

The Simmental Breed: Population Structure and Generation Interval Trends

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Summary

Pedigree data from the American Simmental Association from 1986-2008 were used to analyze the pedigree structure and changes in generation intervals over time within the Simmental breed. The number of breeders that accounted for 10% of sires of sires (SS), sires of dams (SD), dams of sires (DS), and dams of dams (DD) were 3, 5, 5, and 16, respectively. States with the greatest influence on the four pathways of selection (SS, SD, DS, and DD) included Montana, South Dakota, Kansas, and Texas. In general, generation intervals for the four pathways decreased by year of birth over the time span of the data analyzed, albeit numerically slight. Average generation intervals for sires and dams also decreased by year of birth, while animals increased slightly.

Introduction

The fundamental breeding pyramid that is evident in other species by design is less clear in beef cattle. Although not clearly delineated, nucleus and multiplier levels of the beef seedstock industry do exist. The identification of producers within each segment is beneficial, especially within the nucleus level, as this is where the accumulation of breeding value occurs before dissemination to commercial herds. Generation interval (GI) is a key component to the overall rate of genetic change. Estimating trends in GI helps to benchmark progress and identify areas for improvement prior to implementation of genomic selection. The objective of the current study was to determine the population structure

of the Simmental breed, contributions by breeders and states to the four pathways of selection (grandparents), and changes in GI over time.

Procedure

Pedigree data were obtained from the American Simmental Association from animals born between 1986 and 2008. For computational ease, data were edited such that only three years per decade were used. The pedigree file utilized for analysis included 652,249 animals from 19,097 breeders. Population structure was determined by analyzing four pathways of selection including sires of sires (SS), sires of dams (SD), dams of sires (DS), and dams of dams (DD). Breeders with the greatest contribution to a particular pathway were accumulated until they accounted for 10, 25, 50, 75, or 100% of animals in the pathway. States or provinces with breeders that contributed the greatest to each pathway were also determined based on the percentage of animals in a particular pathway that originated from a specific state or province. The average generation

interval, or the average age of parents when the animal is born, of animals, sires, dams, SS, SD, DS, and DD were calculated and averaged by the animal's year of birth.

Results

The number of breeders that accounted for 10, 25, 50, 75 and 100% of total animals in the four individual pathways is depicted in Table 1. The five states with breeders contributing the greatest to each pathway are reported in Table 2. Trends in sire and dam GI show an overall decrease, with the slope being more dramatic in sires than in dams. Unexpectedly, animal GI increased slightly since 1997 (Figure 1). The difference between the birth year with the greatest mean GI and the least mean GI (RANGE) for sires, dams, and animals were 0.47, 0.22, and 0.24 years, respectively. GI measurements were associated with considerable variation as the mean standard deviations pooled across years for GI of sires, dams, and animals were 2.1, 2.4, and 1.9 years, respectively. Across the four pathways,

Table 1. Number of breeders accounting for 10, 25, 50, 75, and 100% of animals in a pathway.

	SS ^a	SD	DS	DD
10%	3	5	5	16
25%	9	19	22	81
50%	29	81	100	361
75%	102	369	419	1,360
100%	3,466	8,169	7,179	15,291

^aSS=sire of sire; SD=sire of dam; DS=dam of sire; DD=dam of dam.

Table 2. The top five states (percentage) for each pathway of selection.

SS ^a	SD	DS	DD
Montana (14.6)	Montana (12.1)	Montana (16.9)	Texas (11.8)
South Dakota (7.9)	Texas (8.2)	South Dakota (9.4)	South Dakota (8.7)
Texas (6.5)	Kansas (7.7)	Texas (9.1)	Montana (8.6)
Kansas (6.4)	South Dakota (6.7)	Kansas (6.7)	North Dakota (7.4)
North Dakota (6.4)	Nebraska (5.6)	North Dakota (5.5)	Kansas (6.6)

^aSS=sire of sire; SD=sire of dam; DS=dam of sire; DD=dam of dam.

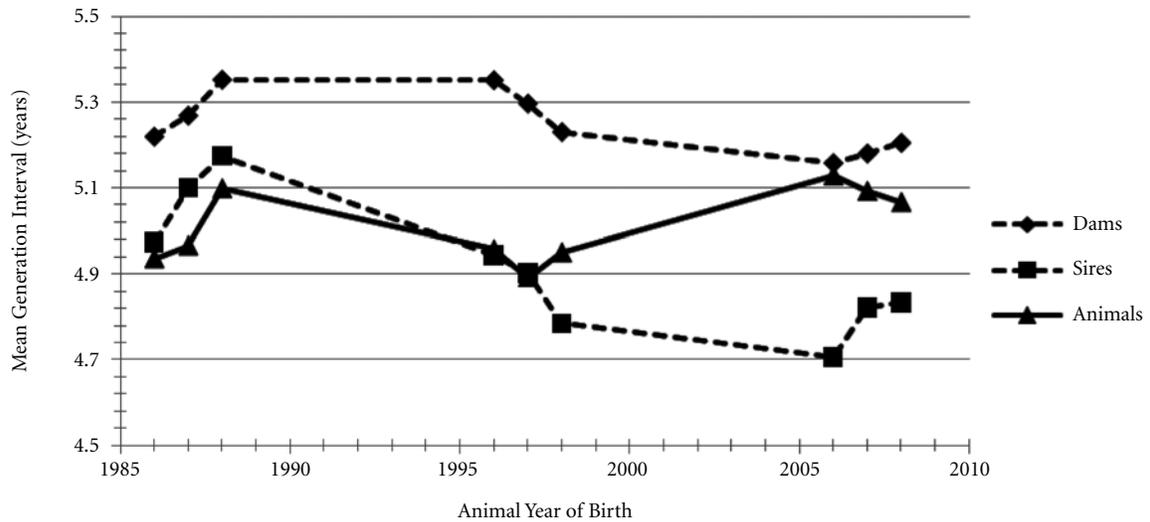


Figure 1. Mean generation interval for animals, sires, and dams by year of birth.

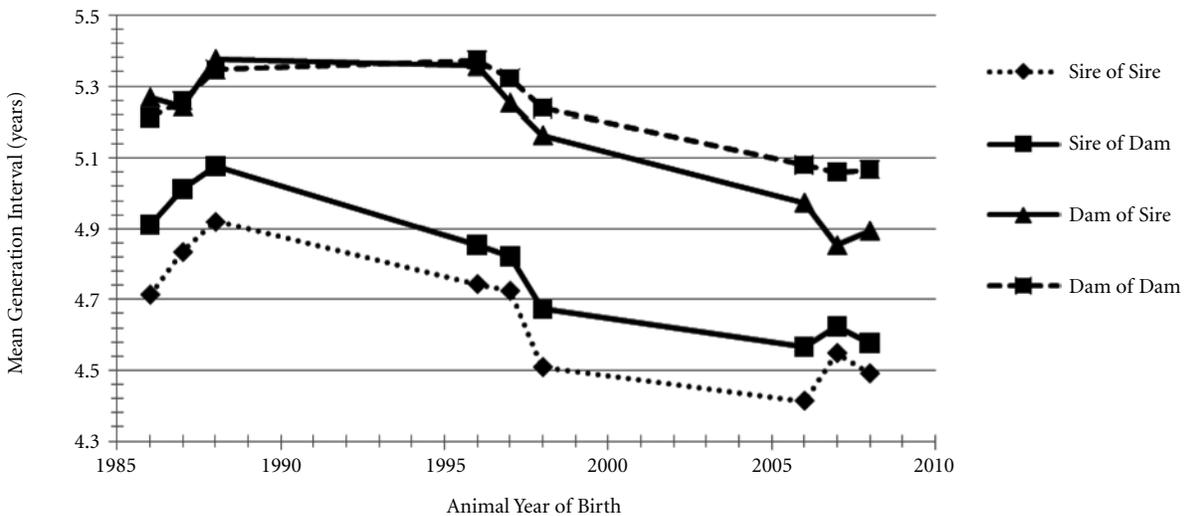


Figure 2. Mean generation interval for the four pathways of selection by year of birth.

GI shows a decreasing trend overall (Figure 2). As expected, SS generation intervals were the shortest and DD generation intervals were the longest. RANGE for SS, SD, DS, and DD were 0.51, 0.51, 0.52, and 0.31 years, respectively. The mean standard deviations pooled across years for GI were 2.0, 2.1, 2.2, and 2.3 years for SS, SD, DS, and DD, respectively.

Implications

There is a clear delineation of the Simmental breed into nucleus and multiplier levels, and genetic change is controlled by a small number of breeders. The GI for SS was the lowest of the four pathways and illustrates the importance of sire selection within nucleus herds. Although modest

improvement has been made, there is room for improvement in GI within the Simmental breed, either via reproductive or genomic technologies.

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