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USING HISTORICAL POPULATION DATA TO ESTIMATE THE INBREEDING COEFFICIENT IN THE DAIRY CATTLE POPULATION USING A SIMULATION TECHNIQUE

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Abstract

This study aimed to simulate the effects of genetic variation and pedigree structure on the estimation of the inbreeding coefficient (FX). Dairy cow populations of 2,000 , 5,000 and 10,000 cows were simulated with varying numbers of sires (1, 5, 10, 20 and 4), three levels of heritability (low, medium, and high) and two litter sizes (1 and 2 calves per litter). Four pedigree structures were considered: 1) constant population size, 2) increasing population size by 1% per year, 3) bottlenecked population with a 1% annual increase followed by 1% annual decrease and 4) current population representing 10% of the actual dairy cattle population. QMSim software was used for analysis. The results indicated that the constant population structure produced the lowest average FX, whereas the current population has the highest average FX, with mean values of 0.602, 0.609, 0.616, and 0.627 across the four structures, respectively. Increasing the number of sires and maintaining greater population numbers were effective ways to reduce inbreeding. Populations with higher heritability and larger size have broader genetic bases, making it easier to manage inbreeding. Estimating the heritability of variables linked with inbreeding, like fertility, milk production, and disease resistance, might help breeders make better educated breeding decisions to eliminate inbreeding and maintain healthy genetic pools. Additionally, cows with single calves displayed lower average inbreeding than those with twins, suggesting that reproductive patterns may influence genetic diversity within herds.

INTRODUCTION

Reproductive technologies are increasingly used in modern animal production, including semen cryopreservation, embryo transfer, sexed semen and artificial insemination. These technologies have been frequently employed to rapidly increase the population of animals with desirable genetic features. For example, sperm from a single genetically superior sire can be utilized to fertilize a huge number of dams. However, without proper mating management, there is a possibility of future inbreeding (mating between related individuals). Inbreeding can reduce fertility, survival rate, and production (Rokouei et al., 2010; Hinrichs and Thaller, 2011; Fuerst-Waltl and Fuerst, 2012). It also increases the probability of expressing genetic disorders while reducing genetic diversity due to a higher proportion of homozygous compared with heterozygous genotypes. Genetic diversity is vital for animal breeding. Populations without sufficient diversity cannot undergo genetic improvement when all individuals share genetic backgrounds. Maintaining the highest level of genetic variety within a population ensures the availability of critical genes for future breeding and decreases the danger of population extinction as environmental conditions change. The primary goal of genetic conservation planning is to retain genetic diversity while decreasing inbreeding (Barker, 2001). Populations that rely heavily on artificial insemination or embryo transfer lose genetic diversity at a faster rate. Consequently, before effective conservation strategies can be implemented, it is essential to understand the pedigree structure and the level of genetic diversity in populations from past to present.

The inbreeding coefficient can be calculated at the molecular or DNA level using the Simple Sequence Repeat (SSR) technique with three loci (Green, Franck, & Oldroyd, 2001). This method allows for the study of the genetic level of an entire population, but it incurs significant analytical expenditures. Another method is to use pedigree information to evaluate genetic diversity (Leroy 2011). This method analyzes existing pedigree data from farms using computer algorithms. The advantage of this approach is that it allows for the estimation of inbreeding trends across past generations without requiring physical samples from animals, as is necessary in molecular genetic studies. Boichard et al. (1997(proposed the use of pedigree information to estimate genetic diversity in populations based on the principle of probabilities of gene origin, which considers that the probability of an animal inheriting a given autosomal gene from its sire or dam is 0.5, and from its grandsire or granddam is 0.25. As a result, measuring the inbreeding coefficient in dairy cattle populations reveals information about both genetic determinants and pedigree structure, providing an additional way for assessing inbreeding in Thai dairy cattle populations.

MATERIAL AND METHODS

Simulation of Pedigree Structure in Dairy Cattle Populations

Different pedigree structures of dairy cattle populations were simulated using different sex ratios. For the first parental generation, sires and dams were chosen at random from an unrelated base population. Table 1 shows how the pedigree structures were divided into four kinds.

Table 1. Data for Simulating Pedigree Structures of Dairy Cow Populations for Inbreeding Coefficient (FX) Analysis

Population Structure Characteristics (Number of Dairy Cattle/Generations)			
Unchanged	Changes[1]	Bottleneck[2]	Current[3]
10,000 [1]	10,000 [1]	10,000 [0]	13,278 [25]
10,000 [5]	10,510 [5]	9,510 [5]	28,725 [31]
10,000 [10]	11,045 [10]	9,045 [10]	27,635 [32]
10,000 [15]	11,610 [15]	8,600 [15]	30,287 [33]
10,000 [20]	12,202 [20]	8,178 [20]	28,267 [35]
10,000 [25]	12,825 [25]	7,777 [25]	29,755 [36]
10,000 [30]	13,480 [30]	8,012 [30]	34,525 [38]
10,000 [35]	14,168 [35]	8,421 [35]	38,398 [40]
10,000 [40]	14,891 [40]	8,851 [40]	38,493 [42]
10,000 [45]	15,650 [45]	9,302 [45]	53,967 [47]
10,000 [50]	16,450 [50]	9,778 [50]	56,250 [48]
		10074 [53]	50,042 [49]
			49,569 [50]
			49,356 [51]
			55,401 [53]

1 Population increases by 1% per year
2 Population increases by 1% per year and then decreases by 1% per year.
3Current population calculated at 10% of the actual population (based on historical dairy cattle data from the Department of Livestock Development since 1997).

The heritability values (h^2) used in the simulation of dairy cow populations were based on economically important traits (milk production and fertility), as shown in Table 2.

Table 2. Simulation Data on Number of Sires, Population Size, and Heritability for Inbreeding Coefficient (FX) Analysis in Dairy Cow Populations

Numbers of Sires	Population Sizes of Dairy Cattle	Heritability[1]
1	2,000	0.02
5	5,000	0.34
10	10,000	0.43
20		
40		

heritability; Low:0.02, Medium:0.34 and High: 0.43 (Warangkana, 2018 and Pakpoom, 2011)

Calculation of the Inbreeding Coefficient (FX) (Falconer and Mackay, 1989)

$$F_x = \sum \quad \left(\frac{1}{2}\right)^n (1 + F_A)$$

Where F_x = the inbreeding coefficient of animal x
∑ = It is the sum of all possible genetic transmission pathways
F_A = It is the inbreeding coefficient of the common ancestor A
Where A = 1,2,..,N
n = It is the number of individuals in the gene transmission pathway, starting from the sire to the dam through the common ancestor Common ancestor A

This simulation was performed using the QMSim tool (Sargolzaei and Schenkel, 2013). QMSim simulated mating among dairy cow groups. Each level of every factor was reproduced five times. The effects of inbreeding were evaluated using regression coefficients (João Cruz Reis Filho et al., 2015).

RESULTS

Simulation of Dairy Cow Pedigree Structures for Inbreeding Coefficient (FX) Estimation

The results indicated that simulated pedigree structures of dairy cow populations had varying effects on estimating the inbreeding coefficient (FX). Initially, the population's inbreeding appeared to be stable. However, from the second generation onward, inbreeding began and continued to increase. From generation 13 onwards, the bottleneck pedigree structure had higher

FX values than the unchanged and changing structures. Furthermore, the current population structure showed a higher rate of inbreeding than the other three population structures.

In terms of overall mean values of the inbreeding coefficient (FX), the simulated present pedigree structure of dairy cow populations showed higher values than the unchanged, changing, and bottleneck structures, with mean FX values of 0.627, 0.602, 0.609, and 0.616, respectively (Table 3).

Table 3. Simulation of Dairy Cow Pedigree Structures for Inbreeding Coefficient (FX) Estimation

Generations	Population Structure Characteristics (Average / Generations)			
	Unchanged	Changes	Bottleneck	Current
0	0.000	0.000	0.000	0.000
1	0.000	0.000	0.000	0.000
2	0.170	0.170	0.170	0.171
3	0.102	0.102	0.100	0.108
4	0.098	0.101	0.101	0.106
5	0.106	0.112	0.111	0.121
6	0.127	0.144	0.137	0.151
7	0.160	0.179	0.172	0.192
8	0.199	0.214	0.210	0.234
9	0.237	0.251	0.249	0.274
10	0.271	0.287	0.282	0.310
11	0.302	0.319	0.317	0.344
12	0.335	0.351	0.351	0.377

Generations	Population Structure Characteristics (Average / Generations)			
	Unchanged	Changes	Bottleneck	Current
13	0.365	0.379	0.381	0.406
14	0.393	0.409	0.411	0.433
15	0.420	0.436	0.440	0.461
16	0.445	0.461	0.468	0.487
17	0.470	0.484	0.494	0.511
18	0.494	0.507	0.520	0.533
19	0.520	0.530	0.545	0.556
20	0.544	0.552	0.568	0.576
21	0.567	0.574	0.590	0.596
22	0.586	0.593	0.610	0.616
23	0.603	0.611	0.627	0.635
24	0.620	0.626	0.644	0.653
25	0.637	0.641	0.660	0.670
26	0.655	0.657	0.676	0.684
27	0.671	0.673	0.691	0.697
28	0.687	0.687	0.705	0.711
29	0.702	0.701	0.718	0.723

Generations	Population Structure Characteristics (Average / Generations)			
	Unchanged	Changes	Bottleneck	Current
30	0.716	0.715	0.731	0.734
31	0.728	0.728	0.742	0.746
32	0.739	0.741	0.753	0.756
33	0.750	0.752	0.763	0.766
34	0.760	0.763	0.773	0.776
35	0.770	0.773	0.783	0.785
36	0.780	0.783	0.792	0.794
37	0.789	0.793	0.800	0.803
38	0.799	0.802	0.809	0.811
39	0.807	0.811	0.816	0.819
40	0.815	0.818	0.823	0.827
41	0.822	0.825	0.831	0.835
42	0.828	0.832	0.837	0.842
43	0.835	0.840	0.844	0.849
44	0.841	0.847	0.850	0.855
45	0.847	0.854	0.855	0.861
46	0.853	0.860	0.860	0.865

Generations	Population Structure Characteristics (Average / Generations)			
	Unchanged	Changes	Bottleneck	Current
47	0.858	0.866	0.864	0.870
48	0.864	0.872	0.869	0.875
49	0.869	0.877	0.875	0.880
50	0.875	0.882	0.880	0.885
Overall	0.602	0.609	0.616	0.627

Simulation Using Different Numbers of Sires and Dairy Cow Population Sizes for Inbreeding Coefficient (FX) Estimation

The simulation results for different sire population sizes demonstrated a clear relationship between the number of sires and the incidence of the inbreeding coefficient (FX). As the number of sires increased, the FX values showed marked differences across generations. In addition, the simulation of a dam population size of 2,000 with varying sire numbers 1, 5, 10, 20 and 40 indicated that higher sire numbers led to a gradual reduction in FX values across generations. Observing the overall trend, a sire population size of 40 resulted in the lowest mean FX value of 0.170, while populations of 20 and 10 sires had higher mean FX values of 0.295 and 0.460, respectively. These findings highlight the significance of sire diversity in regulating and eliminating inbreeding in populations.

For dam populations of 5,000 and 10,000, the number of sires used per herd had significant effects on the inbreeding coefficient (FX). In particular, using fewer sires relative to the number of dams resulted in cumulative positive genetic influences during the breeding process. In contrast, continually employing the same sires or rotating only a small number of sires resulted in higher FX values (Table 4).

Simulation of Heritability (h^2) and Different Dairy Cow Population Sizes for Inbreeding Coefficient (FX) Estimation

According to Warangkana (2018) and Pakpoom (2011)'s investigation of heritability levels (low, medium, and high) on a dairy cow population of 2,000, high heritability had a lower effect on the inbreeding coefficient (FX) than low and medium heritability. Mean FX values were 0.459, 0.483, and 0.556, respectively (Table 5).

In a dairy cow population of 5,000, the study found that over generations 0-10, medium heritability had less of an effect on the inbreeding coefficient (FX) than low and high heritability. In contrast, higher heredity had a greater influence on FX changes in generations 11-50, with FX values lower than those observed with medium and low heritability. It was additionally found that low heritability resulted in greater FX values as generations rose. Overall, high heritability produced lower mean FX values than medium and low levels, at 0.497, 0.502, and 0.592, respectively (Table 5).

For a dairy cow population of 10,000, high heritability resulted in lower mean inbreeding coefficients (FX) than medium and low heritability across generations 0–2. However, as the population progressed over generations, medium heritability produced lower FX values than high and low heritability in generations 3–10. In generations 11-50, higher heritability resulted in smaller FX changes compared to medium and low levels. However, it was found that low heredity yielded lower mean FX values than medium and high heritability, with mean values of 0.627, 0.524, and 0.512, respectively (Table 5).

Simulation of Different Litter Sizes (LS) in Dairy Cattle for Inbreeding Coefficient (FX) Estimation

The analysis clearly showed that litter size influences the estimation of the inbreeding coefficient (FX). Smaller litter sizes, in particular, corresponded with lower FX values compared to higher litter sizes, indicating that as the number of offspring increases, so does the likelihood of mating within the same lineage. This finding highlights the important role population dynamics plays in understanding genetic diversity (Figure 1).

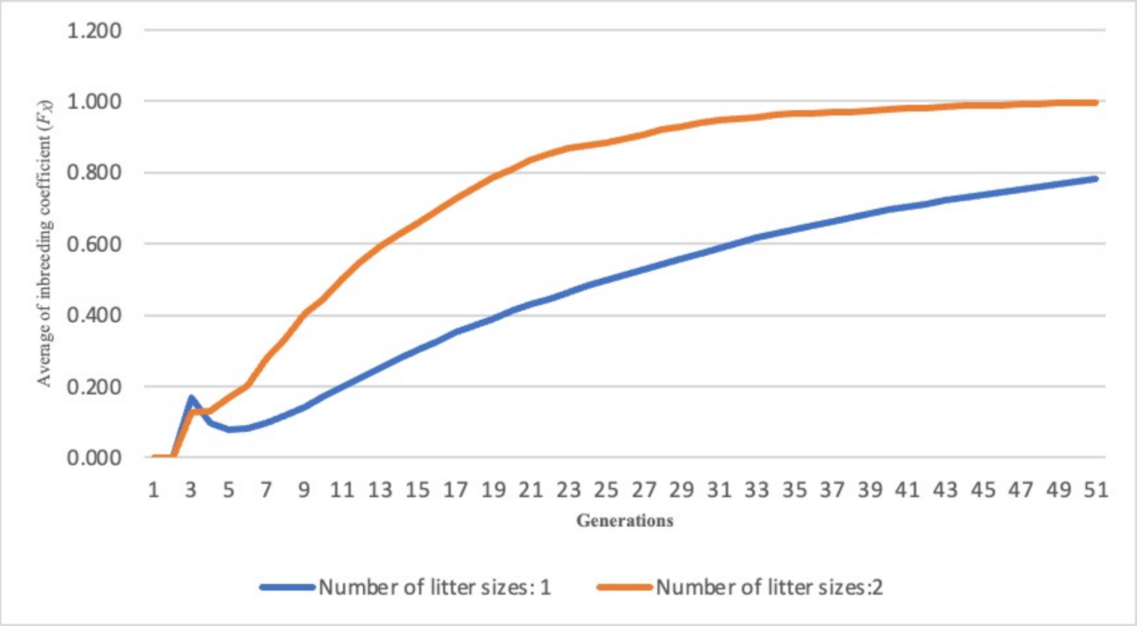

Figure 1. Relationship Between Litter Size and Incidence of the Inbreeding Coefficient (FX) in Dairy Cattle

Table 4. Simulation Using Different Numbers of Sires and Dairy Cow Population Sizes for Inbreeding Coefficient (FX) Estimation

Generations	Different Numbers of Sires and Population Sizes of Dairy Cows[1] (Average / Generations)														
	2,000					5,000					10,000				
	1	5	10	20	40	1	5	10	20	40	1	5	10	20	40
0	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	0.125	0.170	0.179	0.180	0.181	0.125	0.176	0.187	0.186	0.182	0.125	0.174	0.183	0.181	0.178
3	0.097	0.103	0.099	0.089	0.088	0.098	0.117	0.106	0.099	0.086	0.134	0.108	0.099	0.088	0.083
4	0.095	0.097	0.071	0.063	0.051	0.137	0.101	0.078	0.067	0.049	0.157	0.097	0.077	0.060	0.048
5	0.127	0.106	0.067	0.049	0.036	0.150	0.115	0.080	0.047	0.032	0.167	0.103	0.076	0.054	0.033
6	0.180	0.124	0.074	0.047	0.033	0.224	0.134	0.092	0.047	0.029	0.222	0.125	0.088	0.053	0.028
7	0.220	0.156	0.087	0.053	0.034	0.284	0.159	0.111	0.053	0.030	0.273	0.172	0.109	0.059	0.031
8	0.283	0.195	0.104	0.061	0.038	0.339	0.193	0.132	0.065	0.034	0.314	0.211	0.130	0.073	0.037
9	0.340	0.238	0.124	0.071	0.043	0.376	0.223	0.156	0.077	0.040	0.372	0.247	0.151	0.089	0.044
10	0.397	0.268	0.140	0.082	0.052	0.427	0.256	0.180	0.088	0.047	0.419	0.288	0.172	0.103	0.050
11	0.442	0.296	0.157	0.093	0.058	0.470	0.289	0.204	0.102	0.054	0.462	0.322	0.192	0.117	0.058
12	0.491	0.330	0.174	0.105	0.063	0.512	0.323	0.231	0.114	0.060	0.505	0.357	0.213	0.131	0.064
13	0.528	0.355	0.191	0.120	0.069	0.557	0.356	0.257	0.126	0.067	0.551	0.388	0.238	0.150	0.072
14	0.573	0.379	0.213	0.132	0.076	0.597	0.392	0.280	0.138	0.075	0.596	0.421	0.258	0.167	0.080
15	0.604	0.403	0.233	0.144	0.082	0.635	0.427	0.302	0.149	0.083	0.632	0.450	0.282	0.185	0.087
16	0.631	0.430	0.248	0.153	0.087	0.665	0.459	0.324	0.162	0.091	0.671	0.478	0.304	0.199	0.094
17	0.665	0.454	0.266	0.161	0.092	0.697	0.489	0.340	0.177	0.102	0.700	0.507	0.323	0.211	0.104
18	0.693	0.485	0.289	0.170	0.099	0.726	0.516	0.356	0.192	0.112	0.732	0.540	0.345	0.225	0.113
19	0.716	0.513	0.309	0.182	0.106	0.746	0.544	0.375	0.205	0.120	0.757	0.571	0.366	0.242	0.123
20	0.744	0.538	0.330	0.194	0.112	0.769	0.571	0.397	0.219	0.128	0.782	0.604	0.386	0.258	0.131
21	0.766	0.568	0.352	0.207	0.119	0.789	0.596	0.418	0.234	0.136	0.803	0.631	0.407	0.274	0.139

Different Numbers of Sires and Population Sizes of Dairy Cows[1]

(Average / Generations)

Generations	2,000					5,000					10,000				
	1	5	10	20	40	1	5	10	20	40	1	5	10	20	40
22	0.787	0.594	0.376	0.220	0.125	0.810	0.622	0.438	0.248	0.145	0.822	0.655	0.427	0.288	0.148
23	0.807	0.617	0.397	0.233	0.132	0.829	0.647	0.464	0.264	0.153	0.836	0.680	0.450	0.302	0.158
24	0.821	0.641	0.416	0.246	0.139	0.847	0.671	0.488	0.278	0.162	0.850	0.704	0.473	0.319	0.170
25	0.834	0.661	0.436	0.258	0.146	0.859	0.694	0.508	0.295	0.171	0.863	0.724	0.500	0.336	0.182
26	0.845	0.681	0.452	0.273	0.154	0.870	0.717	0.526	0.314	0.181	0.873	0.744	0.527	0.353	0.192
27	0.861	0.701	0.473	0.284	0.162	0.881	0.739	0.542	0.331	0.192	0.882	0.763	0.553	0.373	0.203
28	0.873	0.719	0.494	0.294	0.171	0.892	0.759	0.558	0.345	0.202	0.891	0.779	0.578	0.393	0.215
29	0.885	0.734	0.510	0.306	0.178	0.904	0.777	0.578	0.358	0.213	0.898	0.798	0.601	0.409	0.228
30	0.895	0.751	0.527	0.320	0.186	0.913	0.793	0.596	0.371	0.223	0.906	0.816	0.619	0.424	0.240
31	0.906	0.766	0.543	0.334	0.193	0.921	0.807	0.613	0.386	0.231	0.912	0.832	0.638	0.440	0.252
32	0.915	0.782	0.559	0.345	0.199	0.929	0.821	0.631	0.400	0.241	0.917	0.846	0.657	0.456	0.263
33	0.924	0.798	0.574	0.357	0.205	0.937	0.834	0.648	0.416	0.250	0.923	0.859	0.673	0.473	0.272
34	0.933	0.813	0.592	0.369	0.211	0.943	0.847	0.666	0.430	0.256	0.929	0.871	0.690	0.492	0.283
35	0.939	0.827	0.609	0.382	0.216	0.949	0.859	0.683	0.444	0.265	0.932	0.881	0.708	0.511	0.292
36	0.944	0.839	0.625	0.395	0.221	0.954	0.871	0.699	0.457	0.274	0.937	0.890	0.725	0.528	0.301
37	0.948	0.851	0.641	0.407	0.228	0.957	0.881	0.714	0.471	0.284	0.939	0.898	0.741	0.544	0.312
38	0.953	0.862	0.658	0.418	0.235	0.961	0.892	0.729	0.484	0.295	0.944	0.906	0.759	0.558	0.323
39	0.956	0.873	0.675	0.433	0.243	0.965	0.900	0.743	0.499	0.307	0.949	0.913	0.774	0.570	0.335
40	0.959	0.883	0.689	0.446	0.250	0.968	0.908	0.757	0.515	0.321	0.953	0.920	0.789	0.583	0.344
41	0.962	0.891	0.704	0.459	0.258	0.971	0.914	0.770	0.532	0.333	0.958	0.927	0.802	0.597	0.355
42	0.965	0.898	0.716	0.473	0.264	0.974	0.920	0.782	0.547	0.343	0.962	0.933	0.814	0.610	0.365
43	0.968	0.904	0.729	0.486	0.272	0.977	0.926	0.794	0.563	0.354	0.966	0.939	0.824	0.622	0.375
44	0.971	0.910	0.744	0.498	0.283	0.979	0.933	0.807	0.579	0.364	0.970	0.944	0.833	0.634	0.389

Generations	Different Numbers of Sires and Population Sizes of Dairy Cows[1] (Average / Generations)														
	2,000					5,000					10,000				
	1	5	10	20	40	1	5	10	20	40	1	5	10	20	40
45	0.974	0.916	0.757	0.510	0.290	0.981	0.940	0.819	0.590	0.372	0.974	0.949	0.842	0.647	0.402
46	0.976	0.922	0.770	0.523	0.299	0.983	0.947	0.830	0.600	0.381	0.977	0.953	0.852	0.662	0.412
47	0.979	0.928	0.781	0.536	0.308	0.985	0.952	0.838	0.611	0.390	0.979	0.957	0.862	0.674	0.423
48	0.981	0.933	0.792	0.548	0.315	0.987	0.957	0.846	0.621	0.400	0.982	0.961	0.870	0.686	0.435
49	0.983	0.939	0.802	0.562	0.322	0.988	0.961	0.853	0.632	0.410	0.984	0.964	0.879	0.697	0.446
50	0.984	0.944	0.812	0.573	0.331	0.990	0.965	0.861	0.645	0.420	0.985	0.967	0.887	0.708	0.456
Overall	0.743	0.630	0.460	0.295	0.170	0.763	0.656	0.521	0.337	0.206	0.759	0.672	0.525	0.381	0.221

1the current population of dairy cows

Table 5. Simulation of Heritability (h²) and Different Dairy Cow Population Sizes for Inbreeding Coefficient (FX) Estimation

Generations	Different Heritability and Population Sizes of Dairy Cows (Average / Generations)								
	2,000			5,000			10,000		
	Low[1]	Medium[2]	High[3]	Low[1]	Medium[2]	High[3]	Low[1]	Medium[2]	High[3]
0	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	0.171	0.169	0.167	0.170	0.168	0.171	0.171	0.170	0.168
3	0.103	0.102	0.095	0.100	0.096	0.101	0.108	0.100	0.102
4	0.095	0.087	0.075	0.092	0.079	0.086	0.106	0.086	0.088
5	0.096	0.088	0.077	0.101	0.081	0.085	0.121	0.085	0.087
6	0.120	0.109	0.091	0.124	0.096	0.105	0.151	0.100	0.103
7	0.154	0.129	0.110	0.157	0.119	0.128	0.192	0.126	0.129
8	0.189	0.156	0.136	0.192	0.143	0.153	0.234	0.151	0.153
9	0.220	0.180	0.163	0.230	0.172	0.174	0.274	0.179	0.181

Different Heritability and Population Sizes of Dairy Cows

(Average / Generations)

Generations	2,000			5,000			10,000		
	Low[1]	Medium[2]	High[3]	Low[1]	Medium[2]	High[3]	Low[1]	Medium[2]	High[3]
10	0.252	0.205	0.188	0.264	0.199	0.200	0.310	0.205	0.206
11	0.281	0.228	0.209	0.298	0.225	0.224	0.344	0.233	0.230
12	0.308	0.249	0.233	0.327	0.252	0.248	0.377	0.259	0.254
13	0.337	0.271	0.252	0.359	0.277	0.272	0.406	0.286	0.280
14	0.362	0.292	0.275	0.392	0.303	0.296	0.433	0.313	0.304
15	0.389	0.314	0.293	0.422	0.327	0.319	0.461	0.337	0.327
16	0.415	0.335	0.310	0.451	0.350	0.340	0.487	0.360	0.349
17	0.439	0.356	0.327	0.477	0.370	0.361	0.511	0.381	0.369
18	0.462	0.376	0.347	0.502	0.390	0.380	0.533	0.402	0.391
19	0.483	0.396	0.365	0.525	0.410	0.398	0.556	0.421	0.412
20	0.502	0.414	0.384	0.547	0.430	0.417	0.576	0.441	0.432
21	0.521	0.430	0.402	0.565	0.447	0.435	0.596	0.461	0.451
22	0.540	0.448	0.421	0.584	0.464	0.453	0.616	0.479	0.468
23	0.558	0.464	0.437	0.602	0.481	0.471	0.635	0.498	0.485
24	0.574	0.480	0.452	0.618	0.498	0.489	0.653	0.516	0.503
25	0.590	0.495	0.467	0.634	0.514	0.506	0.670	0.534	0.521
26	0.604	0.510	0.481	0.649	0.529	0.522	0.684	0.551	0.538
27	0.617	0.524	0.496	0.665	0.544	0.537	0.697	0.568	0.555
28	0.630	0.537	0.510	0.678	0.559	0.551	0.711	0.583	0.571
29	0.643	0.550	0.523	0.692	0.574	0.566	0.723	0.598	0.587
30	0.656	0.562	0.536	0.703	0.587	0.579	0.734	0.614	0.601
31	0.669	0.574	0.548	0.714	0.602	0.592	0.746	0.630	0.615
32	0.681	0.586	0.560	0.724	0.616	0.604	0.756	0.645	0.628

Generations	Different Heritability and Population Sizes of Dairy Cows (Average / Generations)								
	2,000			5,000			10,000		
	Low[1]	Medium[2]	High[3]	Low[1]	Medium[2]	High[3]	Low[1]	Medium[2]	High[3]
33	0.692	0.598	0.572	0.734	0.627	0.617	0.766	0.659	0.640
34	0.702	0.609	0.584	0.744	0.639	0.628	0.776	0.672	0.653
35	0.711	0.619	0.595	0.752	0.650	0.640	0.785	0.684	0.665
36	0.720	0.631	0.605	0.761	0.662	0.651	0.794	0.696	0.676
37	0.727	0.641	0.615	0.770	0.674	0.662	0.803	0.705	0.687
38	0.735	0.652	0.625	0.778	0.684	0.672	0.811	0.716	0.698
39	0.742	0.662	0.636	0.786	0.695	0.683	0.819	0.726	0.708
40	0.749	0.672	0.645	0.793	0.704	0.694	0.827	0.735	0.718
41	0.756	0.681	0.655	0.800	0.713	0.704	0.835	0.744	0.728
42	0.763	0.689	0.663	0.807	0.721	0.713	0.842	0.754	0.737
43	0.770	0.697	0.672	0.814	0.729	0.723	0.849	0.762	0.745
44	0.777	0.704	0.681	0.820	0.737	0.733	0.855	0.770	0.754
45	0.784	0.712	0.690	0.826	0.745	0.740	0.861	0.778	0.763
46	0.789	0.720	0.698	0.832	0.753	0.748	0.865	0.786	0.771
47	0.795	0.727	0.706	0.837	0.760	0.755	0.870	0.794	0.779
48	0.800	0.735	0.714	0.843	0.767	0.762	0.875	0.801	0.787
49	0.806	0.742	0.721	0.848	0.774	0.769	0.880	0.807	0.794
50	0.811	0.748	0.729	0.853	0.782	0.776	0.885	0.813	0.801
Overall	0.556	0.483	0.459	0.592	0.502	0.497	0.627	0.524	0.512

23 heritability; Low:0.02, Medium:0.34 and High: 0.43 (Warangkana, 2018 and Pakpoom, 2011)

DISCUSSION

The simulation of genetic variation and pedigree structures in dairy cow populations showed different impacts on the estimation of the inbreeding coefficient. In the initial stages, the inbreeding coefficient was relatively stable across all pedigree structures. However, starting with the second generation, the coefficient showed an ongoing increase.

Importantly, the bottleneck pedigree structure of dairy cow populations showed inbreeding coefficients that remained stable, comparable to other population structures, for the first 11 generations. However, starting with generation 13, the bottleneck population showed higher average inbreeding coefficients than the other groups. Furthermore, the current population structure exhibited increasing inbreeding coefficients starting with generation 2. According to William et al. (2009), Lande (1988), and Lynch et al. (1995), a population bottleneck occurs when population size rapidly decreases due to environmental events or human activity such as genocide, population fragmentation, widespread violence, or intentional selection. Such events can drastically reduce genetic variation within a population, allowing groups with lower genetic diversity to transmit their genes to subsequent generations. Genetic diversity in these populations remains low and only increases when new alleles are introduced through gene flow from other populations or more slowly through random mutation over time. The reduction of genetic variety may have an impact on the population's resilience and ability to adjust to environmental changes such as climatic shifts or changes in resource availability. In some circumstances, if the animals that survive the bottleneck have the highest genetic fitness, the frequency of these beneficial genes will rise. Conversely, the entire gene pool would shrink, and the bottleneck's random distribution of alleles may cause the loss of specific alleles. Furthermore, the likelihood of inbreeding and genetic homogeneity may increase, potentially resulting in inbreeding depression, the severity of which depends on the heritability of the trait in question (Natthaphon, 2004). Moreover, smaller population sizes may promote the accumulation of harmful mutations (Barros et al., 2017). In general, population structure is determined by calculating individual animal allele frequencies. Potential changes in genetic variation distribution should be monitored on a regular basis to prevent linebreeding or inbreeding within herds.

Simulations of sire population sizes revealed a direct correlation between the number of sires and the occurrence of the inbreeding coefficient (FX). As the number of sires increased, there were significant changes in FX across generations. Simulations with dam population sizes of 2,000, 5,000, and 10,000 demonstrated that increasing sire numbers resulted in a progressive drop in FX incidence across generations. The overall trend showed that a sire population of 40 produced the lowest mean FX values. Similarly, Sofa Nyman et al. (2022) undertook the first systematic examination of genetic diversity and inbreeding levels in Red dairy cattle, finding that as population size declined, inbreeding increased. McParland et al. (2007) and Bouchard (1997) further indicated that although the Red dairy cattle population was larger, the smaller number of effective ancestors compared with other Red dairy breeds suggested that the population originated from fewer individuals. A greater number of effective ancestors relative to the total number of ancestors may also indicate historical bottlenecks that caused a loss of genetic diversity during the development of Red dairy cattle populations in Europe. Moreover, the use of multiple sires can reduce the impact of recessive genetic disorders by lowering the probability of closely related animals mating. For effective management of linebreeding, it is essential to balance the number of sires used with careful selection practices to maximize genetic diversity while preserving desirable breeding traits.

Furthermore, Bayode et al. (2019) found that the effective population size (Ne) based on linkage disequilibrium was 58 and 120 for Holsteins and Jerseys, respectively. Over a decade, genomic selection in Holsteins increased ΔF each generation by 1.19% to 2.06%, based on pedigree and genomic data. Given the increased rate of linebreeding following the introduction of genomic selection, it is critical to apply techniques and procedures to regulate annual rates of inbreeding, hence assisting in the management and preservation of genetic resources in farming animals. According to Gutiérrez et al. (2008), pedigree information is critical since it influences numerous population metrics, including inbreeding coefficients and average relatedness. The completeness of pedigree records for animals born within the past ten years was as follows: One generation equals 76.2%; two generations equals 66.3%; three generations equals 57.8%; four generations equals 49.8%; five generations equals 42.1%; and six generations equal 35.6%. In a research by Malhado et al. (2008b) on Brazilian water buffalo populations of Mediterranean provenance, inbreeding due to imbalanced utilization of ancestors was estimated at 0.06%, with 414 ancestors accounting for 50% of genetic diversity. In contrast, the figures reported in the current study were 0.79% and 19 ancestors, indicating flaws in the population structure, such as failures in breeding plans, extensive usage of a small number of animals for reproduction, and a reduction in effective population size.

Warangkana (2018) and Pakpoom (2011) conducted a study of heritability levels defined as low, medium, and high, using dairy cow populations of 2,000, 5,000, and 10,000, and found notable results in terms of inbreeding rates. The study revealed that populations with high heritability had lower average inbreeding coefficients than those with low or medium heritability. These findings emphasize the importance of heritability levels in managing inbreeding across various dairy cattle population sizes, highlighting that not only heritability, but also population generation, is critical in determining inbreeding coefficients. This is because inbreeding increases the proportion of homozygous genotypes, leading to loss of genetic diversity. More importantly, increased levels of inbreeding lead to inbreeding depression, which has a deleterious impact on dairy cattle productivity and reproductive qualities. To avoid these negative consequences and sustain the competitiveness of genetic diversity, diversity must be maintained at acceptable levels (Doekes et al., 2020; Makanjuola, Maltecca et al., 2020; Martikainen et al., 2017). Heritability is critical in evaluating the prevalence of inbreeding across different dairy cow population sizes. In general, heritability refers to the proportion of observed variation in a feature that can be traced back to genetic rather than environmental influences. Maintaining genetic diversity is crucial in breeding programs that aim to increase productivity and health. Smaller populations have a higher probability of inbreeding due to limited genetic variety, which can lead to inbreeding depression as deleterious alleles are paired more frequently, limiting population fitness. In contrast, larger populations typically have broader genetic bases, allowing for better inbreeding management.

The relationship between litter sizes may be quite significant. Dairy cows typically give birth to a single calf every pregnancy, limiting their litter size. However, understanding the effect of breeding strategies on inbreeding rates is vital for maintaining herds health. When closely related animals mate, the inbreeding coefficient rises, resulting in a variety of genetic diseases and a decrease in the overall fitness of dairy cattle groups. In contrast, introducing unrelated or distantly related cattle can reduce the harmful effects of inbreeding depression. Furthermore, litter size, while normally one in dairy cows, can have an impact on management and genetic selection. Herds that prioritize productive attributes may accidentally favor some lineages, increasing the inbreeding coefficient over time. Thus, maintaining genetic diversity is critical in dairy farming to preserve herd health and productivity in the long run. Genetic drift leads to the loss of diversity by removing alleles, resulting in increased genetic homogeneity, also known as inevitable inbreeding (Oldenbroek et al., 2014). Genetic drift has a greater influence in small populations because sampling errors affect allele frequencies more strongly than in big populations. In the absence of dominance or epistasis, genetic variety is lost at the same rate as heterozygosity, i.e. 1/2Ne every generation (Honnay, 2012). In tiny populations, even with an allele frequency of 0.5, a specific gene may eventually become fixed or perish. This suggests the possibility of losing beneficial genes, such as those linked to fertility, or fixing harmful genes that jeopardize health, such as those associated with disease. This provides a reason to avoid inbreeding (Ishiki, n.d.). As per Stachowicz et al. (2011), inbreeding and loss of genetic variety continue to be serious concerns in current dairy cattle breeds. According to Holstein data, the average rate of inbreeding each generation has decreased in recent years, compared to the 1990s. The current effective population size for Holsteins is projected to be around 115, and it is unlikely to alter considerably soon if the current generation gap continues constant, as inbreeding rates grow and shared ancestry decreases.

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CONFLICT OF INTEREST STATEMENT

The author declares no conflict of interest.

REFERENCES

- Barros, E. A.; Brasil, L. H. A.; Tejero, J. P.; Delgado-Bermejo, J. V. and Ribeiro, M. N. 2017. Population structure and genetic variability of the Segureña sheep breed through pedigree analysis and inbreeding effects on growth traits. Small Ruminant Research 149:128-133.
- Barker JSF. 2001. Conservation and management ofgenetic diversity: a domestic animal perspective.Can J For Res 31: 588–595.
- Bayode O. Makanjuola, Filippo Miglior,Emhimad A. Abdalla, Christian Maltecca, Flavio S. Schenke and Christine F. Baes. 2019. Effect of genomic selection on rate of inbreeding and coancestry and effective population size of Holstein and Jersey cattle

populations. J. Dairy Sci. 103:5183–5199. https://doi.org/10.3168/jds.2019-18013Boichard D (1997)

- Doekes, H.P.; Veerkamp, R.F.; Bijma, P.; De Jong, G.; Hiemstra, S.J.; Windig, J.J. 2019. Inbreeding depression due to recent and ancient inbreeding in Dutch Holstein-Friesian dairy cattle. Genet. Sel. Evol. 2019, 51, 54. [CrossRef]
- Fuerst-Waltl B, Fuerst C (2012) Effect of inbreeding depression on survival of Austrian Brown Swiss calves and heifers. J Dairy Sci 95: 6086–6092
- Falconer, D. S., Mackay, T. F., & Frankham, R. 1989. Introduction to quantitative genetics (4th Ed.). Trends in Genetics, 12, 280.
- Green, L.C.,Franck, P.&Oldroyd, B.P. 2001. Characterization of Microsatellite Loci for Trigona carbonaria, a Stingless Bee Endemic to Australia. Molecular Ecology Notes. DOI: 10.1046/ j.1471-8278.2001.00041.x.
- Gutiérrez, J. P.; Cervantes, I.; Molina, A.; Valera, M. and Goyache, F. 2008. Individual increase in inbreeding allows estimating effective sizes from pedigrees. Genetics Selection Evolution 40:359-378. https://doi.org/10.1051/gse:2008008
- Hinrichs D, Thaller G. (2011). Pedigree analysis and inbreeding effects on calving traits in large dairy herds in Germany. J Dairy Sci 94: 4726–4733.
- Hiroshi Isshiki._________. Genetic Drift and Mutation.
- João Cruz Reis Filho, Rui da Silva Verneque, Robledo de Almeida Torres, Paulo Sávio Lopes, Fernanda Santos Silva Raidan and Fabio Luiz Buranelo Toral. 2015. Inbreeding on productive and reproductive traits of dairy Gyr cattle. R. Bras. Zootec., 44(5):174-179, 2015
- Kor Oldenbroek, Liesbeth van der Waaij. 2014. Textbook animal breeding: animal breeding and genetics for BSc students. Centre for Genetic Resources and Animal Breeding and Genomics Group, Wageningen University and Research Centre, the Netherlands. Groen Kennisnet. 311 N.
- K. Stachowicz, M. Sargolzaei, F. Miglior and F. S. Schenkel. 2011. Rates of inbreeding and genetic diversity in Canadian Holstein and Jersey cattle. J. Dairy Sci. 94 :5160–5175
- Lande, R. 1988. "Genetics and demography in biological conservation". Science. 241 (4872): 1455–1460.Bibcode:1988Sci.241.1455L.doi:10.1126/science.3420403. PMID 3420403
- Leroy G (2011) Genetic diversity, inbreeding and breeding practices in dogs: Results from pedigree analysis. Vet J 189: 177–182.
- Makanjuola, B. O., Miglior, F., Abdalla, E. A., Maltecca, C., Schenkel, F. S., & Baes, C. F. 2020. Effect of genomic selection on rate of inbreeding and coancestry and effective population size of] Holstein and Jersey cattle population. Journal of Dairy Science, 103, 51835199.Martikainen et al., 2017;
- Mc Parland, S.; Kearney, J. F.; Rath, M. and Berry, D. P. 2007. Inbreeding effects on milk production, calving performance, fertility, and conformation in Irish Holstein-Friesians. Journal of Dairy Science 90:4411-4419. https://doi.org/10.3168/jds.2007-0227

- Nattapol Chongkasikit. 2004. Animal Breeding. Department of Animal Science, Faculty of Agriculture, Chiang Mai University, Chiang Mai. 135
- Olivier Honnay. 2013. Genetic Drift. University of Leuven, Heverlee, Belgium. This article is a revision of the previous edition article by J Arnold, volume 2, pp 832–834,
- Pakpoom Kitingern and Nattaphon Chongkasikit. 2010. Estimation of Genetic parameters and breeding value for dairy cattle population in Chiang Mai Province. Agriculture Journal 26: 173-181
- Rokouei M, Torshizi RV, Shahrbabak MM, Sargolzaei, Sorensen AC. 2010. Monitoring inbreeding trends and inbreeding depression for economically important traits of Holstein cattle in Iran. J Dairy Sci 93: 3294–3302
- Sargolzaei, M. and F.S. Schenkel. 2013. QMSim: a large-scale genome simulator for livestock. Bioinformatics 25: 680-681.
- Sofa Nyman, Anna M. Johansson, Valentina Palucci, Anna A. Schönherz, Bernt Guldbrandtsen, Dirk Hinrichs and Dirk-Jan de Koning. 2022. Inbreeding and pedigree analysis of the European red dairy cattle.Nyman et al. Genetics Selection Evolution (2022) 54:70. https://doi.org/10.1186/s12711-022-00761-3
- Vasconcellos LPMK, Daniella T, Pereire AP, Coutinho LL, Regitano LC (2003) Genetic
  - characterization of Aberdeen Angus cattle using molecular markers. Genet Mol Biol 26: 133–137.
- Warangkana Kitpipit, Manatsanun Nopparatmaitree and Sayan Buaban. 2018. Genetic parameters for fertility traits of dairy cows in Thailand. Khon Kaen AGR. J. 46 SUPPL. 1: 628-633.
- William R. Catton, Jr. "Bottleneck: Humanity's Impending Impasse" Xlibris Corporation, 2009. 290 pp. ISBN 978-1-4415-2241-2