Multi-Trait and Multi-Source Selection Indices for Milk Production and Reproductive Traits in a Herd of Holstein Cattle in Egypt

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ABSTRAK

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Penelitian Ini dilakukan dengan tujuan mencari kemungkinan meningkatkan produksi susu dan reproduktifitas sapi Holstein melalui pemanfaatan metode indeks seleksi yang meliputi indeks berikut: umum, tidak lengkap, sub dan multi informasi (*Own-Performance, Full-Sibs and Half-Sibs*). Data diperoleh dari peternakan komersial (Safi Masr for Developing the Animal Resources), berlokasi di Delta sungai Nil, Dakahlia, Mesir. Data meliputi 4791 catatan dari 1797 ekor sapi, 794 induk dan 67 pejantan yang mewakili catatan pada kurun waktu 2002 sampai 2012. Estimasi parameter genetika dan phenotipik untuk penelitian trait/sifat dihitung dan digunakan untuk membentuk 18 indeks seleksiguna meningkatkan produksi susu dan reproduksi. Indeks penuh melibatkan produksi susu 305 hari (305-dMY), periode laktasi (LP), days open (DO) dan umur beranakn pertama (AFC) mempunyai korelasi paling tinggi dengan nilai aggregate breeding (R_{ih} = 0.518; RE=100%). Korelasinya berada pada 0,455 bila 305-dMY dihilangkan dari index. Index umum mempunyai pendugaan genetic yang maximum pada 305-dMY (132.6 kg) per generasi diikuti dengan menurunnya LP (-4,679 hari), DO (-3.449 day) dan AFC (-1,41 bulan) jika ke empat sifat dimasukkan ke dalam index (I_1). Pendugaan genetik untuk 305-dMY menurun sampai 26,84kg/generasi bila 305-dMY dihilangkan dari dari index 5 (I_5). Selanjutnya menggunakan informasi multi-sumber akan meningkatkan korelasi dengan nilai *aggregate breeding* (R_{ih}= 0.740; RE=142.91%) dan meningkatkan pendugaan peningkatan genetik tiap generasi untuk 305-dMY (209 kg) dan menurunkan pendugaan peningkatan genetik untuk LP (-6,37 hari), DO (-4,244 hari) dan AFC (1,843 bulan) apabila keempat trait/sifat dimasukkan kedalam index (I_{16}). Dapat disarankan untuk menggunakan indeks yang lebih tinggi untuk Rih (I_1 $_{(RE=100)}$) untuk meningkatkan produksi susu dan sifat reproduksi pada sapi Holstein berdasarkan strategi performannya sendiri dan menggunakan (I_{16} $_{(RE=142.91)}$) berdasarkan strategi multi-sumber untuk mendapatkan akurasi yang tinggi dan perubahan genetik harapan yang tinggi per generasi dibandingkan dengan indeks general.

Kata Kunci: Bobot Badan, Parameter Genetik, *Selection Index*, Sapi Holstein

ABSTRACT

Faid-Allah E. 2015. Multi-trait and multi-source selection indices for milk production and reproductive traits in a herd of Holstein cattle in Egypt. JITV 20(3): 159-167. DOI: http://dx.doi.org/10.14334/jitv.v20i3.1182

The main aim of this study was explore possibility to improve milk production and reproductive traits of Holstein cattle via selection index method which include general, reduced, sub and Multi-source of information indices (Own-Performance, Full-Sibs and Half-Sibs). Data was obtained from a commercial farm (Safi Masr for Developing the Animal Resources), located in the Nile Delta, Dakahlia, Egypt. Data included 4791 records of 1797 cows, 794 dams and 67 sires that represented the period from 2002 to 2012. Estimates of genetic and phenotypic parameters for studied traits were computed and used to construct 18 selection indices to improve milk production and reproductive traits. Full index incorporating milk yield at 305d (305-dMY), lactation period (LP), days open (DO) and age at first calving (AFC) had the highest correlation with aggregate breeding value (R_{ih} = 0.518; RE=100%). The correlation fell to 0.455 when 305-dMY was omitted from the index. The general index has the maximum expected genetic gain in 305-dMY (132.6 kg) per generation were accompanied by decrease of LP (-4.679 day), DO (-3.449 day) and AFC (-1.41 month) when all four traits were included in the index (I_1). The expected genetic gain for 305-dMY decreased to 26.84 kg/generation when 305-dMY was excluded in index 5 (I_5). In addition, Using multi-source of information will enhance correlation with aggregate breeding value (R_{ih}= 0.740; RE=142.91%) and raised the expected genetic gain per generation for 305-dMY (209 kg) and decreasing the expected genetic gain for LP (-6.37 day), DO (-4.244 day) and AFC (1.843 month) when all four traits were included in the index (I_{16}). It could be suggested using the higher indexes of Rih (I_1 $_{(RE=100)}$) to improve milk production and reproductive traits in Holstein cattle under own-performance strategy and using (I_{16} $_{(RE=142.91)}$) under multi-source strategy to get high accuracy and higher expected genetic changes per generation compare to general index.

Key Words: Body Weight, Genetic Parameter, Selection Index, Holstein Cattle

INTRODUCTION

Breeding programs are basically designed to identify superior genotypes for different traits of economic interest, based on performance information of animals and their relatives, in order to disseminate their genes in the population. Literature shows that the implementation of selection indexes was an important step in the evolution of the dairy industry in the developed countries (Cardoso et al. 2014).

Increasing use of selection indices and greater scope in number of traits has been observed in dairy cattle populations in the past two decades included main components related to production, durability, health and reproduction in each selection index (Miglior et al. 2005). The traits that were considered for selection were milk yield, daily gain, weaning weight, calving interval, milk fat yield, productive lifetime, pre-weaning survival rate, post-weaning survival rate and age at first calving. Age at first calving and calving interval are important because they determine the days a cow is in milk and the number of calves in the productive lifetime for replacement or sale (Wahinya et al. 2015).

Multiple trait selection index is widely accepted as the method of choice when improvement is desired for more than one trait (Banga 2009). Undesirable effects were observed on traits with unfavorable correlations with milk production, such as decline in fertility. As information on other traits related to health, fertility and longevity started being recorded and genetic evaluations for these traits were performed, they were gradually included as breeding goals of dairy cattle (Norman et al. 2010).

This study was carried out to investigate the possibility to improve milk production and reproductive traits of Holstein cattle via selection index method under two strategies, own-performance strategy to use easy index and multi-source of information strategy to get high accuracy and higher expected genetic changes per generation compare to general index when more information is used.

MATERIALS AND METHODS

Data, Feeding and management: Data of Holstein cattle were obtained from a commercial farm (Safi Masr for Developing the Animal Resources), located at the Nile Delta, Dakahlia, Egypt. Data were comprised of 4791 records of 67 sires and 794 dams from the year 2002 to 2012. Genetic and non-genetic factors as sire, parity (1st to ≥6th), year of calving (2002 to 2012) and calving season (winter from 22/12 to 21/3, spring form 22/3 to 21/6, summer from 22/6 to 21/9 and autumn from 22/9 to 21/12). Animals were housed free in shaded open yards, grouped according to average daily milk yield, and fed on TMR system a round year as recommended by NRC (2001). Holstein heifers were artificially inseminated (imported semen of Holstein sires) for the first time when reaching 350:370 kg of weight and pregnancy was detected by rectal palpation at 60 days after service. The cows were machine milked three times per day. Studied traits are 305-day milk yield (305-dMY) and lactation period (LP) as milk production traits and days open (DO) and age at first calving (AFC) as reproductive traits were expressed in time intervals. These aspects were discussed by Faid-Allah (2015).

Genetic parameters: The genetic parameters were estimated by derivative free REML with a simplex algorithm using the Multiple Trait Derivative-Free Restricted Maximum Likelihood (MTDFREML) program of Boldman et al. (1995). The animal model in matrix notation as follow:

$$Y = Xb + Za + e$$

where:

Y	=	Vector of observations (milk production and reproductive traits)
b	=	Vector of fixed effects (i.e. parity, year and season of calving)
a	=	Vector of random additive genetic direct effects (i.e. sire and dam)
X, Z	=	Known incidence matrices relating observations to the respective traits
e	=	Vector of residual effects $(0, I\sigma_e^2)$

Selection Index: The four traits studied were used in combinations to construct 18 selection indexes grouped under two strategies based on (305-dMY, LP, DO and AFC) as follows: Strategy 1: own-performance. Strategy 2: Multi-source of information (Own-Performance, Full-Sibs and Half-Sibs). The Selection criterion and the selection objectives are the same.

General Selection Index: Selection Index Program (Wagenaar et al. 1995) and Matlab program (Matlab 2002) were used to construct the selection indices. Studied traits were used to construct 18 selection indices. Selection index was obtained by solving the following equation:

$$I = b_1 P_1 + b_2 P_2 + \cdots b_n P_n = \sum_{i=1}^{n} biPi$$

where:

I	=	Selection index
bi	=	Index weights for each trait in the index
P_i	=	Phenotypic measurement for each trait in the index

The general index was obtained by solving the following equations given in matrix expression according to Cunningham (1969):

$$P*b = G*a \quad \text{to give} \quad b = P^{-1} *Ga$$

where:
P = Phenotypic variances (cov.) matrix
G = Genetic variances (cov.) matrix
a = Economic weights column vector
b = Weighting factors column vector

Reduced selection index: The reduced selection index can be developed by omitting one or more traits from the original index. In relation to the original index the efficiency of the new index, the reduced one, is expected to be decreased depending on the value of the omitted trait in the original index.

Sub Selection index: The sub-index of each trait was achieved by solving the following equation according to Cunningham (1969):

$$b = P^{-1} G$$

where:
b = Weighting factors vector for the sub index
P^{-1} = P matrix inverse
G = Covariance vector between the variables in the index and the main trait in the aggregate genotypes

Multi-Source selection index: The sources of information used in different combinations for each trait were individual's own phenotypic value (OP), its full (FS) and half sibs (HS) averages. The general outline of the selection indices for ranking of the breeding value was as follow:

$$I = \sum_{i=1}^{n} [b_{i1}(P_{i1}-\mu_i) + b_{i2}(P_{i2}-\mu_i) + b_{i3}(P_{i3}-\mu_i) + b_{i4}(P_{i4}-\mu_i)]$$

where:
n = Number of the traits
μ_i = Population mean of the ith trait
b_{ij} = Partial regression coefficients of ith trait of jth group of relatives (i=1-4) ; (j=1-3). P_{i1}, P_{i2}, P_{i3} and P_{i4}= OP and its FS and HS averages of animal candidates

The P and G matrices, respectively consisting of the variances (cov.) from OP, FS and HS family sources were obtained for animals. Estimation of genetic and phenotypic variances (cov.) for FS and HS performance for the P and G matrix were estimated according to the procedures given by Liljedahl et al. (1979) as follow:

σp_{ij} pi' j'= C1 $\sigma p_i p_i$'+ C2 σ_{AiAi}' for P matrix
σp_{ij} Ai = Cσ_{AiAi}'   (i = i' or i ≠ i') for G matrix

where:
σp_{ij} = Phenotypic variances (cov.) between traits in i and **i'** (i = i' or i ≠ i')
$\sigma_{AiAi'}$ = Additive genetic variances (cov.) or between traits in i and i' (i = i' or i ≠ i')

The procedures for obtaining C1 and C2 values for each element in P matrix and C values for each element in G matrix have been utilized according to Liljedahl et al. (1979).

Properties of the selection index: the properties of the selection index according to Cunningham (1969) were calculated as following:
1. Standard deviation of the index (σi) = $\sqrt{b'Pb}$
2. Standard deviation of the aggregate genotype (σt) = $\sqrt{a'Ga}$
3. Correlation between the index and the aggregate genotype (R_{IH})= $\sigma i/\sigma t$
4. Value of each trait in the index = Vt

$$Vt = 100 - \sqrt{\frac{b'Pb - b_i / W_{ii}}{b'Pb}} \times 100$$

where:
Vt = Value of each trait in the index
P = Phenotypic variances (cov.) matrix
B = Weighting factors column vector
w_{ii} = a diagonal element of p^{-1}

Expected genetic change ΔG (EG): EG for each trait, after one generation of selection on the index ($i = 1$) was obtained by solving either of the following equations (Van der Werf & Goddard 2003):

$$\Delta Gi = (i \, b' \, Gi)/\sigma i$$

where:
i = Selection intensity
σI = Standard deviation of the index
Gi = the ith column of the G matrix

The relative economic value (Rev): The economic values (a) were calculated as one phenotypic standard deviation (σp) as relative economic weight of each trait as reported by Atil (2006) and Faid-Allah & Ghoneim (2012) as shown in table 1. It is Non-objective methods with modification in its charge to be negative for LP, DO and AFC to get higher desired genetic gain for traits under selection depends on the trait phenotypic dispersion.

RESULTS AND DISCUSSION

Descriptive statistics

Table (1) shows the arithmetic mean of milk production traits as 305 day milk yield and lactation period are 6384.95 kg and 332 day, respectively.

The average and coefficient of variability (CV %) of 305-day milk yield for Holstein cows were 4295 (CV=19.7), 9038 kg (CV=13.1) and 8455.4 (CV= 18.2) in Egypt as reported by Ashmawy & Khalil (1990), Salem et al. (2006) and Hammoud (2013), respectively.

Table 1. Descriptive statistics of studied traits for milk production and reproductive status in Holstein cows

Traits	Records №	Mean	SD	CV (%)	#Rev
Milk Production Traits					
Milk Yield at 305d (305-dMY), kg	4791	6384.95	1236.9	19.37	1
Lactation Period (LP), day	4791	332.00	49.38	14.87	-25.05
Reproductive Traits (Time intervals)					
Days Open (DO), day	3108	157.93	35.72	22.62	-34.61
Age at First Calving (AFC), month	2431	30.51	5.12	16.79	-8.05

#Rev= the relative economic value

The lactation period (LP) for Holstein cows was found to vary from 286 to 407 days and it's CV ranged from 5 to 31.74 % as mentioned by El-Arian et al. (2003), Salem et al. (2006), Hammoud (2013) and Osman et al. (2013a) in Egypt.

Usman et al. (2012) reported that LP of Holstein cows ranged from 185 to 514 days with mean of 366.5±76.71 days (CV= 20.93).

The mean (CV %) of reproductive traits as days open and age at first calving (Table 1) are 157.93 day (22.62) and 30.51 month (16.79), respectively. The low age at first calving in a particular dairy cattle herd is a reflection of the good managerial strategy adopted in that herd. High level of management allows the growing heifers to reach the suitable body weight for breeding earlier and this in turn leads to lower age at first calving.

Table (1) shows the mean of 305-dMY were lower than those found by Abou-Bakr et al. (2006) being 10847 kg, respectively and those reported by Salem et al. (2006) being 9038 kg, respectively Holstein cows in Egypt. The mean of LP was lower than the mean of 370 and 407 days obtained by Abou-Bakr et al. (2006) and Salem et al. (2006), respectively. The estimated of DO obtained in this study was shorter than that of 255 days found by Abou-Bakr et al. (2000), but was similar to 154 days obtained by Abou-Bakr et al. (2006). High phenotypic dispersion in the data of studied traits will enhance the selection response in our planned for breeding program by selection index method.

Variance components

Table (2) show estimates of variance components, heritability (h^2) as well as genetic correlations (r_G) and phenotypic correlations (r_P) among different milk production and reproductive traits. The variance components of 305-dMY per kg, LP per day, Do per day and AFC per month are 281500, 273.1 , 134 and 7.471 for genetic variance, 1530000, 2438, 1276 and 26.21 for phenotypic variance, respectively. These estimates are in agreement with Hammoud (2013) working on a herd of Holstein cows in Egypt and reported that the variance components of 305-dMY per kg, LP per day and DO per day were 466296, 2848.64 and 3075.04 for genetic variance, 1102847, 5933.22 and 5741.82 for phenotypic variance, respectively.

Table (2) show estimates of heritability for 305-dMY, LP, DO and AFC are 0.184, 0.112, 0.105, and 0.285, respectively. These estimates are low to moderate and in agreement with most of the previous investigators. Heritability estimated were 0.17, 0.29 and 0.20 as reported by Meyer (1985), Dadpasand et al. (2013), Ghiasi et al. (2013) and Kaygisiz (2013) for 305-dMY; 0.06, 0.07 and 0.184 ±0.161 as reported by Lakshmi et al. (2009), El-Arian et al (2003) and Usman et al. (2012) for LP; 0.20 ±0.06, and 0.23 ±0.105 as reported by Salem et al (2006) for AFC.

Ghiasi et al. (2013) showed that heritability estimated of 305-dMY and DO were 0.32 and 0.076, respectively for Holstein cows. Endris et al. (2013) mention that estimated of heritability for 305-dMY of Holstein crossbred cows was 0.24 ±0.12, respectively.

In Egypt, heritability estimated of LP and DO were 0.38 and 0.42 (El-Shalmani 2011) and 0.04 and 0.20 (Shalaby et al. 2012) for first lactation of Friesian cows. Moreover, Hammoud (2013) showed that heritability estimates of 305-dMY, LP, and DO were 0.42, 0.48 and 0.54 for first lactation Holstein cows, respectively.

Osman et al. (2013b) showed that heritability estimates at the first parity of LP, DO and AFC were 0.107±0.07, 0.313±0.09 and 0.431±0.103, respectively for Holstein cows, respectively. Furthermore, the estimated LP and DO at the second parity were 0.166±0.077 and 0.117±0.071, respectively. Furthermore, Abdel-Gader et al. (2007) in Sudan and Tekerli & Kocak (2009) in Turkey found that heritability estimated of LP were 0.17 and 0.02 of Holstein cows, respectively.

The previous investigations revealed a substantial variation in heritability estimated AFC. High estimates were 0.48 and 0.42 as reported by Suhail et al. (2010) and Ayied et al. (2011), respectively. On the contrary, low heritability estimated of AFC was 0.098 as mentioned by Abdel-Gader et al. (2007).

Table 2. Heritability estimates (diagonal), genetic (below), phenotypic (above) correlation coefficients and variance components of studied traits for milk production and reproductive status in Holstein cows

Traits	305-dMY	LP	DO	AFC
305-dMY	0.184±0.032	0.037	-0.005	0.009
LP	0.406±0.131	0.112±0.025	0.894	0.092
DO	0.413±0.135	0.882±0.035	0.105±0.024	0.145*
AFC	-0.178±0.118	0.601±0.106	0.725±0.095	0.285±0.042
Listing of P-matrix				
305-dMY	1530000	2260	-220.9	57
LP	2260	2438	1577	23.26
DO	-220.9	1577	1276	26.52
AFC	57	23.26	26.52	26.21
Listing of G-matrix				
305-dMY	281500	3560	2536	-258.1
LP	3560	273.1	168.7	27.15
DO	2536	168.7	134	22.94
AFC	-258.1	27.15	22.94	7.471

Estimated genetic correlations (r_G) and phenotypic correlations (r_P) among previous traits were positive in general except between 305-dMY and DO (Table 2). Similar results were obtained by Ghiasi et al. (2013).

Selection index and the expected genetic gain

Heritability is used to calculate genetic evaluations, to predict response to selection, and to help breeders decide if it is more efficient to improve traits through management or through selection and making many practical decisions in breeding methods to predict the animal's estimated breeding value (EBV). By regarding heritability as the regression of breeding value on phenotypic value, an individual's EBV is simply calculated as the product of heritability and the phenotypic value. So, the moderate values of heritability for studied traits (305-dMY and AFC) will enhance the possibility of selection by raising its expected genetic gain per generation. König & Swalve (2009) revealed that correlations between indices and aggregate genotypes (r_{ti}) fall-down for traits with heritability's close to zero. There is a positive relationship between r_{ti} and heritability. Using Non-objective methods with modification in its charge to be negative for LP, DO and AFC to get higher desired genetic gain for traits under selection depends on the trait phenotypic dispersion.

General, reduced, sub as own-performance selection indices and multi-source of information are shown in Table 3. The general index is considered as the main index due to its properties, whereas this index contained all traits under selection program without any reduction. Furthermore, the general index is used as a standard efficient index to determine the relative efficiencies of the other types of selection indices.

Eighteen selection indices were constructed divided according to two strategies; first, strategy one include fifteen indices, and second, strategy two include three multi-source indices (Table 3).

The comparisons of the various selection indices indicated that the general index (I_1) which incorporated 305-dMY, LP, DO and AFC is the most efficient (R_{IH}=0.518; RE=100%) and it is recommended for improving milk Production and reproductive traits in Holstein cattle in Egypt in case of applying own-performance strategy. Similar results were obtained by Atil (2006) working on Friesian cow in Turkey, Using one standard deviation as a relative economic weight found that the general index incorporated 305-dMY, LP and AFC (I=.677*305-dMY+.06*LP-135.59*AFC) (R_{IH}=0.77) was the best and increase the expected genetic gain of 305-dMY by 346 kg/generation, LP increased by 3.37 day/ generation and AFC decreased by -1.62 mo/ generation.

Ghiasi et al. (2013) reported that the sub index which includes milk production trait (I=0.15*305-dMY) had the highest genetic gain for milk production (465 kg/generation), among the other selection indices.

However, the decline in fertility performance and profit was the opposite as observed in the index which had DO with 305-dMY (I=0.193*305-dMY - 1.7*DO) to get lower genetic gains for milk production (423 kg/generation). Similar results were reported by Gonzalez-Recio et al. (2006).

Missanjo et al. (2013) developed selection index which includes milk production and functional traits (I = 0.0004 milk yield + 0.0109 fat yield + 0.0313 protein yield + 1.0004 fat percent + 2.4491 protein percent − 0.1905 somatic cell count) and revealed that animals can be ranked according to this index and selection based on these rankings. The positive signs for production traits and negative sign for functionality trait mean that the index developed will allow breeders to select sires and dams, which will increas the production traits and decrease the functionality trait.

Ghiasi et al. (2015) reported that the fertility sub index which includes DO (I= 1.69*DO) had the highest correlated genetic gain for number of inseminations to conception (−0.25 time/ generation), and days from calving to first service (−8.6 day/generation).

Therefore, this index had the highest profit per US dollar (3.5 US dollar /generation), among the other selection indices. Therefore, in conditions where fertility records are not available, DO can be used efficiently to improve fertility performance. These results suggest that two cows may have the same DO but different fertility performance either in the re-cycling activity post-calving or the ability to get pregnant. Further, censoring must be taken into account in genetic evaluations to improve predictive ability (González-Recio et al. 2006).

The least accuracy; first, in strategy one, [R_{IH} =0.17936 (I_9), 0.1793 (I_{13}), and 0.15827 (I_{14})] would result especially from indices that contain LP and DO in present study; second, in multi-source indices, [R_{IH} = 0.60475 (I_{18})] revealed the lower R_{IH} value in case of using maternal half-sibs as a second source of information. It is clear that the index not including AFC showed a reduction in its accuracy. Similar results were obtained by Khattab & Sultan (1991), Atil & Gevrekci (2005) and Atil (2006).

Table 3. Weighing factors (b-values), standard deviation (σi), efficiencies of selection in absolutes (R_{Ih}) and relative values (RE) in indices used to improve body weight at weaning in Holstein cattle

Selection index	Selection criterion				b-values				σi	R_{Ih}	RE (%)
					305-d MY	LP	DO	AFC			
GI											
I $_1$	MY	LP	DO	AFC	0.1267	-4.084	3.374	-52.77	326.47	0.518	100
RI											
I $_2$	MY	LP	DO	----	0.123	-3.039	0.985	----	188.85	0.300	57.85
I $_3$	MY	LP	----	AFC	0.123	-1.913	----	-51.27	322.09	0.511	98.66
I $_4$	MY	---	DO	AFC	0.120	----	-1.707	-51.24	313.92	0.498	96.15
I $_5$	----	LP	DO	AFC	----	-3.418	2.517	-52.22	286.78	0.455	87.84
I $_6$	MY	LP	----	----	0.122	-2.401	----	----	188.19	0.299	57.65
I $_7$	MY	---	DO	----	0.118	----	-2.772	----	176.58	0.280	54.09
I $_8$	MY	---	----	AFC	0.120	----	----	-52.96	308.07	0.489	94.36
I $_9$	----	LP	DO	----	----	-2.403	0.178	----	113.03	0.179	34.62
I $_{10}$	----	LP	---	AFC	----	-1.801	----	-51.1	283.99	0.451	86.99
I $_{11}$	---	---	DO	AFC	----	----	-1.733	-50.95	276.7	0.439	84.76
SI											
I $_{12}$	MY	---	----	-----	0.118	----	----	----	146.21	0.232	44.79
I $_{13}$	----	LP	----	-----	----	-2.288	----	----	112.99	0.179	34.61
I $_{14}$	----	---	DO	-----	----	----	-2.792	----	99.741	0.158	30.55
I $_{15}$	----	---	----	AFC	----	----	----	-52.7	269.84	0.428	82.65
MS											
I $_{16}$	OP* MY	LP	DO	AFC	0.076	-2.484	1.955	-30.01	466.55	0.740	142.91
	FS** MY	LP	DO	AFC	0.426	-16.15	11.26	-78.46			
	HS*** MY	LP	DO	AFC	0.105	-3.72	3.124	-33.98			
I $_{17}$	OP MY	LP	DO	AFC	0.084	-2.69	2.113	-33.84	447.51	0.710	137.08
	FS MY	LP	DO	AFC	0.461	-17.41	12.52	-91.14			
I $_{18}$	OP MY	LP	DO	AFC	0.110	-3.615	3.019	-44.18	381.11	0.605	116.74
	HS MY	LP	DO	AFC	0.151	-5.417	4.878	-50.49			

OP*= Own performance; FS**= Full sibs; HS***= Half sibs; GI= General index; RI= Reduced index; SI= Sub index; MS= Multi-source

Table 4. Expected genetic changes (eg) per generation and value of each trait in the index (vt) when using indices to improve body weight at weaning (*i = 1.0) in Holstein cows

Selection index	Selection criterion				Expected genetic changes (EG)				Value of each trait in the index (Vt %)			
					305-d MY (Kg)	LP (Day)	DO (Day)	AFC (Mo.)	305-d MY	LP	DO	AFC
GI												
I 1	MY	LP	DO	AFC	132.6	-4.679	-3.449	-1.410	12.16	3.84	1.34	42.15
RI												
I 2	MY	LP	DO	-----	139.1	-1.199	-0.367	-0.485	40.15	6.50	0.35	-----
I 3	MY	LP	-----	AFC	127.4	-4.585	-3.685	-1.449	11.83	4.35	-----	41.57
I 4	MY	-----	DO	AFC	135.8	-3.989	-3.504	-1.443	11.86	-----	1.86	43.75
I 5	-----	LP	DO	AFC	26.84	-6.717	-5.011	-1.483	-----	3.51	0.97	60.59
I 6	MY	LP	-----	-----	136.7	-1.181	-0.512	-0.513	39.96	22.31	-----	-----
I 7	MY	-----	DO	-----	148.0	-0.273	-0.411	-0.532	43.52	-----	17.2	-----
I 8	MY	-----	-----	AFC	154.2	-3.278	-2.954	-1.385	12.41	-----	-----	52.54
I 9	-----	LP	DO	-----	-71.7	-5.541	-3.376	-0.541	-----	11.76	0.03	-----
I 10	-----	LP	-----	AFC	23.88	-6.617	-5.197	-1.517	-----	4.99	-----	60.21
I 11	-----	-----	DO	AFC	31.64	-6.055	-5.063	-1.519	-----	-----	2.48	63.95
SI												
I 12	MY	-----	-----	-----	227.6	2.878	2.051	-0.209	-----	-----	-----	-----
I 13	-----	LP	-----	-----	-72.09	-5.531	-3.417	-0.550	-----	-----	-----	-----
I 14	-----	-----	DO	-----	-71.00	-4.723	-3.751	-0.642	-----	-----	-----	-----
I 15	-----	-----	-----	AFC	50.42	-5.302	-4.48	-1.459	-----	-----	-----	-----
MS												
I 16	#OP MY	LP	DO	AFC					1.85	0.65	0.21	4.65
	##FS MY	LP	DO	AFC	209.0	-6.37	-4.244	-1.843	5.24	2.32	0.47	3.11
	###HS MY	LP	DO	AFC					1.15	0.44	0.16	2.10
I 17	OP MY	LP	DO	AFC	200.1	-6.121	-4.082	-1.769	2.47	0.84	0.27	6.65
	FS MY	LP	DO	AFC					6.91	3.03	0.65	4.72
I 18	OP MY	LP	DO	AFC	161.1	-5.331	-3.827	-1.608	6.29	2.16	0.78	17.72
	HS MY	LP	DO	AFC					3.72	1.44	0.59	7.47

OP*= Own performance; FS**= Full sibs; HS***= Half sibs; GI= General index; RI= Reduced index; SI= Sub index; MS= Multi-source;
*j= Selection intensity

A positive relationship was found between 305-dMY and AFC (Table 2). It is necessary to select against the increase of LP more than 305 day, DO more than 60 days after calving and AFC more than 28 month of age as breeder's targets.

Strategy two includes four indices; the best restricted indices were I18, I17. It is suggested using I18, I17 to improve milk Production and reproductive traits in Holstein cattle under restriction strategy. In case of populations that have already reached optimal 305-dMY, we suggest using completely restriction index (I19) to get zero genetic gain in 305-dMY.

The original selection index (I1) which included 305-dMY, LP, DO and AFC was suggested to be used for improving milk Production and reproductive traits in case of own-performance strategy.

The expected genetic change per generation (EG) in each trait assuming the selection intensity of 1.00 is given in table (4). The expected genetic change per generation (EG); first, in strategy one, ranged between -71.7 to 136.7 kg for 305-dMY, -0.2733 to -6.717 day for LP, -0.4109 to -5.197 day for DO and -0.2087 to -1.519 month for AFC; second, in multi-source indices, ranged between 161.1 to 209 kg for 305-dMY, -5.331 to -6.37 day for LP, -3.827 to -4.244 day for DO and -1.608 to -1.843 month for AFC.

The expected genetic gain after one generation through the general index (I1) will be (1) increase in 305-dMY by 132.6 kg, (2) decrease in LP by -4.679 day, (3) decrease in DO by -3.449 day, (4) decrease in AFC by -1.41 month. This index is very simple and easy to construct, therefore, its use is recommended for selection for milk Production and reproductive traits in Holstein cattle in case of applying own-performance strategy.

The expected genetic gain after one generation through the full multi-source index (I16) will be (1) increase in 305-dMY by 209 kg, (2) decrease in LP by -6.37 day, (3) decrease in DO by -4.244 day, (4) decrease in AFC by -1.843 month. This index is very useful to magnify the expected genetic gain, therefore, its use is recommended for selection for milk

production and reproductive traits in Holstein cattle in case of applying multi-source strategy.

Value of each trait in the index (Vt) as a percentage were illustrated in table (4) The Value of each trait in the index; first, in strategy one, ranged between 11.83 to 43.52 % for 305-dMY, 3.51 to 22.31 % for LP, 0.03 to 2.48 % for DO and 42.15 to 63.95 % for AFC; second, in multi-source indices, ranged between 1.15 to 6.91 % for 305-dMY, 0.44 to 3.03 % for LP, -0.21 to 0.78 % for DO and 2.10 to 17.72 % for AFC. These results reveal the importance of 305-dMY and AFC in the index because of the higher values of each trait in the index for these traits.

Atil (2006) working on Friesian cow in Turkey, Using one standard deviation as a relative economic weight reported that the expected genetic change per generation ranged from 321 to 402 kg for 305-dMY, 3.37 to 10.29 d for LP and 0.62 to -1.62 month for AFC. These results were lower than those reported by Atil & Gevrekci (2005) using another set of that herd and used actual economic values for and ranged from 363 to 411 kg for 305-dMY, 16.78 to 29.92 d for LP and from -0.35 to -0.65 mo for AFC. Also in this respect Khattab & Sultan (1991) working on Friesian cow in EGYPT, Using actual economic values found that the expected genetic gain per generation ranged from 88 to 235 kg for 305-dMY, from 21 to 27 d for LP and from -0.26 to – 1.96 month for AFC.

CONCLUSION

Results of this study suggested using the higher indexes of Rih (I_1 $_{(RE=100)}$) to improve milk production and reproductive traits in Holstein cattle under own-performance strategy and using (I_{16} $_{(RE=142.91)}$) under multi-source strategy to get high accuracy and higher expected genetic changes per generation compare to general index.

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