

Original Article

Mating system change reduces the strength of sexual selection in an American frontier population of the 19th century^{☆,☆☆}

Jacob A. Moorad^{a,b,*}, Daniel E.L. Promislow^a, Ken R. Smith^c, Michael J. Wade^d

^aDepartment of Genetics, University of Georgia, Athens, GA, USA

^bDepartment of Pathology, University of Michigan Medical School, Ann Arbor, MI, USA

^cHuntsman Cancer Institute, University of Utah, Salt Lake City, UT, USA

^dDepartment of Biology, Indiana University, Bloomington, IN, USA

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Abstract

Sexual selection, or competition among members of one sex for reproductive access to the other, is one of the strongest and fastest evolutionary processes. Comparative studies support the prediction that sexual selection is stronger in polygamous than in monogamous species. We report the first study of the effect on sexual selection of a change in mating system, from polygyny to monogamy, within a historical human population. Here we show that over the reproductive lifetimes of Utahns born between 1830 and 1894, socially induced reductions in the rate and degree of polygamy correspond to a 58% reduction in the strength of sexual selection. Polygyny conferred a strong advantage to male fitness as well as a weak disadvantage to female fitness. In contrast, mating with multiple males provided little benefit to females in this population. Polygamy benefitted males by increasing reproductive rates and by lengthening reproductive tenure. Each advantage contributed to roughly half of the increased total lifetime reproductive success. This study illustrates both the potency of sexual selection in polygynous human populations and the dramatic influence that short-term societal changes can have on evolutionary processes.

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1. Introduction

Sexual selection is the process identified by Darwin (1859) where the members of one sex, generally males, compete with one another for reproductive access to members of the other sex. Theory predicts that sexual

selection should be a much stronger evolutionary force in polygamous than in monogamous mating systems (Shuster & Wade, 2003; Wade, 1979; Wade & Shuster, 2004b). Support derives primarily from extensive comparisons across taxa with different mating systems (Andersson, 1994; Bateman, 1948; Jones & Avise, 2001; Lofredo & Borgia, 1986; Shuster & Wade, 2003). We report the first study of the effects on sexual selection of a change in mating system, from polygyny to monogamy, within a population of a single species, *Homo sapiens*.

Polygynous marriage, where a man would simultaneously take on multiple wives, was a practice throughout much of the 19th century for some members of the Church of Jesus Christ of Latter-day Saints (LDS or Mormons). In the Utah Territory in the early part of the century, our estimates from the Utah Population Database indicate that the frequency of polygamous men as a fraction of all married men reached a maximum of 17.8% among men born in 1833 (Fig. 1), a figure consistent with previous estimates

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* Corresponding author. Department of Biology, Duke University, Durham, NC 27708, USA.

E-mail address: jacob.moorad@duke.edu (J.A. Moorad).

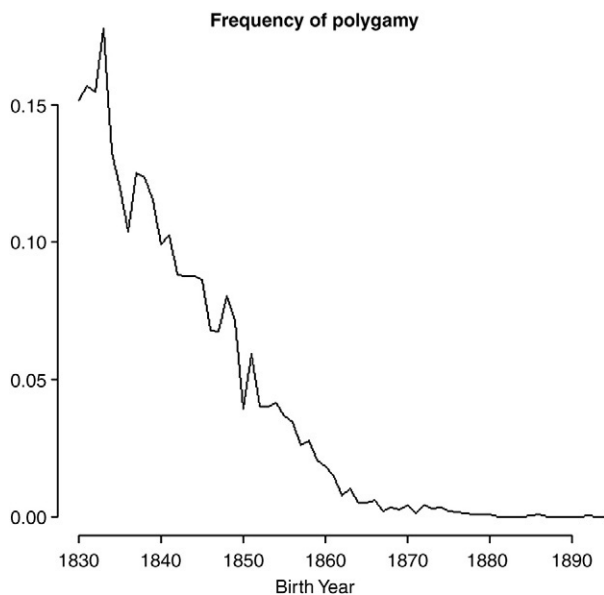


Fig. 1. Polygamous men in the UPDB as a frequency of all married men by birth year.

(Smith & Kunz, 1976). Subsequently, changes in social pressures over the next few decades reduced the frequency of such marriages to less than 1%. New strictures on the practice of polygyny began with the Morrill Anti-Bigamy Act of 1862 outlawing plural marriage throughout the US territories. The US Supreme Court upheld the ban in the face of a freedom of religion challenge in 1878 and, in 1890, the Mormon Church issued the Woodruff Manifesto which officially banned polygyny.

Data from this population afford a unique test of the role of polygyny in sexual selection in four ways. First, until now, the primary source of empirical support for sexual selection theory has been comparative studies across taxa with different mating systems (Andersson, 1994; Bateman, 1948; Jones & Avise, 2001; Lofredo & Borgia, 1986; Shuster & Wade, 2003). Second, previous human studies have compared relationships between social mating customs and sexual selection across geographically and culturally distinct populations (Brown, Laland & Mulder, 2009), whereas this study uses temporally defined cohorts that differ in mating system within the same population. Third, our sample size (180,082 parents) is 18 times larger than that in all other human studies of sexual selection combined (Brown et al., 2009), giving unprecedented power to describe sexual selection in a human population. Finally, these data span an important part of the demographic transition (Borgerhoff-Mulder, 1998) where natural fertility conditions prevailed early but reproductive rates rapidly fell over a few generations.

To determine the strength of sexual selection that acts on a population and to best understand how it is influenced by mating system, we need to quantify the associations

(e.g., the variances and covariances) between mating success and reproductive success in both males and females. In populations with an equal sex ratio of females to males, the rates of polygyny are necessarily and positively associated with the frequency of males who do not mate (Wade, 1979; Wade & Shuster, 2004b). As a result, polygyny increases the *variation* among males in mate number (mating success or MS). Using results from fruit fly experiments, Bateman (1948) was the first to argue that variation among males in mate numbers was the most important cause of a sex difference in the variance in reproductive success (RS). Wade (1995) derived the general relationship between the variance in male and female RS, showing that the sex difference in σ_{RS}^2 was a function of male MS. Shuster and Wade (2003) reviewed and extended this theory and applied it to several different taxa (Andersson, 1994; Bjorklund, 1991; Lofredo & Borgia, 1986; Shuster & Wade, 2003), including sex-reversed species with polyandry among territory-holding females (Jones & Avise, 2001), to show how mating system affected the strength of sexual selection. A recent comparative study using 18 geographically diverse human populations, a collection that included both monogamous and polygamous societies (Brown et al., 2009), showed that σ_{RS}^2 and σ_{MS}^2 tended to be higher in males than in females. Following the methods described in the Methods section, we examine these relationships within a single population during a period of change in the practice of plural marriage that affected mating success.

2. Methods

Our extract of the Utah Population Database (UPDB) included birth and death years of the 89,034 fathers and 96,407 mothers recorded in the UPDB born before 1900 (the majority of the UPDB reflecting Utah parents born after 1900 was not available to us). Note that the Utah population was not a strict closed society since potential wives could be recruited via religious conversion and migration into Utah (Daynes, 2001). We used only those individuals with known death year. There were very few individuals born before 1830 and these were excluded from our analysis. Fathers born after 1894 had missing data on their wives who were often born after the cutoff year of 1900. These exclusion criteria meant we had a sample of 72,812 fathers and 75,366 mothers born between 1830 and 1894. Our extract also included the 322,551 sons and 307,754 daughters who were born to parents represented in the UPDB extract. These parents were divided into 65 single birth-year cohorts from 1830 to 1894. Because the UPDB is derived from descendent genealogies, we could not expect it to include reliable counts of nulliparous individuals. We used US census data and a few reasonable assumptions (see Section 2.1 below) to estimate the size of this class of individuals for each sex and birth years. The

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