conflict of interest

The authors have declared no conflict of interest.

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