



Accurate Estimation of Effective Population Size in the Korean Dairy Cattle Based on Linkage Disequilibrium Corrected by Genomic Relationship Matrix

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- Supplementary Data -

Table 1. Distance classes and bin ranges for the linkage disequilibrium summary

Class	Minimum distance (Mb)	Maximum distance (Mb)	Within class bin distance range (Mb)	No. of bins
1	0	0.5	0.01	50
2	0	5	0.1	50

Table 2. Chromosome-specific centimorgan to megabase (cM/Mb) conversion ratios

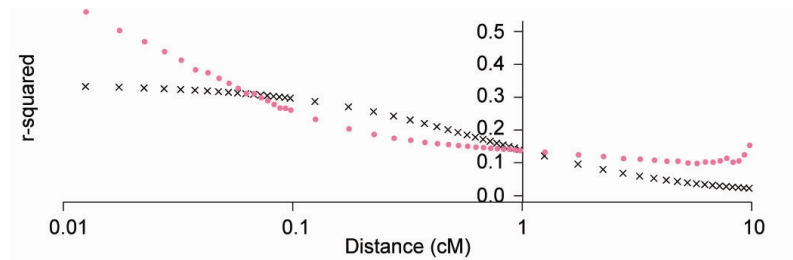
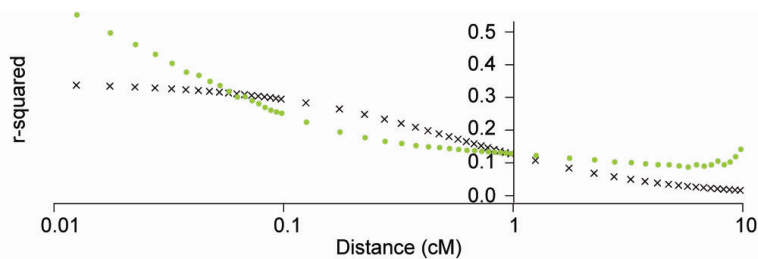
Chromosome	Length (Mb)	Length (cM)	cM/Mb ratio	Chromosome	Length (Mb)	Length (cM)	cM/Mb ratio
1	158	166	1.05	16	82	112.4	1.37
2	137	148	1.08	17	75	97	1.29
3	121	141.8	1.17	18	66	103.2	1.56
4	121	132.5	1.10	19	64	100.8	1.58
5	121	130	1.07	20	72	73.7	1.02
6	119	134.2	1.13	21	72	90.2	1.25
7	113	125.5	1.11	22	61	91.4	1.50
8	113	124.4	1.10	23	53	90	1.70
9	106	110.3	1.04	24	63	85.8	1.36
10	104	118.9	1.14	25	43	62	1.44
11	107	129.9	1.21	26	52	69.8	1.34
12	91	117.3	1.29	27	45	60.9	1.35
13	84	118.3	1.41	28	46	57.3	1.25
14	85	127.4	1.50	29	52	68	1.31
15	85	110.3	1.30				

Table 3. Description of the generation binning process

Generation range applied to	No. of generations represented by each bin	Example for first bin		
		Generation	Generation range	Corresponding distance range (Morgans)
5 to 10	5	5	4.5 to 5.5	0.11 to 0.09
20 to 100	10	20	15 to 25	0.02 to 0.033
200 to 1,000	100	200	150 to 250	0.002 to 0.0033
2,000 to 10,000	1,000	2,000	1,500 to 2,500	0.0002 to 0.00033
20,000 to 100,000	10,000	20,000	15,000 to 25,000	0.00002 to 0.000033

Table 4. Number of registered semen per country in Korea (domestic and imported)

	Estimated number of reliable semen	Estimated number of non-reliable semen	Total	%	Domestic or imported
Korea	38	175	213	12.4	Domestic
USA	958	175	1,133	66	Imported
Canada	311	48	359	21	Imported
Australia	5	0	5	0.3	Imported
Japan	5	0	5	0.3	Imported
Total	1,317	398	1,715	100	-

**Figure 1.** Predicted r^2 versus observed r^2 against mean distance between markers (cM, on a log scale) using the typical r^2 in equation (3).**Figure 2.** Predicted r^2 versus observed r^2 against mean distance between markers (cM, on a log scale) using r^2 corrected by the genetic relationship structure based on total single nucleotides in equation (3).

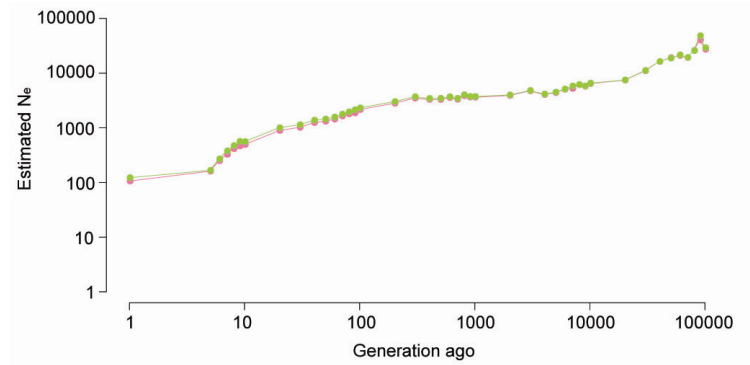


Figure 3. Average estimated effective population size plotted against generations in the past, truncated at 100,000 generations. Estimated effective population size and generations in the past plotted on a log scale. (a) hot pink for the typical r^2 (b) yellow-green for r^2 corrected by the genomic relationship structure based on total single nucleotide polymorphisms.

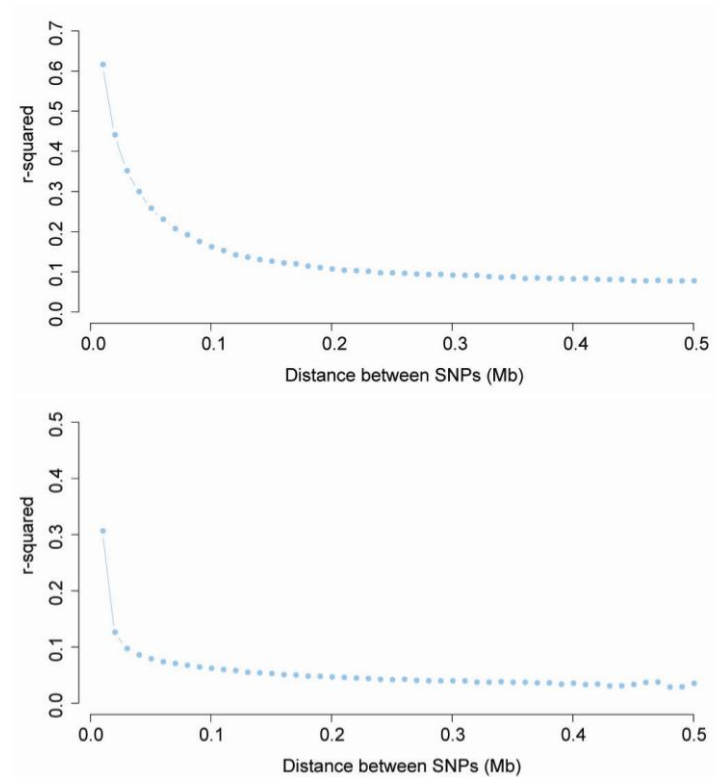


Figure 4. Average linkage disequilibrium (solid line) plotted against the median of the distance bin range (Mb) using r^2 corrected by the genetic relationship structure per chromosome. (a) Distance range from 0 to 0.5 Mb. r^2 values averaged using bins of 0.01 Mb and pooled over autosomes. (b) Distance range from 0 to 5 Mb. r^2 values averaged using bins of 0.1 Mb and pooled over autosomes.

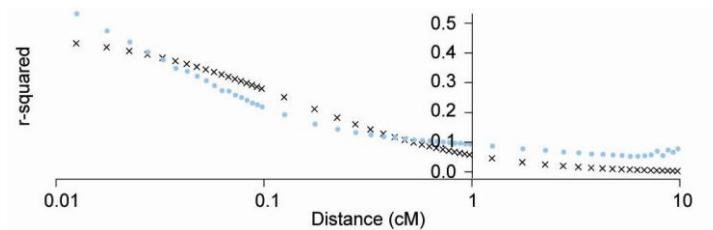


Figure 5. Predicted r^2 versus observed r^2 against mean distance between markers (cM, on a log scale) using the r^2 corrected by the genetic relationship structure per chromosome in equation (3).

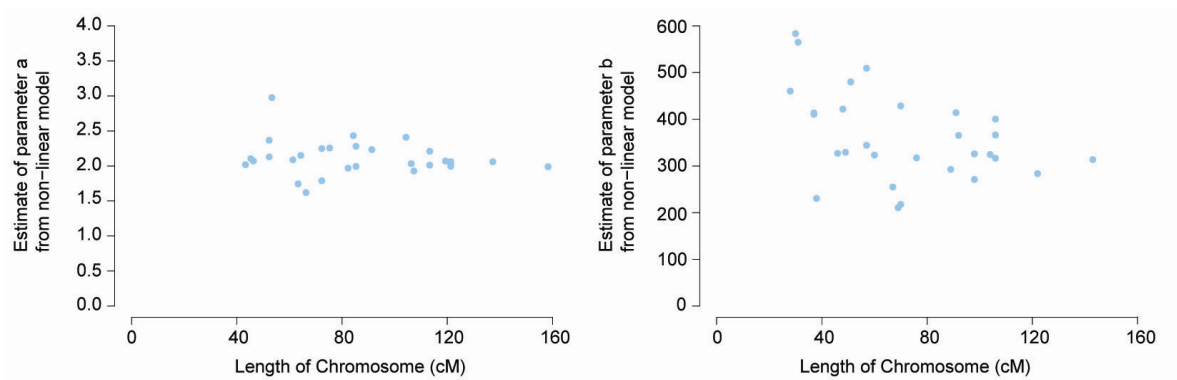


Figure 6. Parameter estimates from equation (3) plotted against chromosome length (cM) according to the bovine linkage map using r^2 corrected by the genetic relationship structure per chromosome. (Arias et al., 2009). (a) Estimates of parameter a plotted against chromosome length (cM) (b) Estimates of parameter b plotted against chromosome length (cM).

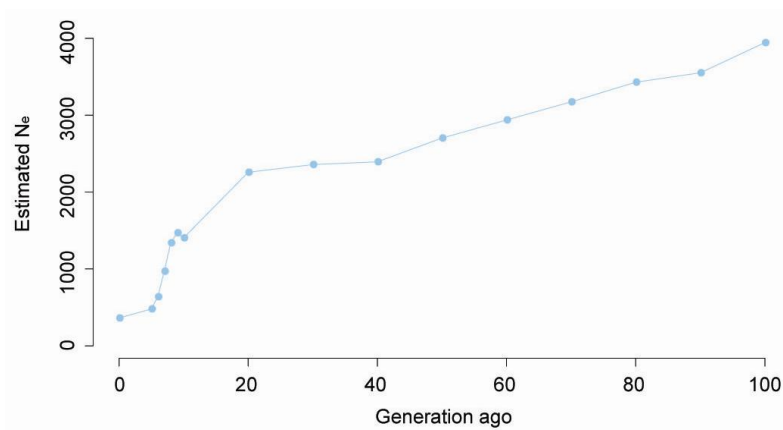


Figure 7. Average estimated effective population size plotted against generations in the past, truncated at 100 generations using r^2 corrected by the genomic relationship structure per chromosome.

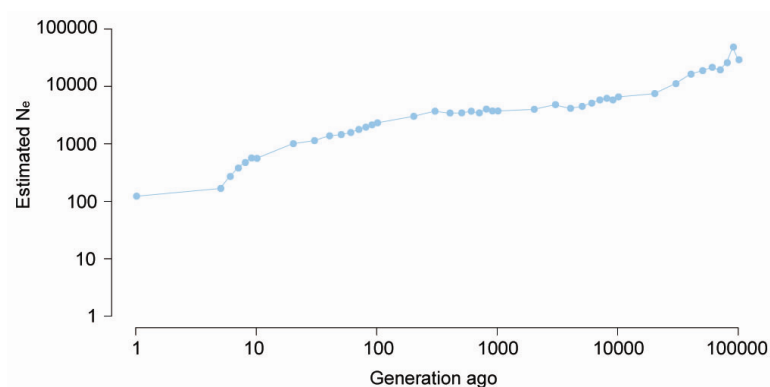


Figure 8. Average estimated effective population size plotted against generations in the past, truncated at 100,000 generations using r^2 corrected by the genomic relationship structure per chromosome. Estimated effective population size and generations in the past plotted on a log scale.