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# TAKING BEEF CATTLE BREEDING INTO THE 21ST CENTURY

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**Summary**

Efficiency of beef production will be the major concern of beef breeders well into the twentyfirst century. The competition from other protein sources will provide the incentive for the beef industry to incorporate current breeding technology and the new emerging biotechnologies into commercial production systems. Considerable effort by the scientific community and expense to the industry will be encountered to make beef a competitive protein source. A number of technologies are developing to enhance beef production efficiency. The key to a successful twenty-first century beef industry will be the incorporation of current breeding technology and emerging biotechnology into a profit maximizing system of production.

Key words: Beef Cattle Breeding, Genetic Manipulation, Reproductive Biotechnology

## *Introduction*

The major area of concern when comparing beef production efficiency with other species is reproductive rate. Price of product is directly correlated with market-share and without efficiency improvements it is not likely that beef production can be profitable or sustainable. The twenty-first century will see the efficiency of beef production and the quality of product improved through a combination of currently available and newly emerging technologies.

## *Genetic resources*

The numerous breeds of *Bos taurus* and *Bos indicus* cattle found throughout the world have distinct advantages and, when comparing the two,

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the environment in which they are to function must be considered. The composites developed from these breeds should have a wider range of adaptability; however, research is not available to conclusively demonstrate the versatility of composites across environments.

Cundiff et al. (1993) and Marshall (1995) have summarized breed comparisons for a large number of breeds in temperate environments. There is a general lack of information concerning functionality comparisons of breeds in most other areas of the world.

*Genetic manipulation*

A number of technologies, which include conventional cattle breeding techniques and biotechnologies, are currently under rapid development.

***National/International Cattle Evaluation (NCE, ICE).*** Within breed and across herd beef cattle genetic evaluation procedures based on mixed model best linear unbiased prediction of additive genetic value (breeding value) techniques originally described by Henderson (1973) are generally established (Benyshek et al., 1988; Benyshek et al., 1994). A multiple trait animal model has become the model of choice for National Cattle Evaluation (NCE) programs throughout the world, with some variation in effects included in and parameters used with the model (Henderson and Quaas, 1976, Quaas and Pollak, 1980, Pollak and Quaas, 1983). These programs have the advantage of utilizing all available recorded information on large numbers of animals including the animal's own performance, its ancestors, and progeny. For the method to be most useful some sires must be used across herds, which requires mating approximately 10% of the breed through artificial insemination. Hough et al. (1985) and Benyshek et al. (1988) indicate that genetic change for yearling weight can occur, using intense selection based on NCE results, at more than twice the rate compared to selection based on information generated within herd.

International beef cattle genetic evaluation became a reality for the U.S. and Canada in 1995 when the American Hereford and the Canadian Hereford Associations published a North American Hereford Genetic Evaluation resulting from a joint analysis of data pooled from both countries. Other breeds are following with joint analyses, and research is being conducted to include data from South America in the North American Hereford analysis.

*Including Dominance and Epistatic Effects in Genetic Evaluation Models.* Considerable research effort has been expended to improve additive genetic value or breeding value prediction models over the last 25 years. One recent development is the inclusion of nonadditive effects in the prediction model

(Misztal et al., 1995). The nonadditive effect of dominance occurs because of the interaction of two alleles at the same locus and epistasis occurs because of interaction between loci. In addition to increasing the accuracy of breeding value prediction, the inclusion of nonadditive effects provides the opportunity to set up mating systems to take advantage of these effects. The issue of across breed genetic evaluations and predicting hybrid vigor will be solved by expanding the genetic prediction models.

*Genetic Selection Using A Quantitative Bioeconomical Model.* If it is assumed that a commercial beef producer is motivated by profit (Melton, 1995), it is possible to describe and quantify the role of genetics in beef production. Melton (1995) states that genetics can affect a producer's profit by affecting (1) quantity of product, (2) cost incurred in production and, (3) the quality of the product and thus, its price. Economic theory indicates that the first two effects are the same, thus if the cost of producing a given product with a particular market or sales price declines, the profit maximizing producer will increase the quantity of that product. Therefore, genetic changes can be thought of in terms of their profit effects on beef quantity and quality. Specific genetic trait economic value is then defined as the sum of these effects on profit arising from an incremental increase in the level of the trait which was originally stated by Hazel (1943).

In a bioeconomical analysis it becomes clear that producers have different levels of resources that distinguish a specific operation from all others. In addition, producers face different prices for both inputs and products, particularly if they market differently, and both prices and resource levels change over time. As Melton (1995) states, the economic value of a genetic trait is not a global constant. Economic values are individualized and apply to a specific producer, the resources or inputs that define that production operation, and the prices faced by that producer at a particular point in time. Economic values may not be appropriate for the aggregate industry since a broad-based genetic change may increase the quantity of beef on the market, ultimately reducing the price of beef. Newman and Melton (1995) discuss the implications of the derivation of economic values for selection indexes. The equation for estimating economic values is most appropriate for short-term genetic changes; however, genetic changes may be complex over time and the economic values may need to be adjusted accordingly for the time that transpires between the selection decision and the actual expression of the characteristic.

***DNA Marker Assisted Selection (MAS).*** Bishop et al. (1995) provides an excellent discussion of the development and use of DNA markers in animal selection. An integrated linkage and physical map totaling several hundred

microsatellite (MS) and restriction fragment length polymorphisms (RFLP) type markers is being developed for each chromosome of the bovine genome. The use of these markers combined with reproductive advancements such as prepubertal oocyte and sperm recovery, IVM (in vitro maturation)-IVF (in vitro fertilization), intracytoplasmic sperm injection, and propagation of embryonic stem (ES) cells offer the promise of tremendous genetic improvement through increased intensity and accuracy of selection and reduction in the generation interval.

MAS implementation is dependent on the systematic dissection of the factors affecting traits of economic importance through genome analysis. Mammals have two genome copies in each nucleus of the individual's somatic cells, one copy from each parent. Obviously, a map detailing the inheritance of genes or markers greatly facilitates genomic dissection and discovery of chromosomal regions affecting a certain trait. Resource families of animals which are segregating interesting traits are required for identifying either the genes causing them (quantitative trait loci, QTLs) where more than one gene may be affecting the characteristic or markers which flank the QTL for use in informative mating schemes. The resulting data can be compiled for the dissected genomes into what is referred to as a "linkage map". This map is constructed from information obtained from analyzing the meiotic linkage relationships of polymorphic loci along a chromosome. The distance between adjacent loci is a function of the frequency of meiotic crossovers that are counted as recombination events between alleles at two adjacent loci. Recombination frequencies determined from analysis of the inheritance of alleles at adjacent loci in large pedigreed families, half or full-sibs. Thus if the recombination frequency is smaller than 0.5, and if the assumption of random segregation at the two loci is correct, it can be concluded that the two loci are linked and on the same chromosome. Statistical techniques are available to help determine whether the hypothesis of linkage can be accepted or rejected. In order to develop a linkage map, polymorphic loci (loci with several alleles segregating in a population) must be identified. Initially, RFLPs were used as markers for this type of map (Botstein et al., 1980). This process was found to be extremely slow and labor intensive for the bovine genome. In human genome work (Weber and May, 1989) hypervariable islands of variable numbers of tandem repeats (VNTRs) known as microsatellites (MS) were discovered embedded in the DNA sequence. MS were found to be highly abundant and variable in size, segregating several alleles at a locus in a population, inherited in a Mendelian fashion and randomly distributed across the chromosomes in several mammalian species. When coupled with the polymerase chain reaction (PCR) technique (Saiki et al., 1985; Saiki et al, 1988) and site specific flanking DNA primer pairs, an excellent genotyping system was developed for rapid construction of linkage maps for any species

using DNA from reference family pedigrees designed to maximize heterozygosity and the number of meiotic events at each loci for estimation of recombination frequencies.

Barendse et al. (1994) and Bishop et al. (1994) have published bovine genetic linkage maps. For cattle, nearly all of the chromosomes have been anchored by polymorphic genes or DNA segments containing MS to the physical and linkage maps (Bishop et al., 1995). These maps are useful for interspecies comparison and to identify "candidate" genes affecting economic traits or for selecting markers for testing in other populations where either desirable or undesirable traits are segregating.

Taylor et al. (1995) describes work at Texas A&M University which is designed to find QTLs for economic traits, particularly those affecting carcass merit. The study uses a resource population involving Angus, Brahman and their crosses. Although the results are interim and unpublished in the scientific literature, evidence is mounting in the project to support the localization of QTLs having, in some cases, sizable effects on quality grade, marbling, Warner-Bratzler shear force, slaughter weight and hot carcass weight, kidney-pelvic-heart fat, dressing percent, cholesterol and amount of saturated and unsaturated fatty acids within the Longissimus dorsi muscle. Work of a similar nature is underway at the U.S. Meat Animal Research Center, Clay Center, NE.

If economical methods of fine mapping procedures leading to universal testing procedures are not discovered, it is likely that this technology will have to be coupled with developing advances in reproductive biology to have major impact in beef cattle (Bishop et al., 1994). This will enhance the introduction of QTLs into different family lines (introgression) and will involve embryo transfer, IVF and IVM and perhaps transgenesis.

*Combining Statistical Quantitative Genetic Evaluation and DNA Marker Assisted Selection.* Much of the practical application of bovine genome mapping will be to enhance traits that are not readily measurable on the live animal, such as carcass traits and characteristics associated with reproductive efficiency. However, as the resolution of the map improves there will be a number of markers identified that will be associated with general production characteristics, such as weaning weight, for which accurate statistical breeding values are currently available. It has been shown that DNA markers can be combined with mixed model best linear unbiased prediction procedures (the latter using objective measurement records) to enhance the accuracy of predicted additive genetic values (Fernando and Grossman, 1989).

***Transgenic Animal Modeling.*** Transgenic animals are the result of either integrating foreign DNA segments into their genome following gene transfer or from the molecular manipulation of endogenous genomic DNA (Pinkert et al., 1995). Transgenic animals, from a molecular biology research perspective, represent unique models that can be actually custom-tailored to answer specific biological questions. This is another ultimate technology, which allows a true genetic engineering of plants and animals by introducing genetic material from outside the animal's genome or altering the existing genetic material in its genome.

Pinkert et al. (1995) discusses a number of methods for gene transfer in mammalian species including DNA microinjection, embryonic stem (ES) cell transfer, retroviral infection, blastomere-embryo aggregation, teratocarcinoma cell transfer, electrofusion, nuclear transplantation, and spermatozoa-mediated transfer.

Eyestone (1994) discusses the unique challenges encountered in the production of transgenic cattle. Survival of microinjected zygotes is low with only 15% of in vivo-derived zygotes developing into morulae and blastocysts; of these, about 18% result in live calves. The integration of transgenes is low at around 3%. Therefore, more than 1000 zygotes must be injected to produce one transgenic calf. Simply obtaining sufficient zygotes for donor cattle to sustain a transgenic cattle program would be, at this time, a logistical nightmare and a financial impossibility. In vitro oocyte maturation and fertilization techniques could be used to alleviate some of the problem; however, in vitro-derived microinjected zygotes are even less viable than those derived in vivo. Although current technology appears to prohibit transgenic programs in cattle, it is important to note that significant breakthroughs are occurring in mice such as the use of embryonic stem cells, which have led to more efficient programs.

*Emerging and developing reproductive biotechnologies*

Seidel (1995) provides a summary of reproductive biotechnologies that have emerged and are presently at varying levels of development and application. Some of these technologies, such as artificial insemination and estrus synchronization are clearly having significant impact in the beef cattle industry, world-wide (Seidel, 1995). These two techniques are relatively simple and inexpensive to use. Artificial insemination and estrus synchronization coupled with NCE/ICE provide an extremely powerful force for genetic change in beef cattle.

***Superovulation, Embryo Cryopreservation and Transfer.*** Seidel (1995) indicates that embryo recovery and transfer result in 40 to 50 thousand beef calves each year in the U.S. and Canada. Research to date has not led to improved superovulation procedures which might more adequately tap the potential of the beef female. Cryopreservation of embryos can help deal with the variability of superovulation and the subsequent cost of maintaining a large nonpregnant recipient population.

***In Vitro Fertilization (IVF).*** Calves are produced annually from this technology, which removes oocytes from the ovary via a technique called transvaginal ultrasound-guided oocyte aspiration (Seidel, 1995). Hasler et al. (1995) provides insight into the production, freezing and transfer of bovine IVF beef embryos.

***Sexing Embryos.*** Seidel (1995) points out that the only way of sexing embryos commercially is to biopsy the embryo and analyze the DNA from a few cells for the presence of the Y chromosome using molecular techniques (Bondioli et al., 1989; Hen and Reed, 1991; Thibier and Nibart, 1995). The key to the usefulness of this technique is a rapid non-invasive and inexpensive procedure.

***Sexing of Sperm.*** Johnson et al. (1994) has shown it is possible to sort sperm with 90% accuracy using flow cytometry. This technology could add considerable efficiency to beef production.

***Bisection of Embryos.*** The procedure provides identical twins and is relatively easy to use although it requires time (Seidel, 1995). Economical sexing of semen and/or cloning by nuclear transplantation would make this technology obsolete.

***Nuclear Transplantation Cloning of Embryos.*** Willadsen (1986) provided the basis for procedures to clone cattle by nuclear transplantation. The current procedure (Seidel, 1995) is to microsurgically remove the chromosomes from in vitro-matured oocytes and then fuse individual cells of morula-stage embryos to these oocytes by electrical pulses (Westhusin et al., 1992). Rates of failure are large because of the high proportion of phenotypically abnormal calves resulting in large percentage of neonatal mortality. It appears likely that some of the problems with abnormal calves from nuclear transplantation can be solved by modifying the media used for the process (Seidel, 1995) as has been shown in sheep (Thompson et al., 1994). This technology can be combined with other technologies such as transgenesis and cryopreservation.

***Cloning of Individuals via Nuclear Transfer.*** While cloning of embryos by nuclear transplantation has received considerable attention, cloning of a sheep using DNA from mammary tissue has produced an individual genetically identical to the donor (Wilmut et al., 1997). The process has received much attention because of the implications for humans; however, the process is a major breakthrough for farm animal breeding if the efficacy can be improved. Wilmut (1996) discusses the usefulness of nuclear transfer in livestock. Nuclear transfer requires an unfertilized egg and a donor cell, with the difference between embryo cloning and cloning of individuals being the source of the donor cell. In the latter the donor cell will come from differentiated tissue, mammary tissue in the case of the cloned sheep described by Wilmut et at., (1997). When the DNA from a differentiated cell is used in nuclear transfer, the precise series of changes in the pattern of gene expression, progressive differentiation must be reversed by a process of "reprogramming" (Wilmut, 1996). The early work and the currently reported work (Wilmut et al., 1997) required considerable resources because of a high failure rate.

Time is the archenemy of beef cattle breeders because it takes years to disseminate superior genotypes. Cloning of elite individuals could speed up dissemination tremendously and move the breeding population average performance closer to the best individuals of the population (Wilmut, 1996). In addition, gene targeting in livestock should become more feasible by nuclear transfer from modified cell populations (Wilmut et al., 1997).

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## S UZGOJEM MESNOG GOVEDA U 21. STOLJEĆE

**Sažetak**

Djelotvornost proizvodnje govedine bit će glavna briga uzgajača goveda dobrano u 21. stoljeće. Takmičenje s drugim izvorima bjelančevina bit će poticaj mesnoj industriji da uvede modernu uzgojnu tehnologiju i novonastale biotehnologije u sustave komercijalne proizvodnje. Znanstvenici će uložiti znatan trud a industrija sredstva da bi govedina postala konkurentan izvor bjelančevina. Razvijaju se brojne tehnologije za povećanje djelotvornosti proizvodnje govedine. Ključ za uspješnu industriju govedine u 21. stoljeću bit će spajanje sadašnje uzgojne tehnologije i nove biotehnologije u sustav proizvodnje koja uvećava dobit do skrajnosti.

Ključne riječi: uzgoj mesnog goveda, genetska manipulacija, reproduktivna biotehnologija.

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