ABSTRACT
Micromanipulation of sperm and ova has been suggested as a means to produce progeny of two sires instead of a sire and dam. Selection schemes taking advantage of this technology could produce genetic gains 1.5 to 2 times current gains. An optimum strategy both genetically and economically would be to breed 99% of the population to young sires and 1% to progeny-tested sires. The genetic pathway from sires to sons could become the only pathway affecting genetic gain; this would eliminate problems of cow evaluation and would give artificial insemination organizations more control over quality of young sires. Inbreeding would not be a problem, and few other technologies could offer superior rates of genetic gain.

INTRODUCTION
Many new technologies that may benefit quantitative animal breeders are being investigated. One of these is a technique to produce male and female offspring with only sires as parents (androgenones). Such animals would be produced by removing the female pronucleus of a fertilized ovum immediately after fertilization and replacing it with a male pronucleus (sperm). In this way, new individuals could be created by uniting two sperm instead of a sperm and an egg, with the ovum simply a carrier for the two sperm.

Research on this topic has proceeded quickly, but recently, problems were discovered (5). Actual micromanipulation procedures are not a problem, at least in mice (4). The technique has been more difficult with cattle until recently when a compound causing fluorescence of pronuclei was discovered (6). The problem is that no live mammalian androgenones have been produced, and a large study concluded that such individuals may not be possible (5). Nevertheless, it is worthwhile to speculate on the genetic gains that might result to determine the potential value of further research in this area.

Offspring produced by mating two sires together would consist of a 2:1 ratio of males to females. Another class of YY individuals would be produced one-fourth of the time but likely would not develop or survive to term. This analysis will concentrate on males produced by this method because such males might have a large impact on the artificial insemination (AI) industry. It is assumed that the cost of producing bull calves by androgenesis will be only slightly greater than that of a normal embryo transfer so that the procedure could be used to obtain all the bulls needed for progeny testing. The majority of females would still be produced with parents of two sexes by AI.

METHODS
The objective is to determine rates of genetic gain attainable when offspring can be produced from only sires as parents and to investigate changes that would occur in the AI industry. This is accomplished by proposing alternative strategies, examining the strategies for internal consistency, and determining the steady state for rates of genetic change. Steady-state or asymptotic rates are those achieved when the selection program has been in effect for a few generations and when no further changes occur in size or structure of the population (3). When this phenomenon occurs, average genetic merit of any identifiable segment of the population (such as sires of sons, 1-yr-old heifers, etc.) increases at exactly the same rate, and this rate equals the steady-state rate of genetic gain. This concept first was employed by Rendel and Robertson (8).
Genetic change per year can be calculated (1) as the intensity of selection \((i)\) times the accuracy of selection \((r_{IH})\) times the genetic standard deviation of the population undergoing selection \((\sigma_G)\) divided by generation length \((L)\). These terms are represented in Equation [1].

\[
\Delta G/yr = (i \cdot r_{IH} \cdot \sigma_G)/L \quad [1]
\]

Suppose that all young bulls to be sampled are produced from only sires as parents. A basic principle of quantitative genetics is that expected genetic value of an offspring is equal to the average genetic value of its two parents. From this, average merit of young sires should equal the average merit of progeny-tested sires used to produce young bulls. This implies that the economic value of top bulls might be reduced sharply, because large numbers of young bulls equally as good as their sires could be produced to take their places in about 2 yr. (Two years allows 1 yr for pregnancy and another year until semen is produced.) The young bulls would be equal to their sires on the average but would be dispersed about this mean by Mendelian sampling.

In a population in which new bulls are produced with only sires as parents for generation after generation, the males become a self-perpetuating breeding population. Females would receive genes from the males through AI but would contribute no genes back to the male population. Females would, however, contribute ovum and gestate the new bulls. Proven bulls selected as sires of sons must then be equal in breeding value to the genetic change that has occurred since their own sires were selected, because this is the only pathway for genetic change. This point is demonstrated in Figure 1.

Further explanation of the diagram is needed. In yr 0, sires of sons are chosen and “mated” together more or less at random to produce young sires. In yr 2, these young bulls will be 1 yr old and will be sampled. Four years later, in yr 6, the bulls will obtain progeny tests. If genetic gain is to continue at a steady pace, sires of sons selected from this group must equal the genetic gain that has accumulated over the 6-yr. This graphical approach assumes overlapping generations but produces the same equation for genetic gain as that displayed in [1], which is based on discrete generations.

Steady-state rates of genetic change now are obtained by devising selection schemes and plugging appropriate parameters into equation [1]. Four schemes will be studied. The first approximates sampling now done by the AI industry. The remaining three consider much heavier use of young sires. A large population is assumed, such that total demand for semen is 17 million units. This is arbitrary but represents an amount that the active bulls currently kept by AI studs are capable of producing. The four schemes are outlined in Table 1.

For all schemes, 10 new bulls are chosen as sires of sons each year (60 bulls per generation). This holds inbreeding constant across methods. Genetic variance of the young bulls is reduced considerably from that of a randomly mated, unselected population, because intense selection is placed on parents (sires). Steady-state genetic variance is obtained by setting up parent-offspring recurrence relationships as in [2] and [3] and solving equations simultaneously for \(\sigma_{GO}^2\) and \(\sigma_{GP}^2\). Equation [2] results from the genetic merit of an offspring being the average of its two parents plus a Mendelian sampling effect with variance equal to \(.5\sigma_G^2\). Equation [3] is adapted from Dickerson and Hazel (1).

\[
\sigma_{GO}^2 = .25\sigma_{GP}^2 + .25\sigma_{GP}^2 + .5\sigma_G^2 \quad [2]
\]

\[
\sigma_{GP}^2 = [1 - r_{IH} \cdot i(1 - t)] \cdot \sigma_{GO}^2 \quad [3]
\]

where:

- \(\sigma_{GO}^2\) is genetic variance among offspring,
- \(\sigma_{GP}^2\) is genetic variance among the selected parents.
TABLE 1. Four schemes for meeting national semen needs.

<table>
<thead>
<tr>
<th>Scheme</th>
<th>No. YS</th>
<th>Units/YS</th>
<th>Total units</th>
<th>No. PS</th>
<th>Units/PS</th>
<th>Total units</th>
<th>Total units</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>YS semen</td>
<td></td>
<td>PS semen</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1,000</td>
<td>1,000</td>
<td>1</td>
<td>400</td>
<td>40,000</td>
<td>16</td>
<td>17</td>
</tr>
<tr>
<td>2</td>
<td>1,000</td>
<td>15,000</td>
<td>15</td>
<td>50</td>
<td>40,000</td>
<td>2</td>
<td>17</td>
</tr>
<tr>
<td>3</td>
<td>2,000</td>
<td>8,250</td>
<td>16.5</td>
<td>100</td>
<td>5,000</td>
<td>.5</td>
<td>17</td>
</tr>
<tr>
<td>4</td>
<td>5,000</td>
<td>3,360</td>
<td>16.8</td>
<td>100</td>
<td>2,000</td>
<td>.2</td>
<td>17</td>
</tr>
</tbody>
</table>

1YS = Young sires.

2In millions.

3PS = Proven sires.

\( \sigma_G^2 \) is random-mating, unselected genetic variance, and

\( t \) is the truncation point

Genetic variance among young sires \( (\sigma_{GO}^2) \) can be given in terms of \( \sigma_G^2 \) by [2] and [3] used to produce [4].

\[
\sigma_{GO}^2 = 0.5 \sigma_{GP}^2 = 0.5 \sigma_G^2
\]

\[
\sigma_{GO}^2[1 - 0.5(1 - r_{IH}^2)i(i - t)] = 0.5 \sigma_G^2
\]

\[
\sigma_{GO}^2 = 0.5 \sigma_G^2/[1 - 0.5(1 - r_{IH}^2)i(i - t)] \quad [4]
\]

Repeatabilities \( (r_{IH}^2) \) of eventual proofs of young bulls also will be affected by selection, because repeatability is the proportion of genetic variance or, rather, reduced genetic variance accounted for in the progeny test. In the absence of selection, if 1,000 units of semen are distributed for a bull, his repeatability 4 yr later would be 75% or .75. With reduced genetic variance equal to \( c_1 \sigma_G^2 \) or with more or less semen distributed given as \( c_2 \) times the original 1,000 units, adjusted repeatability is given in equation [5].

\[
r_{IH}^2 = c_1 c_2 / (c_1 c_2 + .75^-1 - 1) \quad [5]
\]

Derivation of [5], with \( R_O \) to represent original repeatability and \( R \) to represent adjusted repeatability \( (r_{IH}^2) \), is. The multiplier of residual variance \( (\sigma_E^2) \) that produces repeatability of \( R_O \) is introduced as \( c_0 \).

\[
R_O = \sigma_G^2 / (\sigma_G^2 + c_0 \sigma_E^2)
\]

\[
R = c_1 \sigma_G^2 / (c_1 \sigma_G^2 + c_0 \sigma_E^2) / c_2
\]

\[
R_O^{^-1} = 1 + c_0 \sigma_E^2 / \sigma_G^2
\]

\[
R = c_1 \sigma_G^2 / (c_1 \sigma_G^2 + c_0 \sigma_E^2) / c_2
\]

\[
R^{^-1} = 1 + (c_0 \sigma_E^2 / \sigma_G^2) / (c_1 c_2)
\]

\[
R = 1 / (1 + (R_O^{^-1} - 1) / (c_1 c_2))
\]

\[
R = c_1 c_2 / (c_1 c_2 + R_O^{^-1} - 1)
\]

Both \( r_{IH} \) and \( c_1 \) are needed to calculate steady-state genetic gain, and both are partial functions of each other. Equations [4] and [5] can be solved for both \( r_{IH} \) and \( c_1 \) as a set of simultaneous nonlinear equations by an iterative procedure. The procedure was simply to choose an initial value for one variable and then to alternate between the two equations until both \( r_{IH} \) and \( c_1 \) converged (failed to change from one iteration to the next). Then, by using these converged solutions, rate of genetic gain can be calculated from [6]. Equation [6] is a slight alteration of [1] to account for reduced genetic variance:

\[
\Delta G / y = i r_{IH} \sqrt{c_1 \sigma_G^2} / L \quad [6]
\]

Steady-state parameters for the four selection schemes outlined in Table 1 are now calculated from [4], [5], and [6]. Repeatabilities, genetic variances, intensities of selection for sires of sons, and rates of genetic gain are in Table 2.

 Reasons for choosing the four particular schemes of Table 1 are that, as stated previously, scheme 1 mimics the selection now practiced in...
TABLE 2. Steady-state parameters reached under the four different selection schemes.

<table>
<thead>
<tr>
<th>Scheme</th>
<th>Repeatability</th>
<th>Variance of young sires</th>
<th>Intensity</th>
<th>Genetic gain</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>.65</td>
<td>.63σ_G^2</td>
<td>2.67</td>
<td>.284σ_G</td>
</tr>
<tr>
<td>2</td>
<td>.96</td>
<td>.53σ_G^2</td>
<td>2.67</td>
<td>.317σ_G</td>
</tr>
<tr>
<td>3</td>
<td>.93</td>
<td>.53σ_G^2</td>
<td>2.89</td>
<td>.339σ_G</td>
</tr>
<tr>
<td>4</td>
<td>.85</td>
<td>.56σ_G^2</td>
<td>3.17</td>
<td>.365σ_G</td>
</tr>
</tbody>
</table>

1 Also referred to as σ^2_{GO} and c_rσ^2_G, reduced additive genetic variance.

2 Intensity of selection of sires of sons.

the United States except that all young sires would be androgenones. Scheme 1 could not be maintained long, because large quantities of proven sire semen could not be sold in the presence of these genetically superior young sires. A valid assumption might be that semen on proven sires could not be sold for bulls whose genetic merit was less than the average merit of young sire semen available.

From Figure 1, the truncation point for selling semen on proven sires can be deduced as the genetic change per year times 4. This is done by constructing another line on the graph to represent genetic change of young sires at the age of sampling, as in Figure 2. Where this line intersects the distribution of proven sires becomes the point of truncation for proven sires. With the rate of genetic change of scheme 1 (see Table 2), truncation would be at 4(.284) = 1.14σ_G. Expressed in terms of the standard deviation of sire evaluations (see Table 2), truncation would be at 1.14/√.65(.63) = 1.78. This would mean that only 3.8% of sires receiving proofs would be superior to available young sires and would be returned to service. One year later (5 yr after sampling), only 1.3% of proven sires would remain above the truncation point because of still better young sires becoming available.

Scheme 1 is then internally inconsistent because the market would be expected to demand more semen from young sires and less from proven sires. A correction of this problem is in scheme 2 simply by more units per young sire sold and number of proven sires limited to those surviving truncation just described.

Compared with scheme 1, selection intensity in scheme 2 is the same, accuracy of the progeny test is increased dramatically, and because of this increased accuracy, genetic variance declines. Net effect is faster genetic progress.

Although scheme 2 is an improvement, it is still internally inconsistent. With only a small proportion of semen coming from proven sires, economic incentives for keeping and feeding these bulls during the 4-yr waiting period are reduced greatly. A European-type sample-and-slaughter program would become attractive, with perhaps 5,000 units of semen per bull being saved instead of the bull. This would reduce costs per bull sampled and might lead to doubling number of sires sampled. These assumptions produce scheme 3.

Scheme 3 gives another small improvement in rate of genetic gain. Because faster gain seems to result from more young sires being sampled, the industry might proceed further in this direction. Scheme 4 increases the number

Figure 2. Determination of truncation for returning proven sires to active service. ΔG = genetic gain.
of young bulls to 5,000 and decreases units saved per bull to 2,000, producing another increase of genetic gain. Further increases of number of young sires result in smaller improvements and eventually in reductions of genetic gain. For instance, 10,000 young sires would give .373 $\sigma_G$/yr, but 50,000 young sires would reduce genetic gain to .347 $\sigma_G$/yr.

One assumption, which may not be valid, was that a substantial increase could be made in the proportion of the population bred to young sires without lowering the ratio of tested daughters to units of semen marketed from young sires. As proportion of semen from young sires rises, more daughters likely would be in herds not on test or in herds with poor identification systems. Table 3 is a repeat of Table 2, but Table 3 assumes that efficiency of sampling (tested daughters/units YS (young sire) semen marketed) is cut in half for schemes 2, 3, and 4. Genetic progress is affected only slightly by this assumption.

These arguments predict that, with inexpensive production of sons with only sires as parents, selection strategies in the United States eventually could approximate scheme 4. Such a scheme would have major consequences for the AI industry. Housing facilities for proven and in-waiting bulls would be needed no longer. The need for sire analysts to search for elite cows also would be eliminated. Corrective mating programs would have little semen from proven sires with which to work and might cease. All bulls could be "manufactured" in a lab right at the stud and carried to term in nearby recipients. This would minimize disease problems, eliminate transportation costs, and provide a more standard environment for raising young bulls. All these items would tend to bring down the cost of semen despite more rapid genetic progress.

Inbreeding Considerations

Rates of inbreeding and effects of inbreeding depression become concerns in schemes with high selection intensities. In the four schemes outlined, 60 bulls were chosen as sires of sons in each generation. If all sires of sons contribute equally to the next generation, $\Delta F$ (change of inbreeding coefficient) is given by $1/2N$ [(2), p. 59)], where N in this case is 60. Rate of inbreeding per year is then $1/[2(60)(6)]$ or .0014 and is within the range predicted from current strategies (7). Inbreeding depression per year, assuming a loss of .05$\sigma_G$/1%F (10), would be only .007$\sigma_G$/yr, offsetting just a small fraction of the genetic gain.

The technology of uniting two sperm together to form a zygote could be used to obtain intense inbreeding rapidly if this were desired. Bulls could be "selfed" much like corn plants, producing 50% inbreeding in one generation. Van Vleck (9) has discussed potential applications of this technology toward increasing the accuracy of evaluation. He concluded that these methods probably would not be economically attractive.

Selfing also could be used for producing more variance among new bulls. This additional

<table>
<thead>
<tr>
<th>Scheme</th>
<th>$r_{II}^2$</th>
<th>Variance of young sires $\sigma_G^2$</th>
<th>Intensity $\dot{G}$</th>
<th>Genetic gain $\Delta G$/yr</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>.65</td>
<td>.63$\sigma_G^2$</td>
<td>2.67</td>
<td>.284$\sigma_G$</td>
</tr>
<tr>
<td>2</td>
<td>.92</td>
<td>.54$\sigma_G^2$</td>
<td>2.67</td>
<td>.316$\sigma_G$</td>
</tr>
<tr>
<td>3</td>
<td>.87</td>
<td>.56$\sigma_G^2$</td>
<td>2.89</td>
<td>.335$\sigma_G$</td>
</tr>
<tr>
<td>4</td>
<td>.75</td>
<td>.59$\sigma_G^2$</td>
<td>3.17</td>
<td>.351$\sigma_G$</td>
</tr>
</tbody>
</table>

1 Half as many tested daughters are produced per unit of young sire semen in schemes 2, 3, and 4.
2 Also referred to as $\sigma_G^2$ and $c_1 \sigma_G^2$, reduced additive genetic variance.
3 Intensity of selection of sires of sons.
variance would result from introducing a perfect covariance between errors of prediction of the two parents when the two parents are the same sire. This increased variance, however, would be more than offset by the decreased variance of Mendelian sampling effects (variance between sperm within a bull) when the inbred bulls themselves are selected as parents. This fact, coupled with any loss of fertility resulting from inbreeding depression, would tend to discourage selfing.

Other Technologies

The analysis has not considered effects of potential competing technologies or the possibility that some females would be desired as gamete donors. These problems were dealt with as follows. First, the technique of cloning was examined and offered little advantage over the system just described if most genetic variance is additive. Second, ignoring cloning and ignoring the possibility of directly transferring desired genes, the remaining challenge was simply to choose the best source of gametes for producing new individuals. For low to moderately heritable traits, this best source might remain always the elite progeny-tested sires.

In a general sense, genetic progress occurs only through repeated application of two steps. These steps are: 1) identification of animals having the best genetic material, followed by 2) propagation of these genes or genotypes. If most of the genetic variance in a population is additive, cloning would not be an attractive method of propagation. It might be desirable to make exact copies of the best available animals, but it would be even more desirable to create animals having the same mean but with additional variance. Clones of elite bulls would be no worse but also no better than the best bulls currently available. Young bulls having elite sires as both parents would, on the average, equal the merit of these elite sires but would be dispersed about this mean to provide for further selection and genetic gain. If cloning is to have an impact, it would be more likely through identification of the best genetic material than through propagation of these genes.

Average genetic merit of dams of sons is not as high as that of sires of sons. This is simply because dams of sons are not evaluated as accurately as sires. Techniques such as embryo transfer or cloning might be used to increase accuracy of cow evaluation, but these techniques would be expensive, and the resulting evaluations likely would suffer from the same biases in single-herd bull proofs. Nicholas and Smith (7) outlined a scheme utilizing controlled production of clones consisting of 8 to 12 identical animals to evaluate quickly and accurately female genotypes. This scheme has the potential of delivering faster genetic gain because of the shorter generation interval. A practical drawback for schemes relying on accurate evaluation of females, though, is that it is much more difficult to achieve widespread propagation of the genes of superior females than of superior males once these are identified.

One group of females might be considered potential gamete donors. These would be the females with two sires as parents that are produced at the same time as and have the same mean as young sires. Females generally are evaluated earlier in life but with less accuracy than males. For parameters from scheme 4 and an original (before selection) heritability of .25, less than 1 out of 10,000 of these females would have evaluations as high as the average sire of sons. If no females were deemed superior to the best males available, females would not contribute gametes to young sires, and rate of genetic gain would not be influenced by any genetic activities or selection programs in the cow population.

CONCLUSIONS

An ability to create sons with only sires as parents would create substantial changes in the AI industry and lead to genetic gains 1.5 to 2 times the current gain based on current attainable rate between .18 and .220 G/yr. Genetic change is easy to evaluate in populations such as we propose because the pathway from sires to sons becomes the only one affecting rate of genetic gain. Reductions of genetic variance and accuracy of selection were accounted for in the analysis, and these effects were substantial. The analysis predicted that semen sales consisting of 99% young sire semen and 1% proven sire semen would be both genetically and economically ideal once production of sons with sires as both parents is available. Other technologies including cloning and any sort of selection program in females probably would
not be economically competitive with this strategy.

It is important to think about such technologies ahead of time. For instance, if this particular technology should become available in 1995, a sample-and-slaughter program should have been implemented in 1990, and capital expenditures for housing of old and in-waiting bulls should have been stopped even earlier.

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REFERENCES