

AN ABSTRACT OF THE THESIS OF

Debra Jo Schons for the degree of Master of Science in
Animal Science presented on July 11, 1984.

Title: Population Analysis of a Commercial Beef Cattle Herd

Abstract approved: **Redacted for privacy** _____
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Twenty-four years of records (1958-1981) from a commercial Angus ranch were utilized in a population analysis to characterize the herd as a biological unit. The herd averaged 632 ± 129 cows and 123 ± 6 replacement heifers with all replacement heifers and many bulls from within the herd. Life tables were calculated for seven full cohorts (1958-1964) and for 15 partial cohorts (1965-1979) with data corrected for a large herd reduction sale in 1967. The model used was female only, for seasonal breeders with overlapping generations, and a time reference of immediately postpartum. Leaving the herd for any reason was equated with mortality. Nine statistics are reported: probability, at birth, of surviving to age x (L_x); age-specific survival and mortality rates (P_x and Q_x); expected herd life (E_x); age-specific birth rate (M_x); reproductive value (V_x); net reproductive rate (R_0); generation interval (T), and instantaneous rate of population increase (r). Average life table statistics were calculated to characterize the herd. The L_x curve was a quadratic curve ($R^2 = .91$); P_x and Q_x reflected culling for replacements and increased mortality after age 11; the highest

Ex was $5.73 \pm .31$ at one year of age (replacement heifers); Mx ranged from .33 to .47 with no age-specific pattern; Ro, T and r equaled $1.26 \pm .18$, $5.62 \pm .13$ and $.03 \pm .03$, respectively. Comparisons were made with two other studies of demographic analysis of beef cattle populations. Descriptive statistics were calculated, overall and by cohort, for productive years in the herd (YIH), total offspring per cow (TOC) and replacement daughters per cow (RDC). The YIH, TOC and RDC statistics averaged $4.49 \pm .09$, $3.78 \pm .09$ and $1.10 \pm .03$, respectively. Descriptive statistics and maximum possible values were calculated for three measures of genetic contribution by the summation of additive genetic relationships between a foundation animal from the 1959 cohort replacement heifers to the 1981 cohort replacement heifers (coefficient of cohort descent, CCD), to the 1981 herd (coefficient of herd descent, CHD), or to all their female descendants (coefficient of gene replication, CGR). The CCD, CHD and CGR statistics had means (and maxima) of $.007 \pm .003$ (17.2), $.06 \pm .021$ (102) and $.486 \pm .086$ (> 400), respectively.

POPULATION ANALYSIS OF A COMMERCIAL
BEEF CATTLE HERD

by

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A THESIS

submitted to

Oregon State University

in partial fulfillment of
the requirements for the
degree of

MASTER OF SCIENCE

Completed July 11, 1984
Commencement June 1985

APPROVED:

Redacted for privacy

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Date thesis is presented _____ July 11, 1984

Typed by Cathy Wermuth for _____ Debra Jo Schons

ACKNOWLEDGEMENTS

I would like to thank Mr. John Rouse for allowing us access to the One-Bar-Eleven records; Sue DeNise, for assisting with data copying and transfer; both Mr. Rouse and Sue DeNise, for their hospitality; Ron Stillenger, for his computer and Fortran programming consulting; Dr. James Hall, for his assistance with demographic methods, and Dr. William Hohenboken, for his overall assistance and support.

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POPULATION ANALYSIS OF A COMMERCIAL BEEF CATTLE HERD

INTRODUCTION

Population analysis is the study of characteristics unique to populations, as opposed to individuals, and is often used in human, fisheries and wildlife research. It can be divided into two major categories: 1) demographic analysis, involving such things as birth and death rates, growth rate (numbers and/or biomass), age structure, sex ratio, production, reproduction, density and dispersion and 2) genetic analysis, measuring patterns of genetic contribution to future generations.

Both categories of population analysis have been applied to research in domestic animal populations. A recent review of research in this area was published by Vu Tien Khang (1983). Demographic analyses have been performed on domestic animal populations to characterize a breed for the purpose of organizing breeding schemes (Wiener, 1961; Lauvergne et al., 1973; Martin, 1975; Basu and Ghai, 1980); to characterize a population for the purpose of developing models to optimize culling and replacement rates (Turner et al., 1959; Hickey, 1960; Basu and Ghai, 1980; Greer et al., 1980) or as a check on management practices (Nadkarni et al., 1983); to utilize the demographic statistics of a herd to develop a model to optimize herd structure for different production objectives, such as meat vs. velvet production in reindeer (Arobio, 1981); to develop hand calculator programs to project dynamics (in total animal units, herd structure and gross income) of a

beef cattle herd (Butterworth and McNitt, 1983); to examine the effect of selection on fitness traits (Turner et al., 1959); for gerontological studies (Comfort, 1958, 1959), and for municipal planning and regulation (Nassar and Mosier, 1980). Genetic breed analyses have been performed by describing the population through genetic contributions of different herds and individuals, and by calculating inbreeding and effective population size, usually for purposes of recording breed history or planning future breeding schemes (Vu Tien Khang, 1983).

The overall objective of this research was to characterize a commercial beef cattle herd as a population. Specific objectives were: 1) to construct age-specific mortality and reproduction life tables for the herd; 2) to calculate descriptive statistics for female life history traits, and 3) to characterize genetic contributions of a foundation group of cows to their female descendents and to the present population.

MATERIALS AND METHODS

Population and Management

Selection of a herd and the associated data set for this research was based on characteristics that would maximize accuracy and applicability of results, as well as demographic and statistical precision. Ideal characteristics were a large, established commercial cow/calf herd, located in an environment characteristic of many other cow/calf operations, with stable herd numbers and consistent management, representative of other producers, and also having detailed

identification and production records extending over many bovine generations. The One-Bar-Eleven herd possessed many of these ideal characteristics.

The One-Bar-Eleven Ranch, located near Saratoga, Wyoming, was purchased in 1955 by John E. Rouse. The ranch, at an average elevation of 2195 m, covers 3036 ha consisting of 607 ha of irrigated alfalfa and native grasses, 810 ha of native grass meadow and riverbottom land and 1619 ha of sagebrush foothills. Yearly rainfall averages 225 mm.

Mr. Rouse purchased a foundation herd of 376 mixed-aged Angus females in 1953. Herd numbers have varied over the years, averaging 632 ± 129 cows and 123 ± 6 replacement heifers. All replacement heifers and many bulls are selected from within the herd. Heifers are selected on weaning and yearling weights, dam's record and, in some years, information on their sire. Bull calves are selected on weaning weight per day of age, dam's record and results of a postweaning gain test. Cows leave the herd for many reasons; the most prevalent are culling for nonpregnancy, poor production records, calving difficulty or poor mothering ability. Unusually high death and culling rates were due to anaplasmosis and vibrio fetus in 1961 and the following few years, and to herd reduction sales in 1967 and 1974. Although the herd is commercial, both feeder calves and breeding stock (mainly young bulls) are marketed. A partial management calendar for the herd is presented in Appendix figure 1.

Computerized production and identification records for the herd have been kept since 1958. Twenty-four years of records (1958-1981) were available for this research. Information utilized included calf birth year, calf number, sex of calf, dam's calf number, dam's

identification number, dam's birth year and dam's disposal day, year and reason. Missing and incorrect information was encountered, generally due to loss of identification tags and recording errors, and was corrected to the extent that the written records allowed.

Demographic Analysis

Within cohort (birth year group) data for number of cows alive at each age, corrected for the 1967 herd reduction sale (to be described), were used in the cohort or horizontal method of life table construction (Caughley, 1966, 1967; J. Hall, personal communication). A life table is an age-specific table of measures of mortality and reproduction developed in actuarial science. The cohort method of life table construction (following an actual cohort from birth to the end of the last member's life) is one of two methods commonly used. The other method is the time-specific (or vertical) method, which uses the age structure at a specific time as representative of the mortality schedule of the whole population. The cohort method was chosen because the necessary data were available, and no assumption of an equilibrium population structure (stable age-distribution and herd numbers) was required as in the time-specific approach (Michod and Anderson, 1980). Seven full cohort life tables (all animals had left the herd; cohorts 1958 through 1964) and 15 partial cohort life tables (some animals were still present in the herd; cohorts 1965 through 1979) were constructed. The model used was female only, for seasonal breeders with overlapping generations, and a time reference of immediately postpartum. Birth was considered age 0, and the time interval was one year. Ages ranged from 0 to 17, but cows of ages 15 and over were

pooled to avoid distortions in the life table statistics due to small numbers. Leaving the herd for any reason was equated with mortality. The assumed biological flow-chart for this model is shown in figure 1. Six age-specific life table statistics and three overall life table statistics were calculated and are defined in table 1 (Caughley, 1966, 1967; J. Hall, personal communication). An additional definition of reproductive value (V_x) is the ratio of the expected size of a herd (at some future time) founded by a cow or group of cows aged x to the expected size of a herd founded simultaneously by a heifer calf or group of heifer calves aged 0 (MacArthur and Wilson, 1967). Mortality and reproductive conditions as represented by the life table of the cohort under investigation are assumed and V_0 must equal 1.

As stated previously, herd numbers on the One-Bar-Eleven Ranch have fluctuated over the years. Most fluctuations were relatively small and not systematic, with minor effects on life table statistics. The 1967 herd reduction sale was the only event with extreme influence on life table statistics, affecting each cohort at a different age. Because the event was abnormal and its effects on life table statistics drastic and widespread, annual cow numbers were adjusted for the sale to improve applicability of results. Corrected numbers of cows of each age for each cohort were calculated by averaging the age-specific survival rate (P_x) of unaffected cohorts for that age, replacing the P_x affected by the 1967 sale with that average P_x and then calculating backwards to the correct number of cows to use for life table construction. In figure 2, actual herd numbers over the years and herd numbers adjusted for the 1967 reduction sale are shown.

To compare cohort life table results, the Lee-Desu D statistic was used (Hull and Nie, 1981). The D statistic is based on a score (U) that compares, between cohorts, the L_x or other statistic for each age group and tests the null hypothesis that the cohorts are samples from the same survival distribution.

Life History Analysis

Descriptive statistics (mean, SE, SD, range and distribution) were calculated, overall and by cohort, for three female life history traits: 1) years in the herd (YIH), a measure of productive longevity equalling age at disposal minus two; 2) total offspring per cow (TOC), counting both male and female offspring, and 3) replacement daughters per cow (RDC). Only cohorts with essentially all cows having full lifetime records were used (1956 through 1967 for YIH and TOC, and 1957 through 1967 for RDC).

Analysis of Genetic Contributions

Genetic contributions to the herd from animals in a foundation cohort, beginning with replacement heifers, were calculated. The 1959 cohort (105 replacement heifers) was chosen because it was the earliest cohort with sufficient pedigree information. Male progeny and more distant male descendants were not used due to lack of information in some instances. Only direct descent was considered; collateral relatives were ignored. Three methods of calculation were utilized. The first method followed each foundation animal, through her female offspring and more distant female descendants, to termination or to the 1981 cohort replacement heifers (1-yr-olds). Additive genetic

relationships were calculated between each foundation animal and each descendant in the 1981 cohort replacement heifers (177 heifers). These relationships were summed if more than one relative existed. This measurement was termed coefficient of cohort descent (CCD). The second method followed each foundation animal, through her female offspring and more distant female descendants, to termination or to the existing herd in 1981. Additive genetic relationships were calculated between each foundation animal and each descendant in the 1981 herd (641 cows and 177 replacement heifers). These relationships were summed if more than one relative existed. This measurement was termed coefficient of herd descent (CHD). The third method calculated additive genetic relationships between the foundation animal and each of her descendants selected as a replacement heifer. These relationships were considered to be the proportion of a foundation animal's genes that were replicated and given further opportunity to make genetic contributions to the herd. Relationships were summed over each foundation animal's lifetime descendants. This measurement was termed coefficient of gene replication (CGR).

RESULTS AND DISCUSSION

Demographic Analysis

To determine the best method of characterizing the life table statistics, Lx curves (the basis of life table construction) of essentially complete cohorts (1958-1966) were tested for significant differences in survivorship (by each possible cohort pair and overall). Significant differences were found overall and between 20 of

36 cohort pairs (figure 3A). Differences in percentage of heifers kept as replacements and yearly fluctuations in herd size could have contributed to these observed differences. To test these hypotheses, the D statistic was first recalculated with data from ages 2 through 15+ only. This resulted in a marked reduction in significant cohort survivorship differences (figure 3B). To test if yearly fluctuations in herd size were also an important factor, the Lx curve for each cohort was adjusted to a stable age-distribution by the equation $S_x = L_x(e^{-rx})$ proposed by Caughley (1967). Testing differences among Sx curves (adjusted Lx curves) of the cohorts for all ages resulted in a large decrease in significant cohort survivorship differences (figure 3C). Similar tests for ages 2 through 15+ only revealed no significant differences among cohort survivorship curves overall and only two of 36 significant differences between specific paired cohort comparisons (figure 3D). These results support the hypotheses that survivorship differences between cohorts were due largely to differences in percentage of heifers kept as replacements and to yearly fluctuations in herd size.

In most studies with more than one cohort, differences between cohorts are not tested. Rather, populations are characterized by constructing a life table pooled across cohorts (Hickey, 1960; Krehbiel et al., 1962; Grubb et al., 1974; Greer et al., 1980; Melton, 1983). A pooled life table was constructed to characterize the One-Bar-Eleven herd using data from all complete cohorts (1958-1964). Another method to cancel out any differences between cohorts and distortions due to small numbers of animals at older ages is to average each life table statistic (at each age if age-specific) over as many cohorts as

possible. For the One-Bar-Eleven herd, L_x (age-specific survivorship), P_x (age-specific survival rate) and M_x (age-specific birth rate) were averaged over cohorts 1958-1966 (essentially complete to age 15), while E_x , V_x , GRR , R_o , T and r (as defined in table 1) were averaged over cohorts 1958-1964 (cohorts for which all cows had left the herd, i.e. were "complete"). Comparison of the pooled L_x curve with the averaged L_x curve using the Lee-Desu D statistic (Hull and Nie, 1981) showed no significant difference ($D = .308$; $P = .5789$). Thus both the pooled and averaged life table statistics describe the population in a similar fashion. Only the averaged life table statistics and standard errors are reported here. Age-specific life table results are shown in table 2.

As defined in table 1, the L_x or age-specific survivorship curve describes the mortality pattern of a population. For the One-Bar-Eleven herd, the L_x curve (figure 4) was a quadratic curve ($R^2 = .91$) showing the average selection of somewhat over half of the female calves as replacement heifers. After age one, the curve gradually decreases with no major disruptions, reflecting the lack of specific culling for age or age related health problems. In figure 4, the One-Bar-Eleven L_x curve is compared to the L_x curve of an earlier study by Krehbiel et al. (1962), using data from the Virginia Beef Cattle Improvement Association (VBCIA). The VBCIA data were from 1939 to 1961, covering Angus, Hereford and Shorthorn cattle from many farms and cohorts. The demographic method used to characterize cattle populations in that study was to construct a life table from age at disposal data pooled over all cohorts, farms and breeds. The VBCIA L_x curve differs only slightly from that of the current study, having a steeper slope that reflects

heavier mortality and(or) culling pressure. The curve also is smooth with no major disruptions.

A single cohort Px or age-specific survival rate curve, as defined in table 1, can show specific environmental effects (e.g. disease, market and management changes, weather, etc.). The averaged One-Bar-Eleven herd Px curve (figure 5) reflects a consistent management practice for percentage of female calves selected as replacements, little mortality and(or) culling between ages 1 and 2 and overall high survival rates up to 11 years of age. This suggests good herd health and management, high pregnancy rates and physically sound cows, with somewhat increased mortality and(or) culling at older ages. Comparison of the One-Bar-Eleven and VBCIA population Px curves shows the percentage of female calves selected as replacements was similar in the two groups, but there was greater mortality and (or) culling pressure in the VBCIA population (figure 5.) Since Qx, or the age-specific mortality rate, equals $(1-Px)$, the Qx curve is not presented graphically, simply being the mirror image of the Px curve.

Ex, or expected herd life as defined in table 1, has been calculated for dairy herds since the early 1930's (Cannon and Hansen, 1939). In beef cattle, only two other studies utilizing Ex were found. Krehbiel et al. (1962) calculated Ex using the VBCIA data described earlier; Greer et al. (1980) calculated Ex for a herd of mostly Hereford cattle from the Livestock and Range Research Station (LARRS), Miles City, MT. Data were pooled over cohorts from 1943 to 1976 with all cows culled after weaning a calf at age 10. The Ex curves from the three studies are presented in figure 6. The One-Bar-Eleven herd has a higher Ex overall (figure 6), showing lack of culling on age

and possibly reflecting superior herd health and management. Both the One-Bar-Eleven herd and the VBCIA population peaked at age one (no data were available at that age for the LARRS population); replacement heifers have the longest expected herd life. The slopes of the One-Bar-Eleven herd and LARRS population E_x curves are very similar, with the VBCIA population curve differing, possibly due to differences in age-specific survivorship.

The M_x curve is not shown since it is fairly consistent (overall average of $.42 \pm .01$) across all ages. As depicted in figure 1, the M_x of the Rouse herd is not influenced by fertility since it is calculated from the number of cows at calving (the beginning of the yearly cycle for this model) and cows are culled for nonpregnancy at the end of the previous year. The M_x though, as defined in table 1, is a function of sex ratio, fecundity and fetal mortality, and is a very important (and possibly variable) aspect of beef cattle production.

The V_x or reproductive value, as defined at table 1, assumes the age-distribution is stable by including the e^{-rx} correction factor in the equation. A comparison of the V_x curve from the One-Bar-Eleven herd and an estimated V_x curve from the Krehbiel et al. (1962) study is presented in figure 7. The VBCIA V_x curve was estimated by setting M_x equal to .42 (the overall average for the One-Bar-Eleven herd) and using the actual L_x from the Krehbiel et al. (1962) results to calculate an r value and finally the V_x using the equations in table 1. For the One-Bar-Eleven herd, the V_x curve peaks at age 4, although ages 2, 3 and 4 are very similar. The initial upward slope of the curve is possibly due to selection of replacement heifers and lack of reproduction until age 2 (M_x equals 0 for ages 0 and 1). The estimated VBCIA V_x curve peaks at

age 2, although the V_x at age 3 is similar, then decreases more rapidly than the One-Bar-Eleven curve until age 11 when there is a sharp increase, possibly due to the extended L_x curve and the r equalling $-.03$ for the VBCIA population. Caughley (1966) observed a high correlation between the P_x and V_x values of a population, possibly due to some evolutionary process. Comparison of figures 5 and 7 supports this observation with correlation coefficients of $.74$ for the One-Bar-Eleven herd and $.89$ for the VBCIA population. It does follow, in the One-Bar-Eleven herd, that as the probability of a cow surviving to the next year decreases, her probability of contributing to future generations also will decrease. This suggests a direct use of V_x , by culling for age when the V_x of a cow is less than one (a newborn female calf's V_x), which would be at age 13 or 11 for the One-Bar-Eleven herd or VBCIA population, respectively. Another option would be to increase culling pressure when the V_x of a cow is less than that of a replacement heifer (age 1), which would be at age 7 or 4 for the One-Bar-Eleven herd or VBCIA population, respectively. This method of culling would decrease the generation interval and could contribute to an increased rate of genetic improvement in the herd.

The R_o , or net reproductive rate as defined in table 1, is a comparative statistic based on sex ratio fecundity, fetal mortality, maximum longevity of the herd and age-specific survivorship (L_x). It can be used as a measure of finite rate of population increase per generation, but only comparatively if the respective generation intervals are known. The average R_o for the One-Bar-Eleven herd was $1.26 \pm .18$ (table 3), with each cow more than replacing herself and resulting in an overall increase in herd numbers. R_o , T and r

statistics were also estimated for the VBCIA population using an M_x equal to .42 (One-Bar-Eleven overall average) and the equations in table 1. An estimate of R_o for the VBCIA population was calculated at .86, suggesting that cows were not replacing themselves and leading to an expected decrease in population number.

The generation interval (T ; table 3), as defined in table 1, averaged $5.62 \pm .13$ years for the One-Bar-Eleven herd and was estimated at 4.76 years for the VBCIA population. Most beef cattle herds average between 4.5 and 6 years per generation (Newmann and Snapp, 1969). The One-Bar-Eleven herd is therefore at the high end of the range, possibly due to sales of breeding stock and preference for more information on each animal rather than a quick turnover. The One-Bar-Eleven cows also apparently remain structurally and reproductively sound, preventing earlier mortality and not requiring earlier culling.

The instantaneous rate of population increase (r), as defined in table 1, averaged $.03 \pm .03$ for the One-Bar-Eleven herd (table 3), and was estimated at $-.03$ for the VBCIA population. An r of zero means population size is stationary, so overall, One-Bar-Eleven herd numbers were increasing slightly and VBCIA population numbers were estimated to be decreasing slightly. According to J. Hall (personal communication), for natural populations, r is a measure of the population's capacity for sustained change in numbers; the higher the r , the more fit the population. Alternatively, the environment where a population has its highest r is the optimal environment for that population. The application of this definition of r to beef cattle or other livestock populations though, is severely restricted by human influence on management for production efficiency.

Life History Analysis

Overall descriptive statistics for YIH, TOC and RDC for the One-Bar-Eleven herd are presented in table 4. A breakdown of the life history statistics, by cohort, is presented in Appendix table 1. YIH (years in the herd), a measure of productive longevity, averaged $4.49 \pm .09$ years. For ease of comparison, the average age of a cow in the One-Bar-Eleven herd from cohorts 1956 to 1967 was 6.49 years. This appears high when compared to the study by Greer et al. (1980), in which the average age of a cow in the LARRS herd was 4.8 years. One reason for this large difference is the management practice at LARRS of culling on age (at 10 years of age). The One-Bar-Eleven herd had quite a few old and productive cows, as shown by the high SD, the range in YIH from 0 to 17 years and the reported gamma distribution. The TOC averaged $3.78 \pm .09$ offspring per cow. The existence of some outstanding cows in the One-Bar-Eleven herd is suggested by the high SD, the range of 0 to 17 offspring and the gamma distribution. Both YIH and TOC reflect the high level of structural and reproductive soundness in the One-Bar-Eleven herd, allowing the relatively low percentage (52%) of female calves retained as replacements (high female selection pressure), possibly making up for a loss of genetic improvement per year due to the extended generation interval. Average RDC ($1.10 \pm .03$ daughters) is somewhat comparable to the R_0 statistic from the averaged life table. Both indicate each cow is more than replacing herself in the herd, resulting in an overall increase in herd numbers.

Analysis of Genetic Contributions

Descriptive statistics for the three methods of calculating genetic contributions from individuals in the 1959 cohort are presented in table 5. A maximum possible value for each coefficient was also calculated to aid in interpretation and comparison. The maximum values were calculated assuming that a cow optimally produced nine replacement daughters (no twinning) and had 17 years in the herd (maximums from the One-Bar-Eleven life history statistics). These average genetic contribution statistics may represent low estimates for the overall herd due to a somewhat high loss of cows at all ages for the 1959 cohort as indicated by lower than average L_x values. For example, only 40% of the female calves were selected as replacements in the 1959 cohort. This difference in the 1959 cohort's L_x curve is also reflected in figure 3, with many significant differences at the $P < .01$ level.

The CCD was the narrowest ranged coefficient, following the 1959 cohort replacement heifers over 22 years to the 1981 cohort replacement heifers. The average CCD was $.007 \pm .003$ or .04% of the maximum possible value (17.2). The largest value for CCD was .219 or 1.27% of the maximum. The CHD followed the 1959 cohort replacement heifers over 22 years to the 1981 herd (cows and replacement heifers). The average CHD was $.06 \pm .021$ or .06% of the maximum (102), with the largest value at 1.47 or 1.44% of the maximum. Descriptive statistics of both CCD and CHD suggest low inbreeding (on the female side) in the One-Bar-Eleven herd, although there are a few outstanding cows with descendants consistently selected as replacements as shown by each range, SD and gamma distribution.

The CGR also spanned from the 1959 cohort replacement heifers to the 1981 herd. The average CGR was $.486 \pm .086$, somewhat less than one gene replication that could contribute again to future generations (.5). This is inconsistent with previous measures of a cow replacing herself in the herd (R_0 , r , mean of RDC), possibly due to the below average survivorship (L_x) for the 1959 cohort. The mean CGR was calculated at .11% of the estimated maximum (450) and the largest value (6.28), at 1.4% of the maximum. The frequency distribution for CGR is presented in figure 8. As shown in table 5, the CGR has a gamma distribution, although much less condensed than either the CCD or CHD. This suggests that although there are a few outstanding individuals who contributed consistently to future generations and are still directly related to the herd in 1981, there are also quite a few cows repeatedly having some part of their genome replicated and possibly contributing to the 1981 herd more through the collateral relatives of their descendants.

Discussion

The utilization of population analysis for beef cattle herd characterization and comparison has been demonstrated in this study. All three sections (demographic, life history and genetic contributions) contributed in describing the One-Bar-Eleven herd as a population.

In the demographic analysis, both mortality and reproductive life table statistics reflected past and existing management practices, and suggested new management procedures, particularly in manipulation of the herd age structure. Comparison of the One-Bar-Eleven herd statistics with beef cattle herds in two previous studies emphasized how

populations, even domesticated populations, can be uniquely characterized. Additional applications of the life table statistics could be to create a herd model to investigate biological and economic effects of genetic and management alternatives and manipulations. For some purposes, male life table statistics might also be useful. Many of the life table statistics could also be modified for more specific studies. For example, the M_x could be converted to pounds of calf produced (or biomass) and the entire life table modified to measure population production. A total input-output biomass model could also be developed. The survival portion of the life table could be changed to days or weeks instead of years to investigate feedlot mortality, as possibly affected by breed or prior management practices. Finally, mortality itself could be divided into separate life table statistics for culling and death. Although life table techniques and mathematics are fairly straightforward, caution must be used in selecting populations with valid, detailed census records.

The life history statistics, although much simpler than the life table statistics, were also used to characterize the One-Bar-Eleven herd and, in a general way, for comparison with other herds. The statistics reflected the relatively high longevity, excellent reproductive capabilities and overall increase in number of the One-Bar-Eleven herd. In a general way, these statistics could be used for modeling to predict the consequences of management or beef industry changes.

The genetic contribution statistics described the female flow of inheritance in the One-Bar-Eleven herd. The statistics reflected low inbreeding (female) in the herd along with the existence of a few outstanding cows having much higher than average genetic contributions

to future generations. The statistics on genetic contribution could also be used for comparison with other herds, could be expanded into a more detailed analysis and could be computerized within limitations of computer time, money and data set size.

TABLE 1. EXPLANATION OF LIFE TABLE STATISTICS^a

Statistic	Symbol	Definition	Equation
Age-specific Survivorship	L_x	P(at birth, of an animal surviving to age x).	$\frac{\# \text{ alive at age } x}{\# \text{ alive at age } 0}$
Age-specific Survival Rate	P_x	P(assuming survival to age x, of surviving to age x+1).	$\frac{L_{(x+1)}}{L_x}$
Age-specific Mortality Rate	Q_x	P(assuming survival to age x, of dying before age x+1).	$1 - P_x$
Expected Herd Life	E_x	An animal of age x is expected to be in the herd E_x more years.	$\frac{\sum_x^n L_{(x+1)}}{L_x} + .5$
Age-specific Birth Rate	M_x	P(of a cow aged x producing a live female calf). A function of sex ratio at birth, fecundity and fetal mortality.	$\frac{\# \text{ calves produced by cows aged } x}{\# \text{ cows at beginning of interval } x}$
Reproductive Value	V_x	Relative contribution of an animal of age x to future generations. Or, age-specific expectation of present and future offspring (Pianka and Parker, 1975).	$\frac{e^{rx}}{L_x} \sum_x^n e^{-rx} (L_x)(M_x)$
Net Reproductive Rate	R_0	Expected number of daughters produced by each animal entering the population. Or, finite rate of population increase per generation.	$\sum_{x=0}^n (L_x)(M_x)$
Generation Interval	T	Mean interval between birth of a parent and birth of its offspring.	$\left[\frac{\sum_{x=0}^n (L_x)(M_x)(x)}{\sum_{x=0}^n (L_x)(M_x)} \right] \div R_0$
Instantaneous Rate of Population Increase	r	A measure of herd number (N) increase or decrease. t=time period. $N_{t1} = N_{t0} e^{rt1}$	Iteration of: $\sum_{x=0}^n (L_x) e^{-rx} (M_x) = 1$

^a x = present age group.
n = oldest possible age group.

TABLE 2. AVERAGE AGE-SPECIFIC LIFE TABLE STATISTICS \pm SE
FOR THE ONE-BAR-ELEVEN HERD

AGE	L_x^b	P_x^b	Q_x^b	E_x^a	M_x^b	V_x^a
0	1.00	.52 \pm .06	.48 \pm .06	4.09 \pm .40	-	1.00
1	.52 \pm .06	.96 \pm .02	.04 \pm .02	5.73 \pm .31	-	1.88 \pm .12
2	.50 \pm .04	.84 \pm .02	.16 \pm .02	4.99 \pm .30	.39 \pm .02	2.02 \pm .06
3	.43 \pm .05	.82 \pm .02	.18 \pm .02	4.79 \pm .20	.41 \pm .03	2.02 \pm .09
4	.35 \pm .04	.85 \pm .02	.15 \pm .02	4.72 \pm .15	.47 \pm .02	2.04 \pm .12
5	.30 \pm .04	.84 \pm .04	.16 \pm .04	4.53 \pm .21	.45 \pm .03	1.94 \pm .15
6	.25 \pm .03	.86 \pm .02	.14 \pm .02	4.49 \pm .29	.45 \pm .03	1.90 \pm .21
7	.22 \pm .03	.83 \pm .03	.17 \pm .03	4.12 \pm .33	.42 \pm .03	1.72 \pm .20
8	.18 \pm .02	.84 \pm .02	.16 \pm .02	3.70 \pm .25	.39 \pm .04	1.56 \pm .14
9	.15 \pm .02	.78 \pm .03	.22 \pm .03	3.34 \pm .30	.44 \pm .04	1.44 \pm .18
10	.11 \pm .01	.86 \pm .03	.14 \pm .03	3.29 \pm .33	.39 \pm .04	1.36 \pm .17
11	.10 \pm .01	.81 \pm .07	.19 \pm .07	2.55 \pm .30	.34 \pm .03	1.13 \pm .15
12	.08 \pm .01	.76 \pm .05	.24 \pm .05	2.12 \pm .17	.44 \pm .06	1.06 \pm .11
13	.06 \pm .01	.68 \pm .05	.32 \pm .05	1.67 \pm .07	.46 \pm .08	.88 \pm .05
14	.04 \pm .01	.65 \pm .12	.35 \pm .12	1.18 \pm .13	.33 \pm .07	.61 \pm .14
15+	.03 \pm .01	0	1.00	.43 \pm .07	.43 \pm .11	.46 \pm .14

^a Averaged over cohorts 1958-1964 (complete cohorts only).

^b Averaged over cohorts 1958-1966 (essentially complete cohorts to age 15).

TABLE 3. AVERAGE, SE AND RANGE OF OVERALL LIFE
TABLE STATISTICS FOR THE ONE-BAR-ELEVEN HERD^a

Statistic	Ro	T	r
Mean	1.26	5.62	.03
SE	.18	.13	.03
Range	.67 - 1.82	5.14 - 6.07	-.07 - .12

^a Averaged over cohorts 1958-1964 (complete cohorts only).

TABLE 4. OVERALL LIFE HISTORY DESCRIPTIVE STATISTICS
FOR THE ONE-BAR-ELEVEN HERD

Statistic	YIH ^a	TOC ^b	RDC ^c
N	1586	1586	1480
Mean	4.49	3.78	1.10
SE	.09	.09	.03
SD	3.63	3.43	1.39
Range	0 - 17	0 - 17	0 - 9
Distribution	Γ	Γ	Γ

^a Years in herd; cohorts 1956-1967.

^b Total offspring per cow; cohorts 1956-1967.

^c Replacement daughters per cow; cohorts 1957-1967.

TABLE 5. DESCRIPTIVE STATISTICS OF GENETIC CONTRIBUTIONS
FROM THE 1959 COHORT REPLACEMENT HEIFERS TO THE 1981
COHORT REPLACEMENTS, TO THE 1981 HERD AND
TO ALL THEIR FEMALE DESCENDANTS

Statistic	CCD ^a	CHD ^b	CGR ^c
N	105	105	105
Mean	.007	.06	.486
SE	.003	.02	.086
SD	.031	.21	.880
Range	0 - .219	0 - 1.47	0 - 6.28
Distribution	condensed Γ	condensed Γ	Γ
Maximum ^d	17.2	102	> 400

^a Coefficient of cohort descent.

^b Coefficient of herd descent.

^c Coefficient of gene replication.

^d Assuming a cow produced nine replacement daughters (no twinning) and had 17 years in the herd.

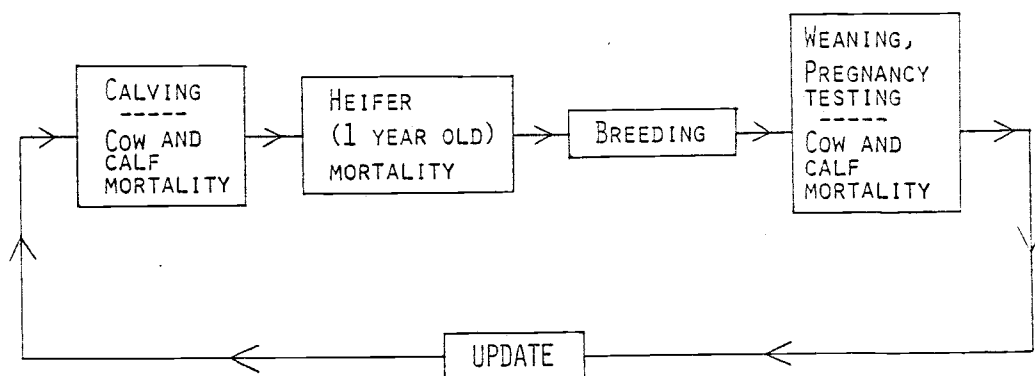


Figure 1. Biological flowchart for the model of the One-Bar-Eleven herd.

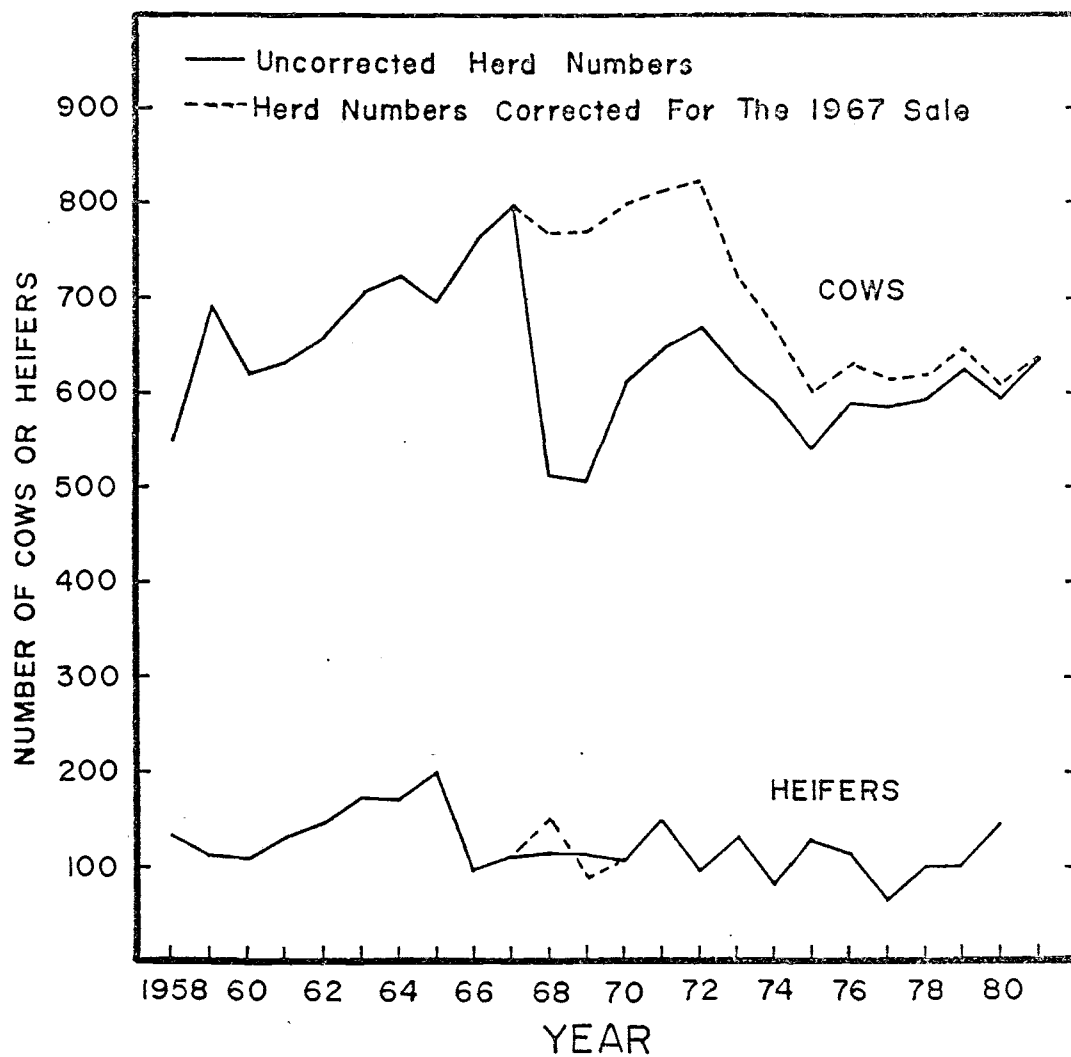


Figure 2. Fluctuations in herd size, from 1958 to 1981, before and after corrections for the 1967 herd reduction sale.

A. LX AGES 0-15+ OVERALL RESULTS										
D=75.424					P=.0000					
58	59	60	61	62	63	64	65	66		
				★★	★	★★		★		
			★★	★★	★★	★★				
				★★	★	★★		★		
						★★		★★		
							★★	★★		
							★★	★★		
	★				★		★★	★★		
				★		★★				
★		★	★	★★	★	★★				

B. LX AGES 2-15+ OVERALL RESULTS										
D=17.786					P=.0229					
58	59	60	61	62	63	64	65	66		
					★					
				★	★★	★★				
					★★	★				
					★		★			

C. SX AGES 0-15+ OVERALL RESULTS										
D=22.364					P=.0043					

D. SX AGES 2-15+ OVERALL RESULTS										
D=8.703					P=.3680					

★ P < .05

★★ P < .01

Figure 3. Results of Lee-Desu D statistic analysis, overall and for each possible cohort pair. Lx is age-specific survivorship and Sx is age-specific survivorship adjusted to a stable age distribution by the equation: $S_x = L_x(e^{-rx})$.

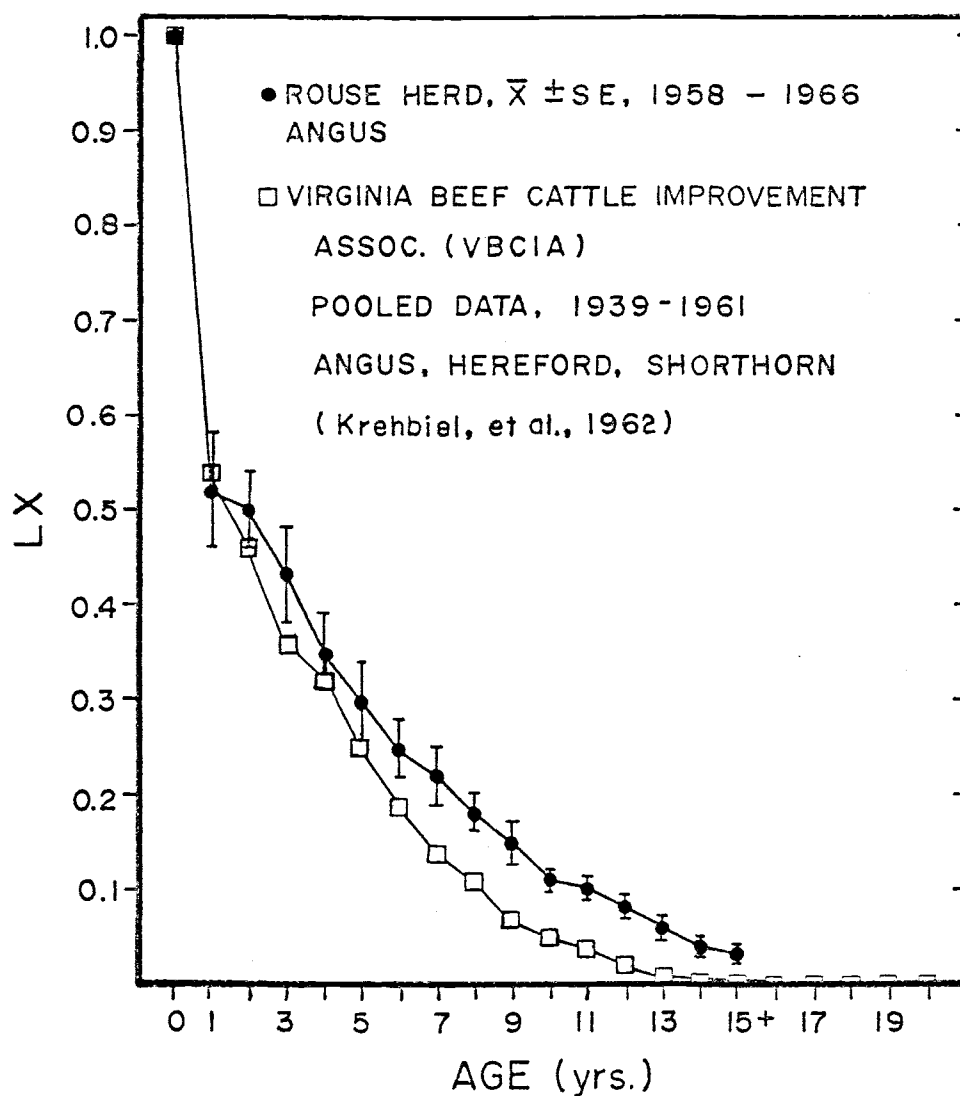


Figure 4. Relationship between age and survivorship (L_x) for the One-Bar-Eleven (Rouse) herd and another study.

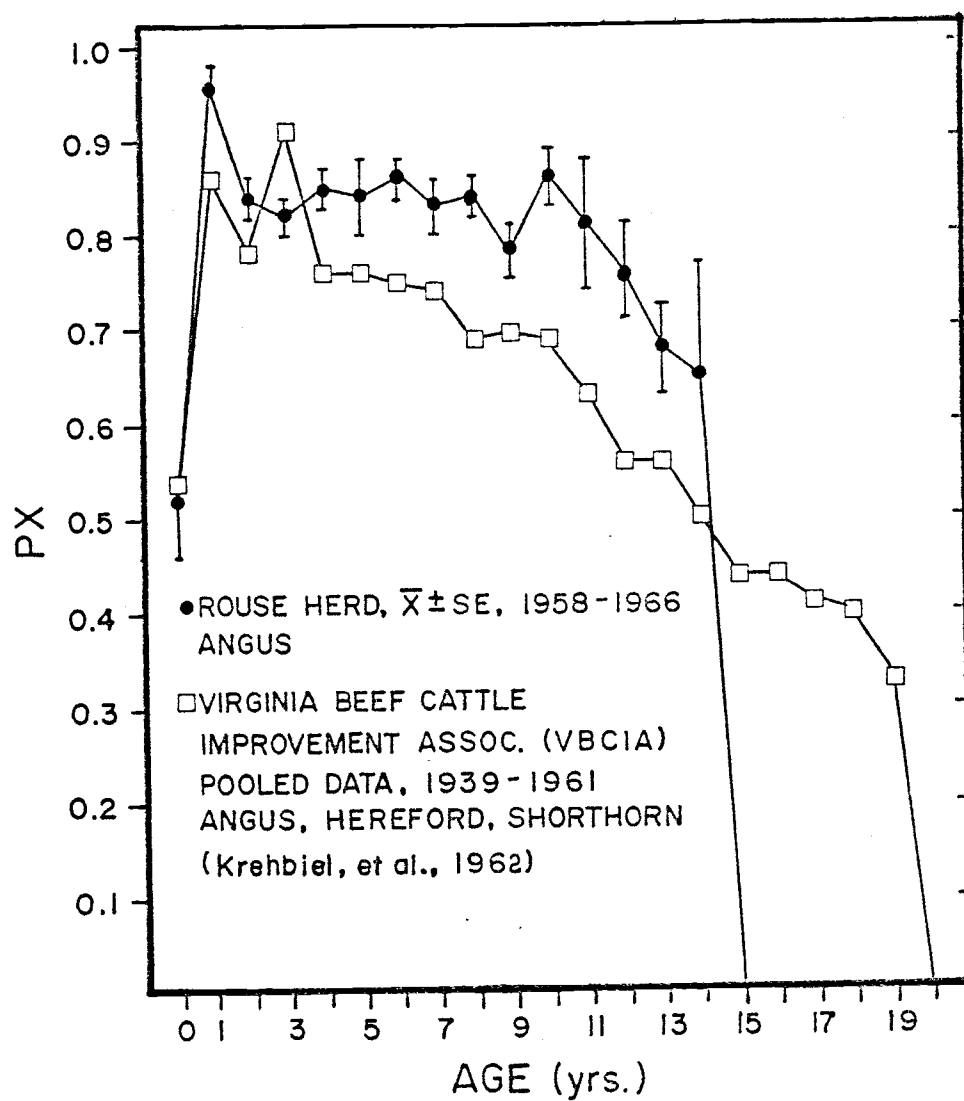


Figure 5. Relationship between age and survival rate (Px) for the One-Bar-Eleven (Rouse) herd and another study.

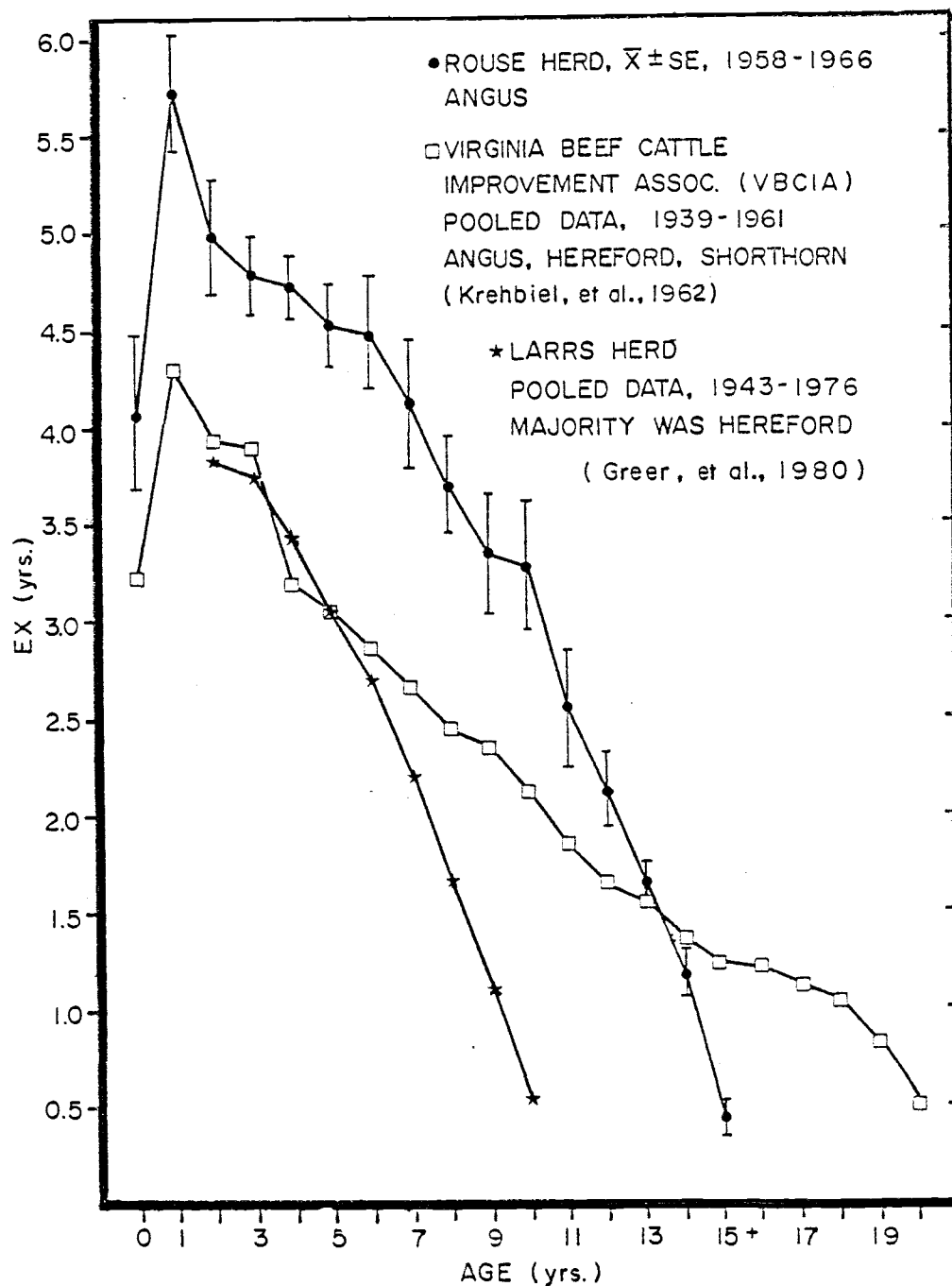


Figure 6. Relationship between age and expected herd life (Ex) for the One-Bar-Eleven (Rouse) herd and two other studies.

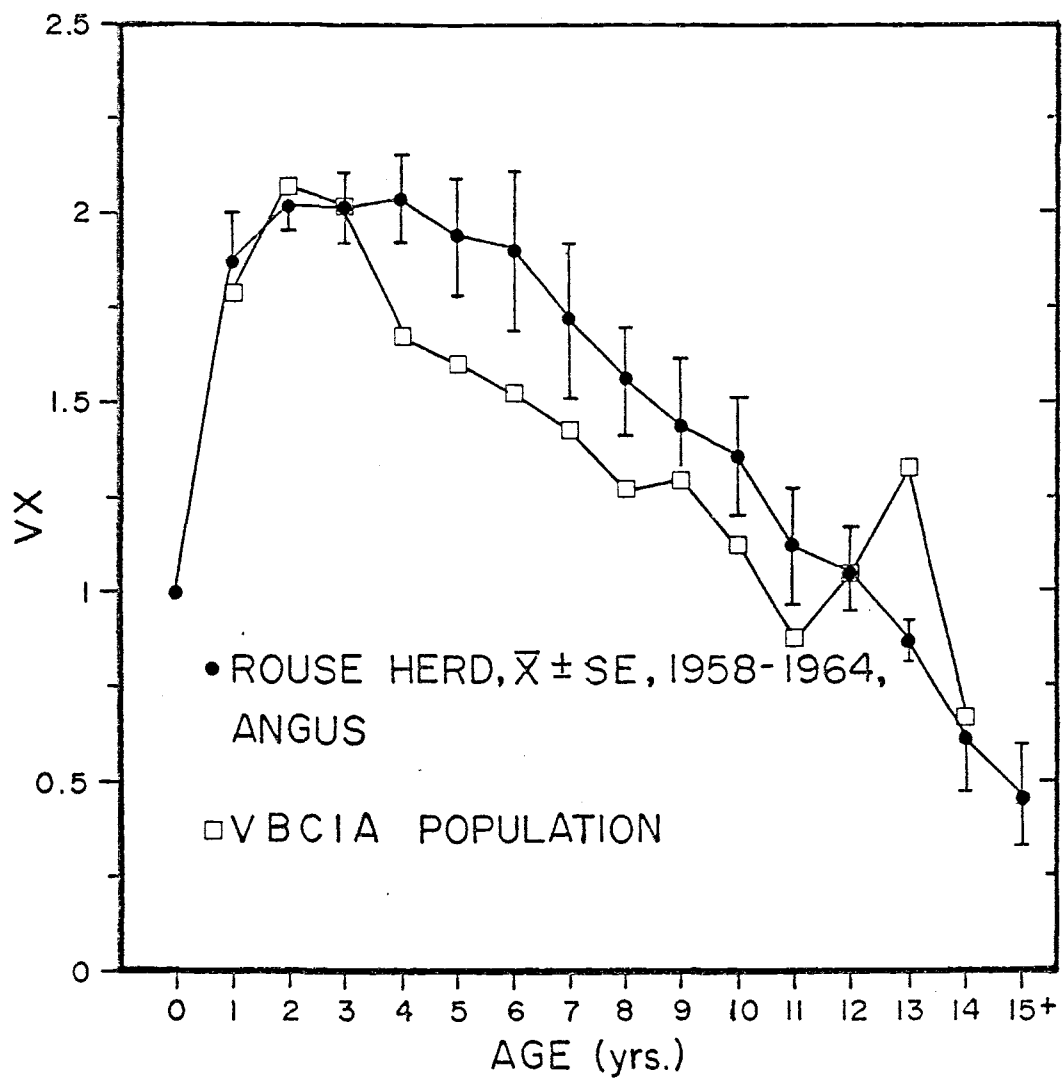


Figure 7. Relationship between age and reproductive value (V_x) for the One-Bar-Eleven (Rouse) herd and an estimate of V_x for the VBCIA population (Krehbiel et al., 1962).

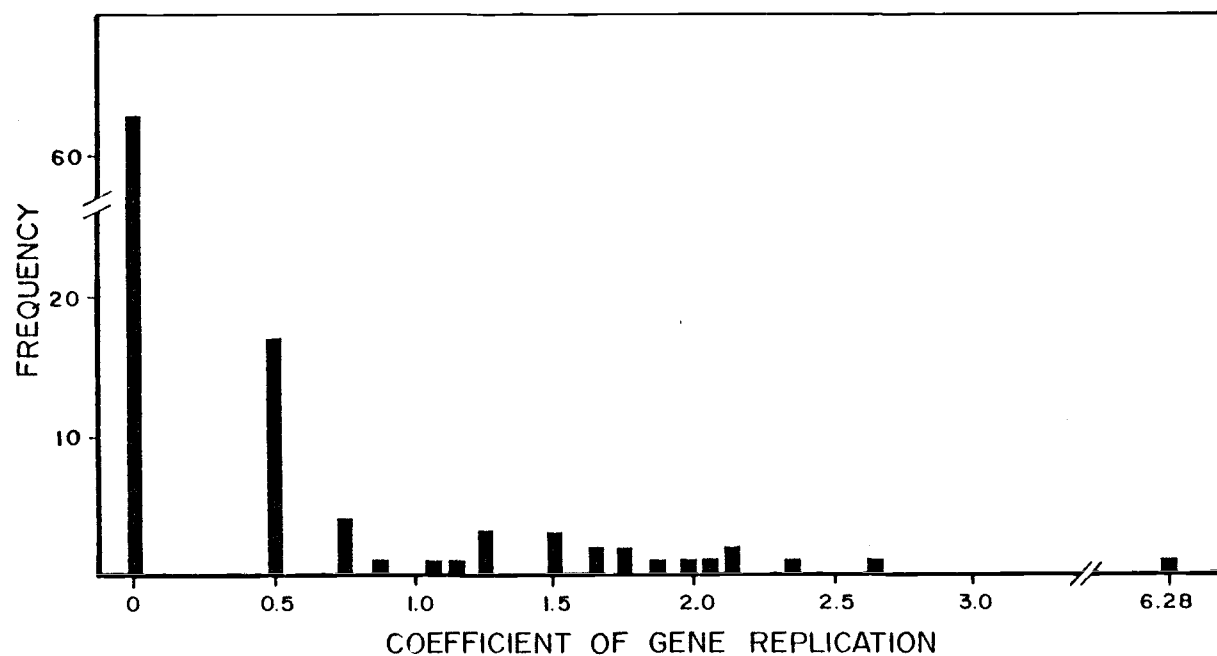


Figure 8. Frequency distribution of the coefficient of gene replication (CGR) for 1959 cohort replacement heifers, spanning 1959 to 1981.

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APPENDICES

APPENDIX TABLE 1. LIFE HISTORY DESCRIPTIVE
STATISTICS, BY COHORT

Cohort	Statistic	N	Mean	SE	SD	Range
1956	YIH ^a	106	4.73	.35	3.58	1 - 17
	TOC ^b	106	3.74	.34	3.32	0 - 16
	RDC ^c	-	-	-	-	-
1957	YIH	133	4.69	.39	4.44	0 - 17
	TOC	133	3.56	.34	3.90	0 - 16
	RDC	133	.84	.14	1.58	0 - 8
1958	YIH	111	4.10	.30	3.15	0 - 13
	TOC	111	3.08	.25	2.68	0 - 11
	RDC	111	.85	.10	1.04	0 - 5
1959	YIH	110	3.74	.36	2.85	0 - 15
	TOC	110	3.04	.29	2.55	0 - 14
	RDC	110	.69	.10	1.03	0 - 4
1960	YIH	130	4.13	.26	2.93	0 - 14
	TOC	130	3.11	.23	2.58	0 - 13
	RDC	130	.85	.10	1.08	0 - 4
1961	YIH	145	5.59	.35	4.18	0 - 17
	TOC	145	5.03	.34	4.10	0 - 17
	RDC	145	1.30	.13	1.56	0 - 7
1962	YIH	173	4.53	.23	2.98	1 - 16
	TOC	173	3.88	.23	2.97	0 - 16
	RDC	173	1.04	.11	1.38	0 - 9
1963	YIH	171	4.80	.28	3.70	0 - 15
	TOC	171	4.24	.27	3.48	0 - 15
	RDC	171	1.31	.11	1.38	0 - 6
1964	YIH	197	3.41	.26	3.63	0 - 16
	TOC	197	3.04	.24	3.37	0 - 16
	RDC	197	.95	.10	1.31	0 - 6
1965	YIH	94	3.14	.36	3.52	1 - 13
	TOC	94	2.71	.37	3.55	0 - 14
	RDC	94	.90	.14	1.38	0 - 5
1966	YIH	105	5.70	.38	3.85	1 - 14
	TOC	105	5.00	.38	3.90	0 - 14
	RDC	105	1.82	.16	1.60	0 - 7
1967	YIH	111	5.50	.31	3.31	0 - 13
	TOC	111	4.95	.32	3.35	0 - 13
	RDC	111	1.56	.13	1.37	0 - 6

^a Years in the herd.

^b Total offspring per cow.

^c Replacement daughters per cow.

MARCH	APRIL	MAY
<div>← HEIFER 2 YEAR</div>	<div>CALVING OLDS.</div> <div>← COW CALVING. →</div>	<div>↔ YEARLING WTS. TAKEN. ADDITIONAL SELECTION OF REPLACEMENT HEIFERS.</div>
JUNE	JULY	AUGUST
<div>← BREED HEIFERS. →</div>	<div>← ARTIFICIALLY INSEMINATE COWS. →</div>	<div>PUT IN CLEAN-UP BULLS.</div>
SEPTEMBER	OCTOBER	NOVEMBER
	<div>↔ WEIGH CALVES. SELECT AND WEAN BULL CALVES. WEAN CALVES FROM HEIFERS. CASTRATE NON-SELECTED MALES. PREGNANCY TEST. MAJOR COW CULLING.</div>	<div>↔ WEAN REMAINING CALVES. SELECT REPLACEMENT HEIFERS.</div> <div>← FEEDER CALVES SOLD. →</div>
DECEMBER	JANUARY	FEBRUARY
<div>←</div>	<div>HERD WINTERED ON GRASS AND ALFALFA HAY FROM THE RANCH.</div>	<div>→</div>

APPENDIX FIGURE 1. PARTIAL MANAGEMENT CALENDAR FOR THE ONE-BAR-ELEVEN HERD.