



J. Dairy Sci. 101:1–4
<https://doi.org/10.3168/jds.2017-13694>
 © American Dairy Science Association®, 2018.

Short communication: Two dominant paternal lineages for North American Jersey artificial insemination sires

C. D. Dechow,^{*1} W. S. Liu,^{*} J. S. Idun,^{*} and B. Manes[†]

^{*}Department of Animal Science, Penn State University, 324 Henning Bldg., University Park 16802

[†]Jersey Origins LLC, 4056-A Commercial St., Stitzer, WI 53835

ABSTRACT

Jersey cattle are the second most prominent breed in the United States and represent a growing portion of the dairy cow population in the United States. The objectives of our study were to determine the male lineages of Jersey sires with official genetic evaluations and to determine whether there are differences in sire conception rate among lineages. Paternal lineages back to the 1950s were extracted from genetic evaluation files of the Council on Dairy Cattle Breeding (CDCB, Bowie, MD) for all sires with an official United States genetic evaluation and that were enrolled with the National Association of Animal Breeders (Madison, WI). Further tracing of male lineages was performed by accessing the pedigree database of Jersey Origins LLC (Stitzer, WI). Only paternal lineages were considered because we were interested in transmission of the Y chromosome. Sire conception rate evaluations were also retrieved from CDCB for 1,116 bulls. Nearly all North American bulls born in the decade beginning 2010 could be traced to Secret Signal Observer or Advancer Sleeping Jester, who together account for 98.9% of paternal lineages. Both bulls plus the 3 additional bulls that account for the remaining 1.1% of current descendants can be traced to a single bull (Champion Flying Fox) born on the island of Jersey in 1898. When considering sires imported into the United States, the majority (71%) trace their paternal lineage to Secret Signal Observer or Advancer Sleeping Jester, and 97% can be traced to Champion Flying Fox. Sire conception rates were higher by 0.30 percentage points in the Secret Signal Observer line than in the Advancer Sleeping Jester line, which was significant. The small number of paternal lineages for recently born artificial insemination Jersey sires indicates that there is limited genetic diversity for much of the Y chromosome, suggesting that autosomal variation may be a more impor-

tant source for differences in male fertility than the Y chromosome.

Key words: Jersey, Y chromosome, paternal

Short Communication

Higher male fertility increases the value of semen (Pecsok et al., 1994) because high reproductive efficiency is essential to profitable dairy production; the value of establishing a new pregnancy was estimated to be \$278 (De Vries, 2006) when comparing the future cash flows of a pregnant cow to those of a nonpregnant cow. Sire conception rate (**SCR**) was established as a national phenotypic predictor of male fertility in 2008 (Kuhn and Hutchison, 2008) and replaced estimated relative conception rate, which had been available beginning in 1986 (Clay and McDaniel, 2001; Kuhn and Hutchison, 2008).

Although substantial phenotypic differences exist among sires in conception rate, the genetic component is relatively small and heritability estimates are low (Kuhn and Hutchison, 2008). Nevertheless, molecular pathways that influence male fertility have been identified (Li et al., 2012; Han and Penagaricano, 2016). Genetic variation on the Y chromosome (**Y-chr**) has also been shown to influence male fertility in cattle (Yue et al., 2013) and male health and fertility in humans (Bellott et al., 2014). In Holsteins, the amount of genetic diversity on much of Y-chr is expected to be limited because nearly all Holstein sires trace through their male lineage to only 2 sires from the 1960s (Yue et al., 2015). However, some variation is expected because the pseudoautosomal region of the Y-chr (~5%) recombines with the X chromosome during meiosis. There are also multiple copy gene families in the male-specific region that vary among Holstein bulls and that can change rapidly (Chang et al., 2013; Yue et al., 2013).

Jersey cattle are the second most prominent breed in the United States and represent a growing portion of the population, with the proportion of Jersey semen sold domestically by National Association of Animal Breeders (**NAAB**; Madison, WI) members increasing

Received August 16, 2017.

Accepted November 7, 2017.

¹Corresponding author: cdd1@psu.edu

from 6% in 2000 to 13% in 2016 (NAAB, 2017). Paternal lineages for Jersey cattle have not been reported on as they have for Holstein. The objectives of our study were to determine the male lineages of Jersey sires with official US genetic evaluations and to determine if differences exist in SCR among Jersey lineages. We focus on male fertility because the Y-chr would not influence cow or heifer conception rate.

Data were extracted from the April 2017 genetic evaluation of the Council on Dairy Cattle Breeding (CDCB, 2017a). The data were used to trace the paternal lineage to the last ancestor born in the 1950s for all AI sires; we considered lineages from the AI era to be modern era Y-chr lineages. Further tracing of male lineages to Isle of Jersey breeding records was performed by accessing the pedigree database of Jersey Origins LLC (Switzer, WI) to identify island founders. Lineages were initially traced for North American-born sires and subsequently for foreign-born sires with semen imported to the United States and with an official genetic evaluation.

We retrieved August SCR evaluations from the CDCB (CDCB, 2017b) every year from 2008 to 2017. The SCR with the highest reliability for bulls from Jester and Observer lineages was retained. Reliability was required to be at least 50% to be included in the analysis, resulting in 1,116 sires with SCR records. The association of paternal lineage with SCR was evaluated using the MIXED procedure of SAS (version 9.4, SAS Institute Inc., Cary, NC). Statistically significant ($P < 0.05$) fixed model effects included paternal lineage, age

of the sire at his SCR evaluation, and bull stud. The interaction of bull stud and year of SCR evaluation was treated as a random effect and improved model fit (lower Akaike information criterion corrected for finite sample size, AICC); year of SCR evaluation was not a significant fixed effect when this interaction was included but was included to maintain a hierarchical model. The reliability of the SCR evaluation was used as a weighting factor. Least squares means were generated for paternal lineage.

The number of Jersey sires born per decade with an official US genetic evaluation is depicted in Figure 1, along with the number of paternal lineages present by decade. The number of North American-born Jersey sires per decade was 431 in the 1970s and 1,778 (to date) in the decade beginning in 2010. The number of total sires born in the 2010s was 1,929 after including those not born in North America. The number of modern era Y-chr lineages that can be traced in the CDCB system declined to 5 for North American-born bulls in the 2010s compared with 44 in the 1970s.

Some decline in the number of lineages over time is expected, because each generation is a subset of the parent generation. More generations can also be traced for later decades, which could inflate the perception of the number of lineages maintained in earlier decades. To test this, we compared the number of lineages over 2 generations for each decade. Of sires with sufficient pedigree depth available, there were 3.4 descendants per lineage in the 1960s, 9.1 in the 1970s, and >15 for the remaining decades. This suggests that paternal

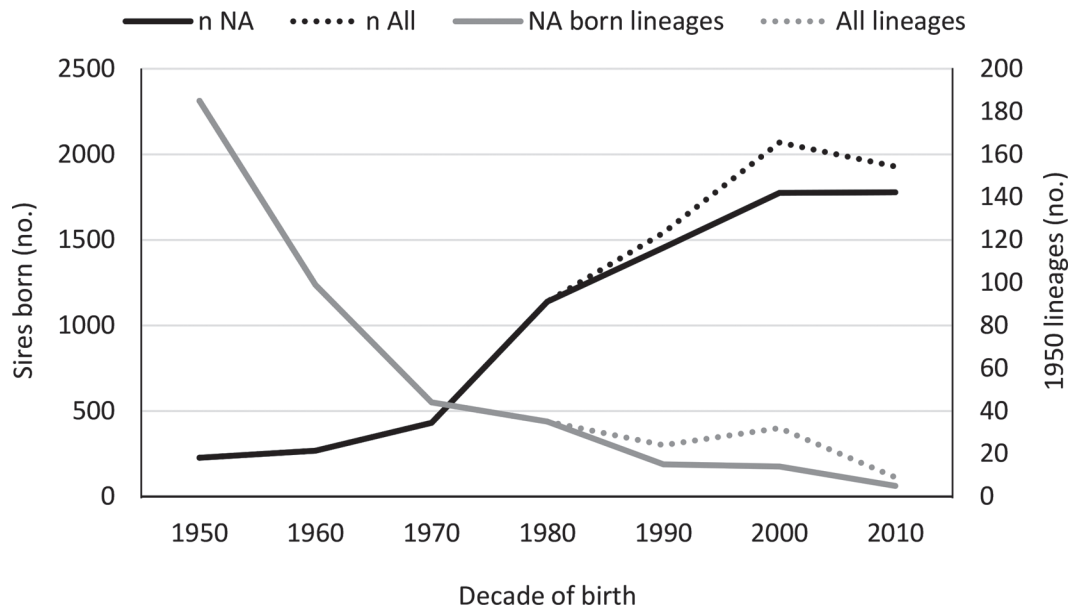


Figure 1. The number of North American born (n NA) and all (n All) AI sires with an official US genetic evaluations, and the number of modern era male lineages (NA born and All lineages) represented by those sires.

Download English Version:

<https://daneshyari.com/en/article/8501408>

Download Persian Version:

<https://daneshyari.com/article/8501408>

[Daneshyari.com](https://daneshyari.com)