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Original article

Comparison of Two Methods of Predicting 305-day Milk Yield for Genetic Evaluation to Design a Tunisian Holstein Reference Population

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Abstract

Various standardized milk yield prediction methods have been developed and used. The objective of this study was to compare two methods for the estimation of 305-day milk yield inthe Holstein breed, in terms of breeding values and their accuracy. Genetic evaluations of milk yield were compared using: 1) adjusted total lactation yield for days in milk, month, and age at calving (adjusted TY305) or 2) adjusted305-day milk yieldestimated by fitting test-day(TD) records to the Wood model(adjusted WY305).The method with better ability to predict standardized milk yield was used to identify a Tunisian cow reference population toward genomic evaluation of milk trait. Three datasets were used. The first data contains 380'709 TD records corresponding to 34'281 three first lactations of 20'758 cows collected between 2008 and 2018 in 33 herds. The second dataset contains 11'175 total first three lactation yields recorded between 2012 and 2017 from 6251 cows belonging to 33 herds.The third data is a pedigree file of 27'487 males and females. The predictive ability of the two methods was assessed by Spearman's rank correlation between predicted breeding values for 305-day milk yield (PBV305) from the full dataset and reduced dataset in which the records from the last calving year were masked. The two methods were compared in terms of rank correlation between PBV305 and the percentage of selected animals in common when different selection intensities were applied based on PBV305.The average gain in accuracy was calculated and a Tunisian reference population was identified. The results showed that heritability estimates were 0.11 (±0.02) and 0.13 (±0.01) for adjusted WY305 and TY305, respectively. The highest correlation for PBVs between full data and reduced data was achieved in TY305 dataset. Rank correlations between PBV305 estimated for adjusted WY305 and TY305 were 0.67. The percentage of animals selected in common was 11% or 21%, respectively, when 1 or 5% of cows were chosen as future dams of bulls, according to PBVs. An average gain in accuracy of 15% was observed for cows when using adjusted TY305 to estimate PBVs for milk yield trait. The obtained results showed that adjustments applied to the total milk yield records could be appropriate for 305-day milk yield prediction and genetic evaluation of milk production in the Tunisian Holstein population. Based on two main designs (extreme yield and top accuracy), a total of 1000 cows were selected to form the Tunisian female reference population using adjusted TY305 records.

Keywords: Adjustments, Dairy cattle, Genetic evaluation, Milk production.

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INTRODUCTION

Genetic evaluation and selection in dairy cattle require the assumption that phenotypic measurements are adjusted for known environmental factors that can affect milk yield (like herd-year of calving, lactation length, lactation order, month of calving, and age at calving). Production variability caused by systematic environmental effects could be removed by using multiplicative corrections for the non-genetic factors. Estimating adjustment factors is important to: 1) obtain reliable results of genetic parameters and breeding values by higher homogeneity of means and standard deviations; 2) allow effective comparisons of individuals that are submitted to different environments (Searle and Henderson, 1959); 3) make dairy records useful for management of within-herd breeding programs (Djemali and Berger, 1992); and 4) increase accuracy in selection by reflecting the animal's genetic structure. In dairy cattle, multiplicative adjustment factors are usually applied on standardized milk yield for lactation length at 305 days (Carta et al., 1998). The 305-day milk yield (Y305) is an important basis for individual genetic evaluation and for the selection and culling of cows during the production process (Kong et al., 2018). However, the genetic evaluation of dairy cows based on random regression models applied to test-day (TD) records has been widely studied (Bohmanova et al.,2008). The total Y305 remains the current basis for the genetic evaluations and the most used information by farmers to make their breeding and management decisions(Dongre and Gandhi, 2014). The first essay to estimate the Y305 was made by Brodyetal (1923), and after this, several researchers have attempted to develop different models to predict the value of this trait. The incomplete gamma function, proposed by Wood (1976), is a widely used method to describe the lactation curve and to estimate its characteristics such as the standardized milk yield. Wood's model parameters are generally determined by the least-squares technique using a logarithmic transformation of the function (Macciotta et al., 2005)or non-linear regression (Wayne Kellogg et al., 1977). The aim of this study was to find an optimal method of predicting Y305 for genetic evaluation of milk trait in Tunisian Holstein population. Hence, the following methods were compared in terms of breeding values and prediction accuracy: 1) Adjustment of the total lactation records for lactation length by applying the estimated coefficients of regression of milk yield on days in milk, and 2) fit the Wood incomplete gamma function on TD records and using its parameters to estimate the 305-day lactation milk yield.

MATERIAL and METHODS

Data

Three datasets were provided by the National Center for Genetic Improvement belonging to the Livestock and Pasture Office (OEP) of Sidi Thabet, Tunis. The first performance data contained 380'709 test-day milk yield (TDMY) records corresponding to 34'281 first three lactations and collected between 2008 and 2018 from 20'758 dairy Holstein cows belonging to 33 herds. The second performance data set contained initially 11'175 complete lactation records registered for over 5 years (2012-2017) from

6251 Holsteincowsraisedin33herds.Each cow with records is milked two times per day under the Tunisian milk recording program. The third data had genealogical information and included the cow, the sire, and the dam. The pedigree file contained all participating cows, whether they contributed progeny or not, giving a total of 27’487 animals. The original two performance datasets were edited, using R software (R Foundation, Vienna, Austria), and only records falling within the range of mean ± 2 × standard deviation were kept. Other criteria for the inclusion of cows in this study were applied to the first data as follows: only TDMY from the first three lactations were kept; to exclude animals with very short lactations and to better estimate the Wood’s incomplete gamma function parameters; lactations with less than 5 TDMY records were deleted; only herds containing more than 5 cows per herd-year of calving combination were considered and only days in milk (DIM) between 5 and 305 were used. The edited first data included 202’497 TD records. Three age subclasses (young, middle, and old) were defined in each lactation, using the quantile function of R-project software(R Core Team. 2017) giving a total of 9 age groups.Filters were also applied to the second data as follows: only DIM from 30 to 450 and coded as terminating normally were used; lactations of order > 3 were excluded and cows with less than six TDMY during the first 305 days of each lactation order were not used to predict cumulative milk production. After the application of these constraints, approximately 20% of the original complete lactation data had been discarded from the second dataset. Twelve calving age subclasses were performed, using SAS software (SAS. 2002), as follows: Lactation 1: 3-month intervals for age 24-35 months; Lactation 2: 3-month intervals for age 36–44 months; ≥45 months and Lactation 3: age ≤48; 49–51; 52–54 and ≥55 months.

Estimation of 305-day milk yield by fitting Wood’s model to TDMY records

To determine the 305-day milk yield in the first three lactations, Wood’s incomplete gamma function was fit to TDMY records of the different age group’s individual cows. This function is written as (Wood. 1976):

$$\mathbf{Y_t = a\, t^b\, (exp)^{-ct}} \quad \mathbf{(1)}$$

Where:

Y_t: The daily milk yield at day **t**;

a: The parameter associated with yield at the beginning of lactation;

b: The parameter associated with the ascending phase before peak yield;

c: The parameter associated with the decreasing phase after peak yield;

exp: The base of the natural logarithm.

Using the non-linear regression, Wood’s incomplete gamma function parameters were determined for each lactation order separately by Marquart method (R Core Team. 2017). Initially, starting values needed for non-linear analysis were defined by fitting Wood's model in form of log-linear. A lactation curve was considered atypical only if b or c is negative. The 305-day milk yield was calculated, after discarding the atypical lactation curves, by the

following equation (Tekerli et al.. 2000):

$$\mathbf{WY305 = a \int_0^{305} t^b \exp(ct)dt} \tag{2}$$

Estimation of 305-day milk yield by adjusting total milk yield for lactation length

The second performance data were analysed by least-squares techniques of the GLM procedure of SAS software (SAS, 2002). Primiparous were analysed separately from multiparous. The following model was used:

$$\mathbf{Y_{ijkl} = \mu + HYS_i + Mo_j + A_k + b_1(305 - DIM_{ijkl}) + b_2(305 - DIM_{ijkl})^2 + e_{ijkl}} \tag{3}$$

Where:

$\mathbf{Y_{ijkl}}$: The total milk production yield;

μ: The overall mean;

$\mathbf{HYS_i}$: The effect of herd-year-production sector;

Moj: The effect of calving month (j = 1… 12);

$\mathbf{A_k}$: The effect of calving age group k (Lactation 2: 3-month intervals for age 33–44 months, ≥45 months; Lactation 3: age ≤48, 49–51, 52–54 and ≥55 months; Lactation 4–7: age ≤58 months, 3-month intervals for 59–70 months, >70 months);

$\mathbf{DIM_{ijkl}}$: The actual days in milk for record l;

b1 and **b2**: The linear and quadratic regression coefficients;

$\mathbf{e_{ijkl}}$: The random residual.

To estimate the 305-day milk yield (TY305), total milk yield records were adjusted for lactation length by using the estimated coefficients of regression of milk yield on DIM.

Animals in common between the first and the second data set

In each lactation order, cows with WY305 and TY305 records were selected to compare the 305-day milk yield prediction methods. Herds containing the selected animals were located in the northern favorite environment (71%) and in the semi-arid environmental conditions in the center of Tunisia (29%). The different farms belong to five production sectors: the state farms (OTD: 50.29%); the private agricultural development enterprise (SMVDA: 24.92%); the Cooperative Agricultural Production Units (UCPA: 13.92%); private owners (5.81%) and the Livestock and Pastures Office (OEP: 5.05%). To adjust 305-milk yield for known non-genetic sources of variation, multiplicative adjustment factors for month and group-age at calving were computed for WY305 and TY305 records relative to the common animals.

Genetic evaluation

To compare genetic evaluations of milk yield in the Tunisian Holstein cows, genetic parameters, breeding values (PBVs), and their accuracies (rTI) were computed by MTDFREML software (Boldman et al., 1995) for the adjusted WY305 and TY305 traits. To predict breeding values, variance components, and their standard errors, the performance datasets and the pedigree file were used to set up the following BLUP animal model:

$$\mathbf{Y_{ijklm} = \mu + HYS_i + Mo_j + AG_k + a_l + pe_m + e_{ijklm}} \qquad \mathbf{(4)}$$

Where:

$\mathbf{Y_{ijkl}}$: The adjusted 305-day milk yield trait (WY305 or TY305);

$\boldsymbol{\mu}$: The overall mean ;

$\mathbf{HYS_i}$: The Herd-year-production sector effect;

$\mathbf{Mo_j}$: The calving month effect;

$\mathbf{AG_k}$: The group of age at calving effect (k= 11, 12, 13, 21, 22, 23, 31, 32 and 33 for WY305 trait and k= (1, …, 12) for TY305 trait);

$\mathbf{a_l}$: The random animal effect;

$\mathbf{pe_m}$: The random permanent environment effect;

$\mathbf{e_{ijk}}$: The random residual effect associated.

Comparison of 305-day milk yield prediction

To show if ranking and selection using PBVs for adjusted WY305 are (or not) similar to those for TY305, the rank correlation between PBVs from the two studied methods was calculated. To point out the best method of 305-day milk yield prediction, the two methods were compared in terms of average gain in accuracy and percentage of animals selected in common when different selection intensities were applied based on PBVs. Further, the predictive ability of each method was assessed by spearman’s rank correlation between PBVs for 305-day milk yield from the full data and five reduced data in which decreasing percentages of the most recent records were masked (only full and reduced first lactation data were used). The rank correlation was calculated as follows(Zar, 2005):

$$\boldsymbol{\rho = 1 - \frac{6\sum d_i^2}{n(n^2-1)}} \qquad \mathbf{(5)}$$

Where:

d_i: The difference between the two ranks;

n: The number of cows.

Reference population design

A cow reference population was identified toward genomic evaluation of milk yield production trait. Breeding values and their accuracy (rTI) were calculated for standardized milk yield trait estimated by the method found more appropriate. The design of the reference population was based on the traditional extreme de-regressed PBV (dPBV) and top accuracy concept (Perez et al., 2019). The dPBVs were determined by the following equation: $dPBV = PBV/rTI^2$ (Garrick et al., 2009). Both genetic merit and accuracy of the indexes were taken into account in order to get promising results when using a small population with few accurate estimates. Moreover, after comparing different cow-genotyping traditional designs,Perez et al, (2019)concluded that best results in accuracy were found for genotyping designs considering cows with extreme dPBV values. To apply this reference population design, three steps were followed (Garrick et al., 2009): 1) animals were sorted by descending dPBVs and two groups of 1000 animals were selected (1000 from the top 'highest dPBVs' and 1000 from the bottom 'lowest dPBVs'); 2) in the two groups, animals were sorted by descending rTI; 3) the most accurate 500 animals were chosen, from each group, giving 1000 candidates in total for the reference population.

RESULTS and DISCUSSION

Estimation of 305-day milk yield by fitting Wood's model to TDMY records

Mathematical means for the estimated lactation curve parameters (a. b. and c) and the WY305, after discarding atypical curves, are given in Table 1. Although insignificant differences between results were found among lactation for b and c, the daily milk increase (a) was higher in lactation 2 and 3 than in lactation 1. Consequently, cows in the second and third parity reached the highest levels of WY305 in comparison to the first parity. These findings outline the typical milking pattern of Holstein cows (Elahi Torshizi, 2016).

Table 1. Means of lactation curve parameters of Wood's incomplete gamma function and 305-day milk yields (WY305) using the first 3 lactations records.

Trait	Lactation 1		Lactation 2		Lactation 3	
	Mean	Sd*	Mean	Sd	Mean	Sd
a	12.54	8.404	14.78	9.9868	14.557	10.2
b	0.338	0.306	0.339	0.326	0.358	0.338
c	-0.004	0.003	-0.005	0.004	-0.006	0.004
WY305	6865	1555	7165	1762	7086	1800
Number of cows	8627		6304		4342	

Sd*: Standard deviation

Estimation of 305-day milk yield by adjusting total milk yield for lactation length

Unadjusted milk yield and DIM in the first lactation showed that Holstein cows raised under southern Mediterranean conditions produced on average 6636 ± 2001 kg milk during 315 ± 71 days (Table 2). Unadjusted average milk yield for second and third lactations was 6848 ± 2168 kg. Average DIM for cows in their second and later lactation was 308 ± 70 days (Table 2). Adjustments for DIM were estimated separately for first calving and multiparous. Recommended adjustments for 305 DIM under Tunisian environmental conditions were developed for cows in first, second, and later lactations as described by equations (6) and (7):

For primiparous:

$$\hat{y}_{adj} = y + 19.46\,(305 - DIM) - 0.03\,(305 - DIM)^2 \qquad (6)$$

For multiparous (second and third lactation):

$$\hat{y}_{adj} = y + 20.93\,(305 - DIM) - 0.03\,(305 - DIM)^2 \qquad (7)$$

Table 2. Means and variation of unadjusted milk yield and days in milk (DIM) in first, second and third lactations.

Lactation order		Lactation 1	Lactation 2	Lactation 3
Milk (kg)	Average	6636	6920	6776
	Standard deviation	2001	2173	2163
DIM (days)	Average	315	310	305
	Standard deviation	72	69	71
Number of cows		2050	2231	1953

General statistics of the common data

After discarding atypical lactation curves, a total of 3664 observations relative to 2820 cows were found in common between the two performance data sets. Means of the two predicted traits, means of records (per herd or HYS), as well as the mean number of cows with records, were shown in Table 3.Higher means of 305-day milk yield were found in Morocco by Boujenane and Hilal (2012)who reported an average of 7135.1 kg for the first lactation and 8756 kg for the second and later lactations. This might be explained by differences in management and environmental factors between the two countries.

Table 3. Characteristics of the final data sets used in the analysis.

Characteristics	Lactation 1		Lactation 2		Lactation 3	
	WY305[(1)] (kg)	**TY305[(2)] (kg)**	**WY305 (kg)**	**TY305 (kg)**	**WY305 (kg)**	**TY305 (kg)**
Means of the trait	6455	6457	6825	5355	6782	6663
Standard deviation of the trait	1476	2435	1696	2946	1695	3011
Minimum	1586	175	1810	2169	1594	2130
Maximum	11287	11165	12920	11868	11990	11728
Means number of records per herd	659.2		712		583	
Means number of records per HYS[(3)]	7.5		7.1		5.6	
Number of cows with records	1197		1350		1116	

(1)WY305: 305-day milk yield estimated by using Wood's incomplete gamma function parameters; (2)TY305: adjusted 305-day milk yield estimated by adjusting total lactation milk yield for lactation length; (3)HYS: herd-year-sector for 305-day milk yield.

Genetic parameters

The heritability estimates in the first three lactations were 0.11 ± (0.02) and 0.13 ± (0.01) for adjusted WY305 and TY305, respectively. These heritabilities were lower than those found in previous studies (Rekaya et al., 2000; Jakobsen et al., 2002;Ben Gara et al., 2006).These results are probably due to the limited number of cows (2820 individuals) used in the present study. Rank correlation betweenPBV305 for the two estimated traits was 0.67. Lower correlation was found by Santos et al, (2014)for the Guzerà breed. This difference in results could be explained by the differences in data consistency requirements, the animal breed and the fixed effects included in the models used for genetic evaluation. In evaluating different dairy cattle breeds in Canada, Schaeffer et al, (2000)reported similar results to the correlation found in this study.

Comparison on predictability of the two methods

The percentage of animals in common was relatively low when 1 or 5% of cows were chosen as dams of bulls, according to PBV305 for adjusted WY305 and TY305 traits (Table5).A higher percentage of the same animals is obtained as selection intensity decreases. Consequently, significant differences are expected between the group of animals selected for WY305 and TY305 at high selection intensities. According to the Cohen's kappa values (Cohen, 1960), the agreement rate between the number of animals selected and the number of animals in common was moderate when selecting 40% to 60% of the animals. However, slight to fair agreement was observed for the other selection intensities. For this reason, errors are expected when choosing dams of future progeny as high selection intensities are commonly used in this case. The ranking of the best 20 cows with known yield was analyzed to verify the differences between the methods of standardized milk prediction (Table6). For example, the cow ranked in the first position based on the PBVs for adjusted WY305 was in the 757th position when cows are ranked according to PBVs for adjusted TY305.Therefore, in a small population such as the Tunisian Holstein breed, genetic contribution to the population could differ significantly between animals ranked in these positions. Gains in accuracy of 14 to 18% were observed for all the cows when adjusted total lactation yield was used to predict breeding values for the studied trait. The average of the whole population showed an average increases in accuracy of 15% for the PBVs when 305-milk yield predicted by adjusting complete lactation milk production was used rather than adjusted WY305. The gain in accuracy when using adjusted TY305 to estimate breeding values was the main reason several countries adopted this method of 305-day milk yield prediction in routine genetic evaluations (Djemali& Berger, 1992).Spearman's rank correlation between PBVs from full first lactation data and five reduced data, for adjusted WY305 and TY305 traits, are shown in Table7. Correlations between full and reduced data for TY305 increased from 0.57 to 0.68 when deleting 50% and 30% of the most recent records, respectively, and then decreased from 0.68 to 0.60 when deleting 30% and 10% of the last records. Rank correlation of PBVs for adjusted WY305 ranged from 0.26 to 0.33 when deleting 10% and 30%, respectively, of the full data and from 0.27 to 0.24 when discarding 40% and 50% of the most recent records. Adjusting the total lactation records for lactation length is recommended for predicting 305-day milk yield in Tunisia. According to this study, this method had the best predictive ability. Future research should consider using adjusted TY305 for genetic evaluation of Tunisian Holstein cattle.

Table 5. Total number of animals (N), number (NC), and percentage (%C) of common animals selected (%SEL) for breeding based on PBV305(1) for adjusted WY305(2) and TY305(3).

%SEL	N	NC	%C	Cohen's k	Agreement
1	28	3	11	0.10	slight
5	141	30	21	0.16	slight
10	282	103	37	0.29	fair
20	564	264	47	0.33	fair
40	1128	839	74	0.57	moderate
60	1692	1299	77	0.42	moderate
80	2256	1979	89	0.38	fair

(1)PBV305: estimated breeding values for 305-day milk yield production; (2)WY305: 305-day milk yield estimated by using Wood's incomplete gamma function parameters; (3)TY305: adjusted 305-day milk yield estimated by adjusting total lactation milk yield for lactation length.

Table 6. Comparison of predicted breeding values (PBVs) and rank of the 20 best cows with known yield obtained with method 1 (WY305) and method 2 (TY305)

WY305			**TY305**			**dAC[2]**
Rank for PBV	**PBV**	**RTi[1]**	**Rank for PBV**	**PBV**	**RTi**	
1	456.172	0.35	757	256.19	0.51	0.16
2	453.852	0.29	235	562.166	0.44	0.15
3	453.258	0.35	458	396.084	0.49	0.14
4	442.369	0.41	160	653.422	0.57	0.16
5	420.866	0.39	26	989.632	0.53	0.14
6	374.928	0.35	175	629.243	0.56	0.21
7	314.840	0.26	513	369.09	0.41	0.15
8	310.721	0.42	77	804.309	0.58	0.16
9	310.603	0.37	262	538.072	0.51	0.14
10	307.876	0.4	827	220.923	0.55	0.15
11	306.593	0.43	34	938.249	0.61	0.18
12	300.674	0.23	1325	20.378	0.38	0.15
13	298.131	0.38	194	607.822	0.55	0.17
14	297.114	0.34	310	500.378	0.49	0.15
15	290.952	0.39	92	766.204	0.56	0.17
16	290.598	0.32	614	314.327	0.47	0.15
17	283.754	0.44	309	500.482	0.6	0.16
18	270.147	0.36	22	1009.246	0.54	0.18
19	268.060	0.34	726	270.239	0.51	0.17
20	265.409	0.4	39	918.768	0.56	0.16

(1)RTi: accuracy of the predicted breeding values; (2)dAC: percent gain or loss in the accuracy of PBVs when the WY05 is replaced with the TY305.

Table 7. Spearman's rank correlation between PBVs for adjusted 305-day milk yield obtained from full and five reduced data.

Percentage of deleted records (%)	**WY305[1]**	**TY305[2]**
50	0.24	0.57
40	0.27	0.59
30	0.33	0.68
20	0.32	0.66
10	0.26	0.60

(1)WY305: 305-day milk yield estimated by using Wood's incomplete gamma function parameters; (2)TY305: adjusted 305-day milk yield estimated by adjusting total lactation milk yield for lactation length.

Female Tunisian reference population design

As a result of this study, applying adjustments to the total lactation milk records to predict 305-day milk yield is more efficient for the genetic evaluation of this trait in the Tunisian Holstein. Therefore, the initial data set containing adjusted TY305 was used to identify a female reference population toward genomic evaluation. A total of 1000 cows were selected to form this population basing on two main traditional designs (extreme yield and top accuracy cows) as described in Figure 1. The majority of the identified cows were distributed on farms belonging to the Office des Terres Domaniales (63%). However, opting for using females to perform reference population could reduce the gap between developing and developed countries in the field of genetic evaluation. Implementing progeny testing dairy of bulls is a required tool to ameliorate the accuracy of the genomic estimated breeding values.

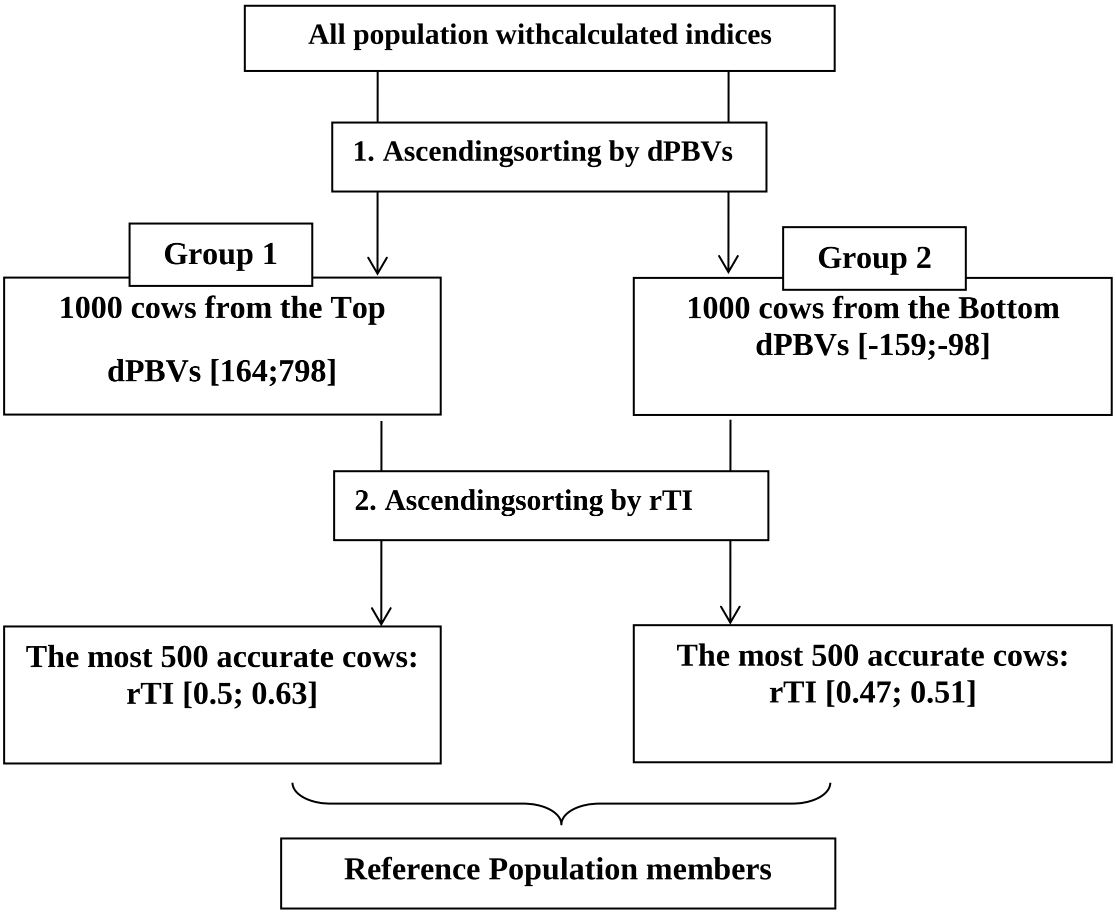

Figure 1. Illustrative scheme describing the strategy of the reference population design considered in the present study.

CONCLUSION

This study showed that adjusting the total lactation records for lactation length by applying the estimated coefficients of regression of milk yield on DIM could achieve reasonable good estimates of genetic parameters and breeding values. Gains in accuracy and differences in animal ranking are obtained with the use of lactation model instead of the Wood model to predict 305-milk yield for genetic evaluations of dairy cattle. Moreover, lactation model had the best prediction ability and presents statistical adequacy indicating its efficiency for genetic evaluations of milk production trait in the Holstein breed. Based on this model, that should be used as an initial model for the estimation of standardized milk yields and for the implementation of a genetic improvement program in the Tunisian Holstein population, a female reference population was identified as a first step toward genomic evaluation.

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