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Evolution of Genetic Improvement Practices in Domestic Animal Populations

M. A. Elzo

Department of Animal Sciences
University of Florida

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M. A. Elzo

Department of Animal Sciences, University of Florida, Gainesville 32611

Introduction

Procedures of genetic evaluation of domestic animals for economically important traits experienced significant changes during the past half a century. These changes will accelerate in the future as a consequence of the emergence of new quantitative genetic tools currently being developed. These new quantitative genetic tools rely on biotechnologies developed from joint research and development efforts in areas as diverse as physical sciences, engineering, material sciences, computer sciences, physiology, molecular genetics, genomics, functional genomics, robotics, and nanotechnology.

The development of collaborations among researchers from a wide range of scientific areas has opened the door for new and innovative solutions to current research problems, and dramatically reduced the length of time between research results and the development of applications in the field. These collaborations have occurred within universities, within private companies, and across universities and private research institutions. Substantial private industry support has probably been the major force behind this trend. Universities have become active participants in research-for-profit endeavors, a trend that is likely to continue and expand in the future.

All these biotechnological developments have had a comparatively small effect on the genetic improvement of domestic animals. Most of its impact, and current funding, have so far been aimed at solving problems related to human beings. However, many research results and techniques developed for humans as well as animal models for human research, are directly applicable to domestic animals. Thus, their impact on animal genetic improvement is likely increase in the future.

The objectives of this discussion are: 1) to characterize in general terms the problem of genetic evaluation of domestic animals, 2) to explain the main characteristics of genetic evaluation procedures used in the recent past, 3) to describe the main aspects of current genetic evaluation procedures, 4) to forecast future developments in genetic evaluation and mating procedures, 5) to analyze the factors contributing to the development of new genetic improvement procedures, 6) to envision potential roles of universities, government institutions, and private industry in future genetic improvement systems, and 7) comment on the impact of globalization on research and development of new genetic improvement procedures and mating systems.

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[1] Invited Presentation, Kasetsart University, Bangkok, Thailand, September 12, 2002.

Characterization of Genetic Evaluation of Domestic Animals

The problem of quantitative genetic evaluation of domestic animals can be organized in the following steps: 1) definition of the population, 2) identification of a set of economically important traits, 3) identification of a set of relevant genetic and environmental effects for each trait, 4) development of a dynamic system for data collection, maintenance, and editing, 5) development of genetic-statistical models for genetic evaluation and estimation of genetic and environmental parameters, 6) development of flexible computing algorithms to obtain estimates of genetic parameters and predictions of genetic effects, 7) use of genetic predictions to select future parents in the population, and 8) development of appropriate within subpopulation and across subpopulation mating strategies.

Definition of the population. The population can be either simple (e.g., a single breed) or complex (e.g., a population composed of various breeds and any number of their crossbred groups). A simple population will be Holstein (unibreed population) and a complex population will be a population composed of Holstein, Brahman, and their crossbreds (multibreed population). In most cases the population will be a mixture of "purebred" and "crossbred" animals, and a decision on whether to analyze this population using a unibreed or a multibreed strategy will need to be made. This decision will depend on amount and distribution of data and on hardware-software capability. In addition, a justifiable set of assumptions will likely need to be imposed.

Identification of a set of economically important traits. Traits of economic interest are biologically complex and usually assumed to be determined by a large number of alleles each having a very small effect. The type of information collected on economically important traits in beef cattle (weights at various ages) and in dairy cattle (milk yield, fat percent, protein percent) has changed little over the last thirty years. Reproduction traits have also been considered to some extent in cattle, but not nearly as much as in multiparous species such as swine.

In recent years interest has increased in defining traits in a more production oriented fashion (e.g., actual weaning weight as opposed to 205-day adjusted weaning weight, actual heifer pregnancy instead of scrotal circumference). Production oriented traits are certainly more economically relevant to producers than classical prediction traits. However, they are usually the result of a larger number of genetic and environmental factors, which may render their genetic predictions less accurate than those of classical prediction traits.

Identification of a set of relevant genetic and environmental effects for each trait. In most cases, this has amounted to defining additive genetic effects for an animal and its ancestors, permanent and transitory environmental effects, and group genetic and environmental effects. A few experimental and field data analyses have accounted for nonadditive genetic effects. Generally speaking genetic and environmental effects could be classified as additive, nonadditive, direct, maternal, intrabreed, and interbreed. More complex classifications can be devised. In particular, with the advent of functional genomics, the usual economically important traits (weights, yields) could be separated into interrelated biochemical traits (each due to one or more pathways), the internal environment of the body of an animal could potentially be subdivided into several environmental regions, which would complicate potential genetic analyses even further.

Development of a dynamic system for data collection, maintenance, and editing. Data needs to be collected not only for traits of current economic interest and their corresponding genetic and environmental effects, but also for traits and effects that might be used for genetic evaluation in the future. The date (and time of day as needed) must be entered together with the trait and effect information in the database. The system used for data maintenance must be flexible and easily adaptable to future changes and improvements in the system. A system of crosschecking of data must be implemented to maximize the accuracy of the information entered in the database. Information on individual animals should be easily retrieved and reports readily created. Thus, it is of paramount importance that a good database program be chosen to maintain such datasets, particularly for large national databases.

Development of genetic-statistical models for genetic evaluation and estimation of genetic and environmental parameters. The form of genetic-statistical models depends on the type of population (unibreed, multibreed) and the type of trait (continuous, categorical). Both linear and nonlinear models have been implemented in national genetic evaluation systems. The vast majority of them has been linear, and have only accounted for additive genetic effects. Nonlinear models are currently used only for some categorical traits (e.g., calving ease). Rapid changes in computer speed and memory capabilities made multitrait linear models the models of choice for national genetic evaluations, and they are still the most prevalent type of model used for national genetic evaluation in the world today.

The vast majority of national genetic evaluation models still assume a single population, and a common set of genetic and environmental parameters, even though in many instances the population being analyzed is composed of several known subpopulations with potentially different means and variances (e.g., several breeds and crossbred groups, several subpopulations of a single breed as for Holstein). Multibreed models have been used to compute genetic covariances and to predict genetic values for straightbred and crossbred animals in several small beef (Colombia, USA) and dairy cattle multibreed populations (Thailand). The only national multibreed model currently in place in the USA is the one for the Simmental-Simbrah-Canadian Simmental multibreed population.

Development of flexible computing algorithms to obtain estimates of genetic parameters and predictions of genetic effects. Computing algorithms are chosen based on the type of population (unibreed, multibreed), the type and number of traits (continuous, categorical), the size of the population (small, large), and the density of the generated set of equations to be solved (dense, sparse). Computing algorithms used in genetic evaluations can be broadly classified into two types: direct and iterative. Most national genetic evaluation systems have traditionally been programmed using iterative systems, and have frequently used a variety of transformations to improve computational efficiency. Direct computational systems have usually been used to obtain predictions of genetic values and to estimate variance components using restricted maximum likelihood procedures in small data sets. The spectacular increase in microcomputer speed and memory capabilities in recent years have made direct computing algorithms that use sparse matrix procedures a feasible alternative to iterative procedures for solving large sets of equations. In addition, advances in computer languages (e.g., FORTRAN 95) have enormously facilitated the creation of software that emphasizes modularity, making computer programs more general, flexible, and easily modifiable to accommodate future changes in model and computational strategies.

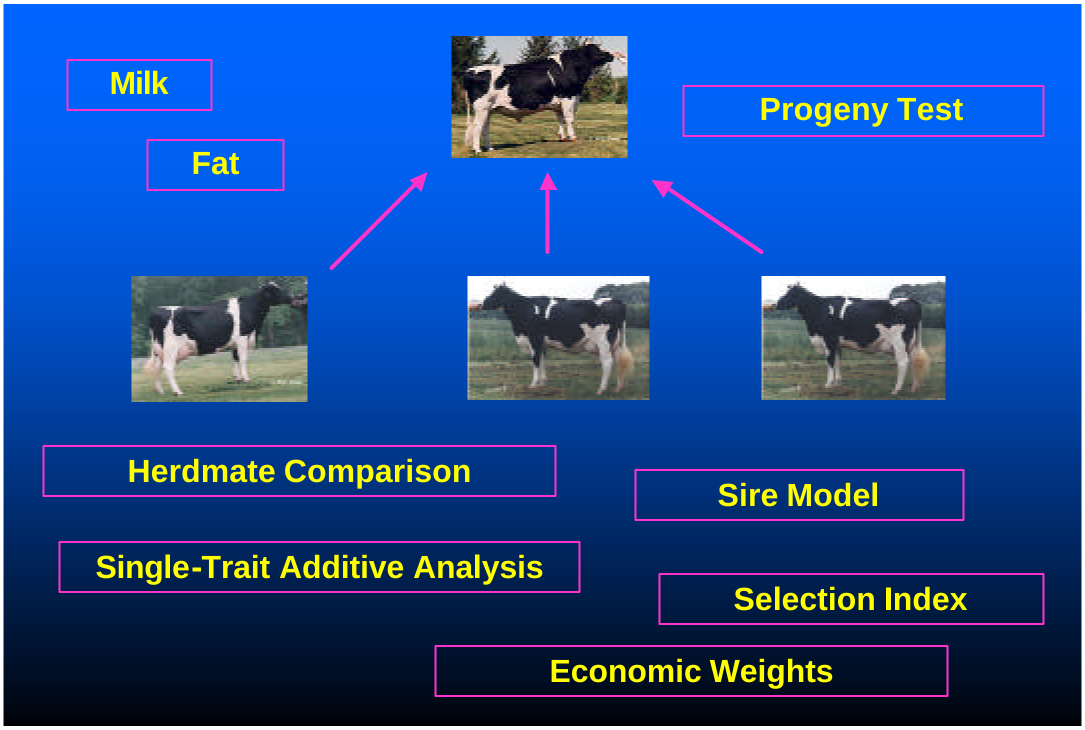
Use of genetic predictions to select future parents in the population. Genetic predictions have been used somewhat differently in beef and in dairy cattle. Indexes have been supplied in dairy cattle sire summaries for decades, in addition to predicted genetic differences. Contrarily, beef cattle summaries have traditionally published only genetic predictions. This is one aspect that needs to be revised in beef cattle evaluation. An indication that this may change is the recent interest in redefining traits of economic importance in beef cattle, and making them more similar to commercial production traits. There is ample evidence that modern genetic predictions have been successfully used in dairy and in beef cattle to significantly change their respective populations over time. In dairy cattle the enormous genetic progress in milk yield is well known. In beef cattle, changes in calving ease and yearling weight have been remarkable over the last fifteen years.

Development of appropriate within subpopulation and across subpopulation mating strategies. Nowadays most mating strategies in beef cattle in the USA and across the world involve some form of crossbreeding. In dairy cattle however, the tremendous advantage of Holstein in milk production has determined a unibreed mating strategy in the USA, and an upgrading mating strategy in the rest of the world. In many tropical and subtropical regions of the world, however, a complete upgrading to Holstein has been found to be in many instances environmentally unfeasible and(or) economically disadvantageous. Thus, the upgrading process has frequently been stopped at somewhere between 62% and 87% Holstein. Thus, the mating scheme applied to a particular population will primarily depend on its feasibility under local environmental conditions and on its net economic advantage over competing mating systems.

Historical Genetic Animal Evaluation Procedures

Genetic evaluation procedures for large unbalanced data sets have traditionally been a compromise between accuracy of prediction of the genetic-statistical models of the time and computational feasibility.

National genetic evaluation procedures until the 1960s were based on Best Linear Prediction (BLP) principles, and considered only additive genetic effects. This type of systems was used in both beef and dairy cattle as well as in other species of domestic animals such as swine and sheep. The last implementation of such systems in dairy cattle was probably the herdmate comparison. The main objective of BLP systems was the prediction of sire genetic values based on data collected on their female progeny (**Figure 1**).



Milk

Fat

Progeny Test

Herdmate Comparison

Sire Model

Single-Trait Additive Analysis

Selection Index

Economic Weights

Figure 1. Historical dairy cattle sire genetic evaluation strategies

Typical traits of economic interest were milk yield, fat percentage, and protein percentage. Analyses were usually single trait. Records were “corrected” for fixed environmental effects, and the resulting residuals were weighted by a BLP regression factor. Selection indices were constructed using actual or relative economic weights.

National beef genetic evaluation followed a BLP strategy similar to the one used in dairy cattle. Their system was called contemporary comparison. It was based on in-farm data collection of weights (birth, weaning, yearling). The objective was to obtain predictions of sire transmitting abilities for various weight traits (usually birth weight, weaning weight, and yearling weight).

Subsequently, some dairy cattle systems changed their genetic evaluation procedures from BLP-based to BLUP-based. The first generation of BLUP genetic evaluation systems considered only sires as random effects in the model (hence the name sire models). Subsequently, maternal grandsires were added to the model to account for differences in the genetic values of dams (sire-maternal grandsire models). The main objective continued to be the genetic evaluation of sires. Genetic predictions for dams were computed using linear combinations of male relatives with BLUP predictions. This procedure was similar to the one used during the BLP era.

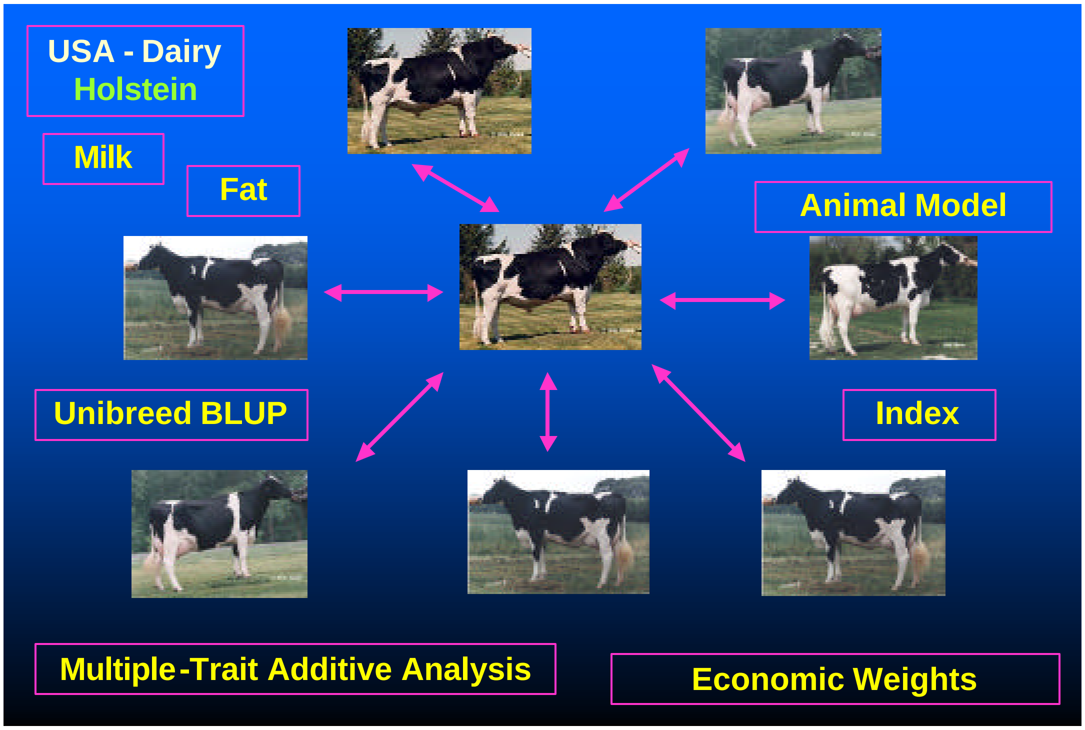
In short, during this period genetic evaluation systems analyzed single traits, utilized limited information from relatives, and were severely restricted by computational resources.

Current Genetic Animal Evaluation Procedures

Progress in national genetic evaluation programs over the last 20 years has been the result of improvements in a number of areas: 1) a tremendous increase in the volume of data available for genetic evaluation, 2) advances in data storage and management, 3) new and(or) improved statistical methodologies (linear, nonlinear, bayesian, multibreed), 4) more complete (and complex) statistical-genetic models, 5) improvement in computational strategies (sparse direct, iterative), 6) large increases in processing speed, memory capability, and affordability of workstations and microcomputers, and 7) increased availability of software packages for genetic prediction and estimation of genetic parameters.

Traits of economic importance have changed little from the BLP period. Much larger numbers of recorded animals, use of additive relationships among individuals, and simultaneous evaluation of multiple traits have substantially improved the accuracy of prediction of genetic values. Increased accuracy of prediction has permitted the identification of large numbers of genetically superior sires that, with the help of artificial insemination, have generated large numbers of superior progeny. Consequently, steeper genetic trends for economically important traits have been observed in both beef and dairy cattle populations. Current sire summaries publish not only genetic predictions for a large number of traits, but also tables of percentiles to help locate the precise ranking of an animal in the population, and graphs depicting genetic trends for many of the evaluated traits. Dairy cattle summaries continue to produce economic indexes. Beef cattle summaries still do not. However, this may change in the near future given the current interest in production-type traits.

The following set of figures is provided to give a pictorial version of current forms of genetic evaluation systems and their associated mating programs. **Figure 2** shows schematically the structure of a national genetic evaluation for the Holstein breed in the USA. The superiority of the Holstein breed for milk yield has persuaded producers in most countries to attempt to upgrade their dairy breeds to Holstein. The genetic evaluation procedure for this breed in the USA and elsewhere is unibreed, multitrait, and uses an animal model. The usual production traits evaluated are milk yield, fat percentage (or yield), and protein percentage (or yield). In addition, in recent years, genetic predictions for a large number of type traits have been published. Economic indexes of net merit are published. The latest manifestation of the dairy animal model is the test-day model that uses random regression to predict milk production traits at any



USA - Dairy
Holstein

Milk

Fat

Animal Model

Unibreed BLUP

Index

Multiple-Trait Additive Analysis

Economic Weights

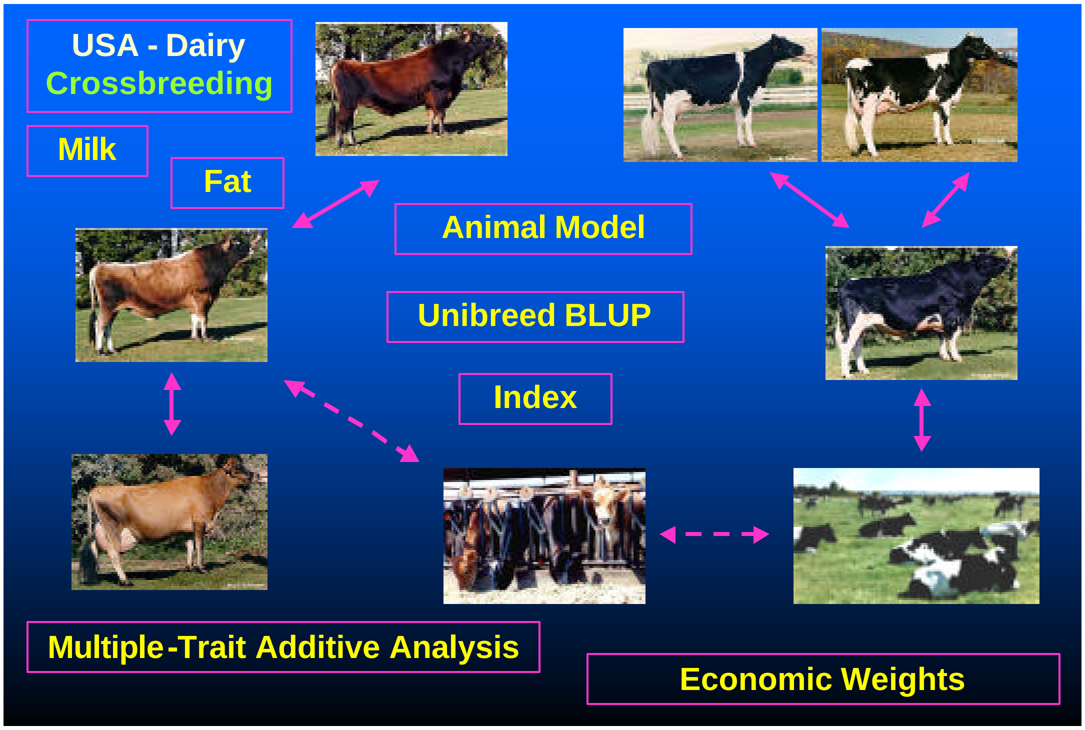
Figure 2. Current dairy cattle genetic evaluation strategy in the USA.

stage of lactation. Lastly, markers for quantitative trait loci have began to be used as part of the genetic evaluation systems in some countries.

Crossbreeding is rarely used for dairy cattle in the USA. Some dairy cattle producers use Jersey sires on Holstein heifers as a means of avoiding calving difficulties (**Figure 3**). These producers frequently maintain two separate herds: one with straightbred Holstein, and another with Jersey and Jersey x Holstein crossbreds. It also appears that some crossbreeding with Brown Swiss and Jersey is being done to counteract losses in milk production and to decrease calf losses due to inbreeding depression in Holstein.

All dairy breeds in the USA (Brown Swiss, Jersey, and Holstein) conduct separate genetic evaluation using only straightbred information. This is not the case however, in countries involved in upgrading to Holstein, where information from straightbred Holstein, straightbred data from the local breed, and crossbred data from animals of various Holstein fractions is frequently used as input for their genetic evaluation systems. Genetic evaluation systems in these countries either ignore the breed composition of crossbred animals and treat them as part of the "population being evaluated" or incorporate breed composition into their genetic grouping strategy. Two countries exemplifying this situation are Chile (temperate climate), and Thailand (tropical and subtropical climate).

Chile has imported Holstein semen from USA, Canada, Great Britain, and New Zealand over the last 20 years. The local breed was European Friesian. Sires from all these



USA - Dairy Crossbreeding

Milk

Fat

Animal Model

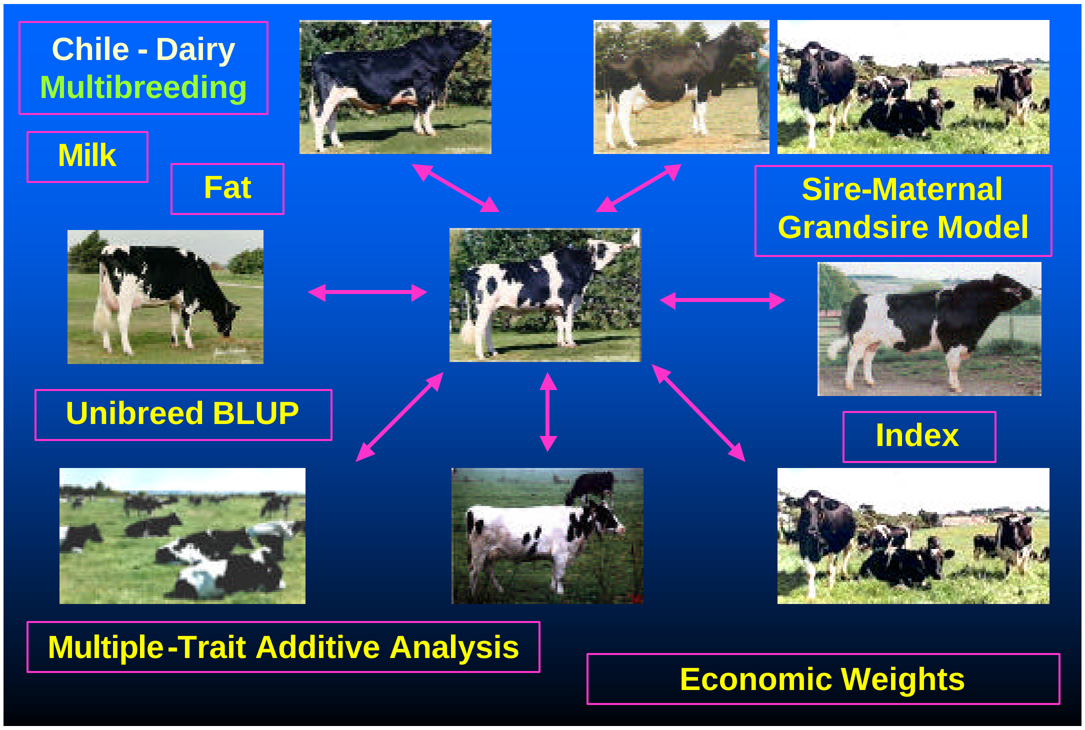
Unibreed BLUP

Index

Multiple-Trait Additive Analysis

Economic Weights

Figure 3. Current dairy cattle crossbreeding practices in the USA.



Chile - Dairy Multibreeding

Milk

Fat

Sire-Maternal Grandsire Model

Unibreed BLUP

Index

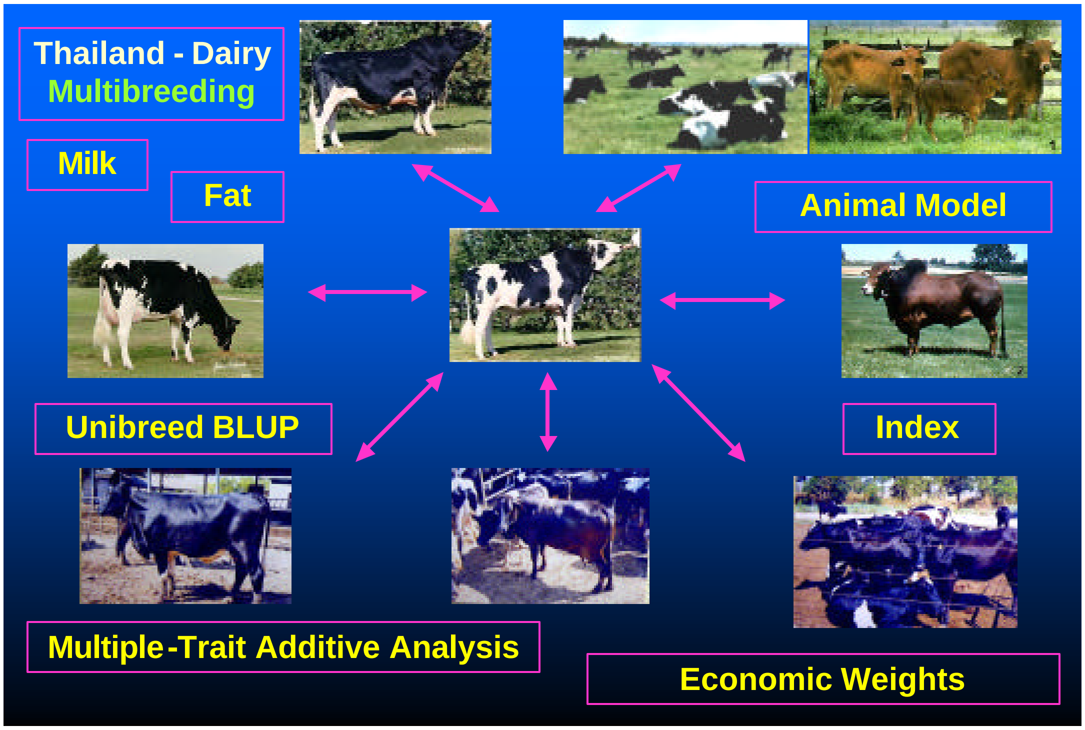
Multiple-Trait Additive Analysis

Economic Weights

Figure 4. Current dairy cattle genetic evaluation strategy in Chile.

countries were used to upgrade the local population. Crossbred sires of various Holstein fractions (.25, .50, .75) were also used a parents (**Figure 4**). The Chilean national genetic evaluation system currently evaluates milk yield and fat percentage using a single-trait sire-maternal grandsire model. It assumes a single population with a single set of genetic parameters. A sizable and well-kept recording system is in place. This recording system should facilitate the migration to a more current genetic evaluation system.

The situation in Thailand is far more complex. Holstein males and females as well as Holstein semen has been introduced into the country. In addition, a variety of other breeds of *Bos indicus* origin (e.g., Red Sindhi, Sahiwal) and *Bos taurus* (e.g., Jersey, Red Dane) have also been introduced. The Thai native breed of cattle is *Bos indicus*. The Thai native breed has been mated to all these breeds. The resulting crossbreds, in turn, have been mated to animals of a third or a fourth breed, as well as used in crossbred x crossbred matings. This has created a complex multibreed population with animals that have alleles of up to seven breeds. The current genetic evaluation system uses a unibreed animal model, it groups animals according to their Holstein fraction, and it evaluates animals for milk yield and fat yield separately. A single set of genetic parameters is used for all breed groups (**Figure 5**). The database system is currently being revised.



Thailand - Dairy Multibreeding

Milk

Fat

Animal Model

Unibreed BLUP

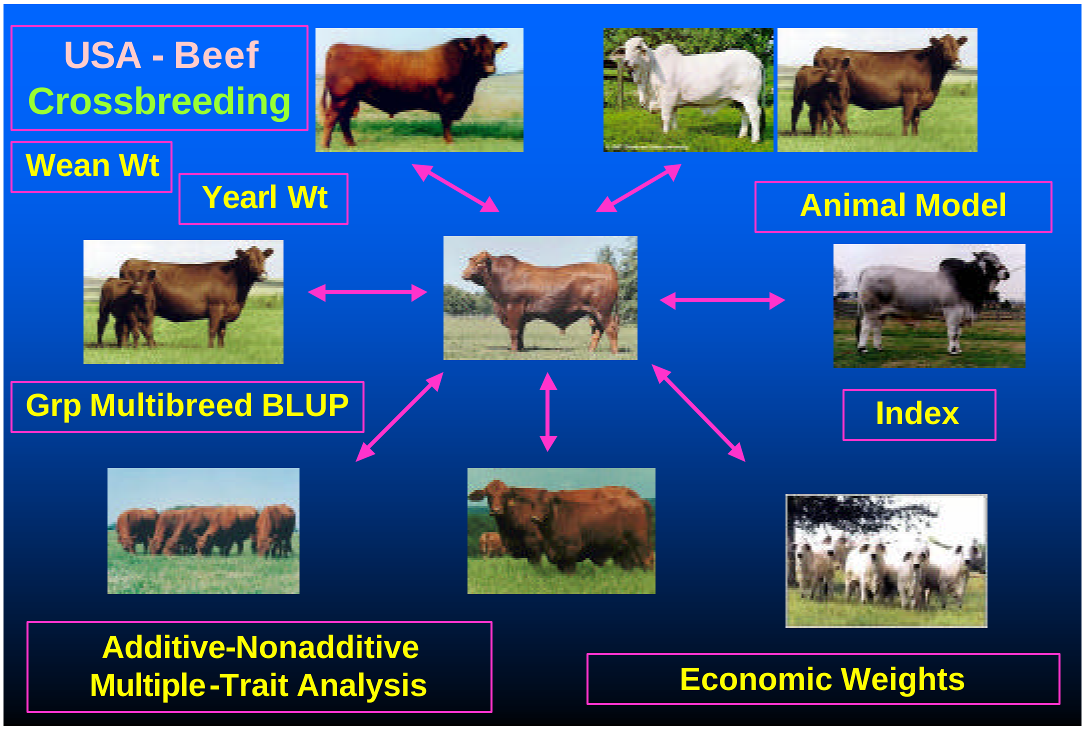
Index

Multiple-Trait Additive Analysis

Economic Weights

Figure 5. Current dairy cattle genetic evaluation strategy in Thailand.

Beef cattle national genetic evaluation procedures have had enormous progress in the USA during the last 20 years. The first multiple trait BLUP systems used sire-maternal grandsire models, and accounted for direct and maternal genetic effects. The first multitrait genetic evaluation system was developed at Cornell University in 1984. This system evaluated sires for birth weight and weaning weight direct and maternal, and postweaning weight direct (five traits). Another system included birth weight and calving ease direct and maternal (four traits). Both system were linear. Subsequently, a nonlinear threshold model was implemented for calving ease, and a combined linear (birth weight direct and maternal) – nonlinear (calving ease direct and maternal) was implemented. Currently the Cornell system uses a multibreed animal model that accounts for interbreed nonadditive group effects (**Figure 6**).



USA - Beef Crossbreeding

Wean Wt

Yearl Wt

Animal Model

Grp Multibreed BLUP

Index

Additive-Nonadditive Multiple-Trait Analysis

Economic Weights

Figure 6. Current beef cattle genetic evaluation strategy in the USA.

Other universities in the USA involved in national beef cattle genetic evaluations currently use intrabreed genetic evaluation procedures. Comparisons with Chile or Thailand cannot be made because currently neither country has implemented national genetic evaluation programs for beef cattle.

Future Genetic Animal Evaluation Procedures

Changes to national beef and dairy genetic animal evaluation procedures will continue to be evolutionary rather than revolutionary. Feasibility and cost-efficiency of field data collection, maintenance, and retrieval are likely to continue to be the most important factors when deciding what traits to collect information for genetic evaluation and for selection purposes. In the near future, markers for quantitative trait loci may become a usual component of genetic evaluation procedures in some countries, particularly those that have small well-controlled populations, where accuracy of prediction of the usual traits may be an issue. In other cases, markers will be used to routinely select animals for genes that control a major component of an economically important trait (e.g., kappa casein in dairy cattle, a tenderness gene in beef cattle). In the more distant future however, when massively parallel biochemical characterization techniques (biochips, microarrays, or some newer parallel biochemical technology) become well developed and efficient (robots), the targets are likely to be groups of genes affecting important sections of the biological make up of economically important traits. When this happens, the accuracy of genetic predictions will be enhanced immensely. However, the random aspect of the distribution of alleles during meiosis will still remain, thus prediction of the genetic and phenotypic behavior of future progeny will still involve a probabilistic component. This probabilistic uncertainty could be decreased by extensive use of cloning and, in the more distant future, by genetic engineering of desirable genotypes coupled with cloning.

Unless there is a major change in the structure and composition of the dairy and beef cattle populations in the USA, genetic evaluation systems in the near future will be similar to the current ones (**Figure 7**). Thus, genetic evaluations in dairy cattle in the USA will continue to be unibreed, for multiple traits, primarily additive, and perhaps nonadditive intrabreed genetic effects might later be included in the model. The major changes to this evaluation system are likely to come from new traits responsible for portions of a traditional economic trait (milk yield, calving ease) and their associated genetic-statistical models and procedures. These new traits will probably be reconstituted traits constructed using genetic-statistical prediction equations based on physiological

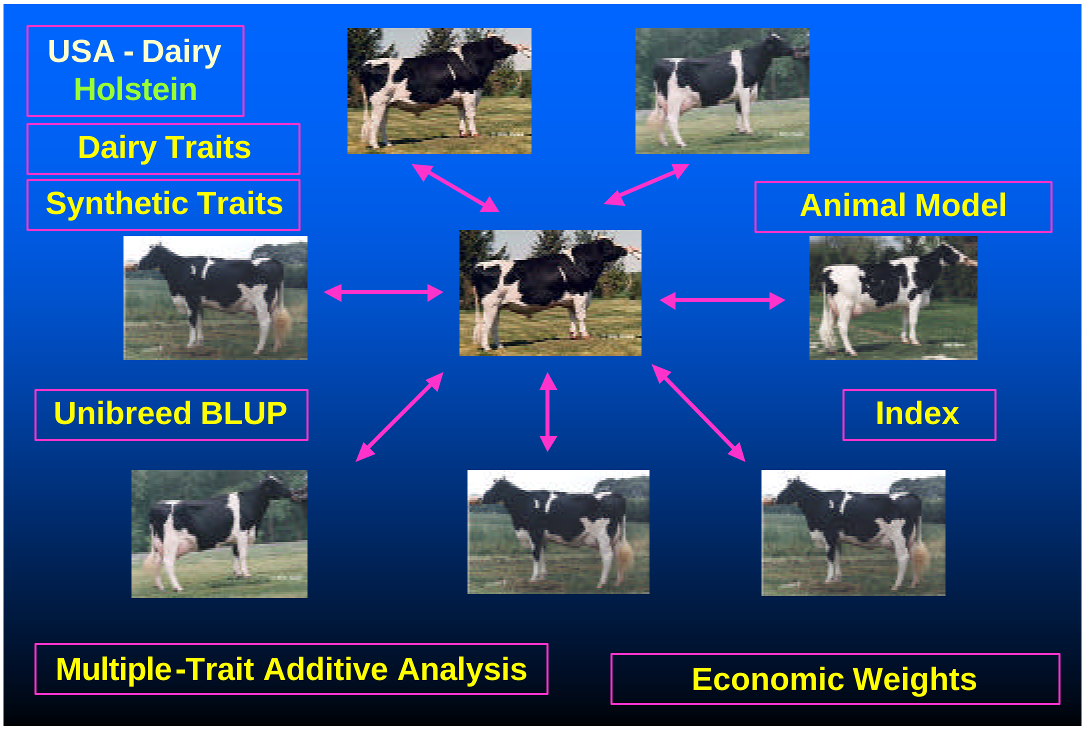


Figure 7. Future dairy cattle genetic evaluation strategy in the USA.

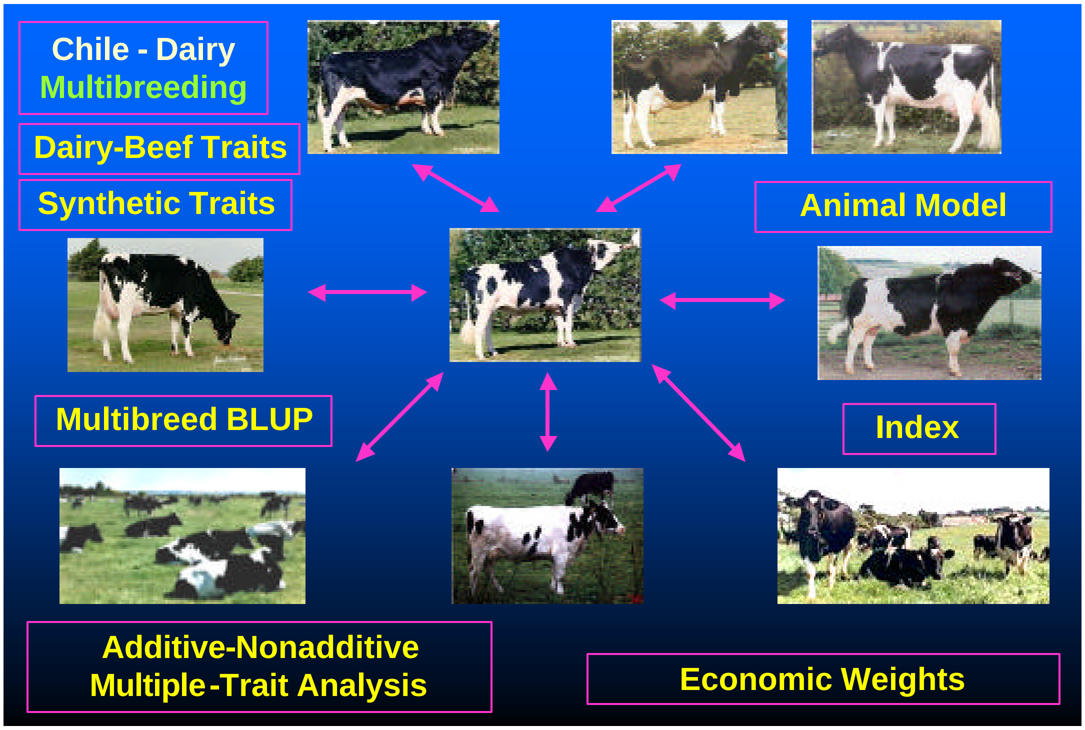
and biochemical relationships among individual biochemical measurements obtained through a massively parallel biochemical procedure.

Crossbreeding in the USA is likely to continue to be used as a genetic management tool to control calving difficulties in Holstein heifers. Further, if the level of inbreeding in the Holstein breed continues to increase, then use of crossbreeding (e.g., with Brown Swiss or Jersey) as a way of counteracting its negative effects on reproduction, survival, and production traits is likely to continue to increase in the future. Some dairy cows may also continue to participate in beef crossbreeding schemes as a means to increasing milk production or milk quality in beef cows. In such cases, it would probably be advantageous to incorporate information from straightbred dairy animals in the beef multibreed genetic analysis.

The situation of Holstein-importing countries with a Holstein-*Bos indicus* or Holstein-*Bos taurus* multibreed population (like Chile and Thailand) is substantially different. The main issue here is whether the ongoing upgrading mating scheme should be continued until all animals in the population have a breed composition close to 100% Holstein. This appears *not* to be the case in either country. Crossbred sires of various Holstein fractions have continued to be used. Furthermore, in various regions of Thailand, economic conditions suggest that crossbred animals with a Holstein fraction close to 50% are better suited to the local conditions better than crossbred animals with high percent Holstein (75% and above). A similar situation may exist in temperate countries like Chile, where some producers may not be willing to adopt the highly controlled management, heavy use of concentrate feed, and environmental conditions (shades, sprinklers) required by high-producing, low heat-humidity tolerant Holstein and high percent Holstein cows.

As a result of the variety of economic environments and goals of dairy farmers in Holstein importing countries around the world, it is likely that some form of a Holstein-Local Breed multibreed population will continue to exist in these countries, at least in the near future. Primarily because of the internal economic environment, some form of a multibreed animal model will be needed both in Chile (**Figure 8**) and in Thailand (**Figure 9**). Unless the beef market conditions change in Chile, straightbred and crossbred animals will be genetically evaluated only for dairy related traits (traditional and new). In Thailand, however, beef traits may become an integral part of a national beef-dairy cattle genetic evaluation system.

National beef cattle genetic evaluation systems in the USA are likely to continue to collect information and to evaluate animals for traditional growth, reproduction, and carcass traits (**Figure 10**) in the foreseeable future. The same as with dairy cattle, these systems are likely to incorporate markers for quantitative trait loci in their genetic evaluation systems initially, and subsequently composite traits responsible for the phenotype of specific portions (subtraits) of traditional economic important traits. The evaluation of the DNA sequences of these genes will permit the identification of the breed of origin of these alleles. Furthermore, measurement of the level of activity of genes responsible for these subtraits in straightbred and in crossbred animals will permit the generation of dramatically more accurate multibreed genetic predictions and estimations of multibreed genetic and environmental levels of variation.



Chile - Dairy
Multibreeding

Dairy-Beef Traits

Synthetic Traits

Animal Model

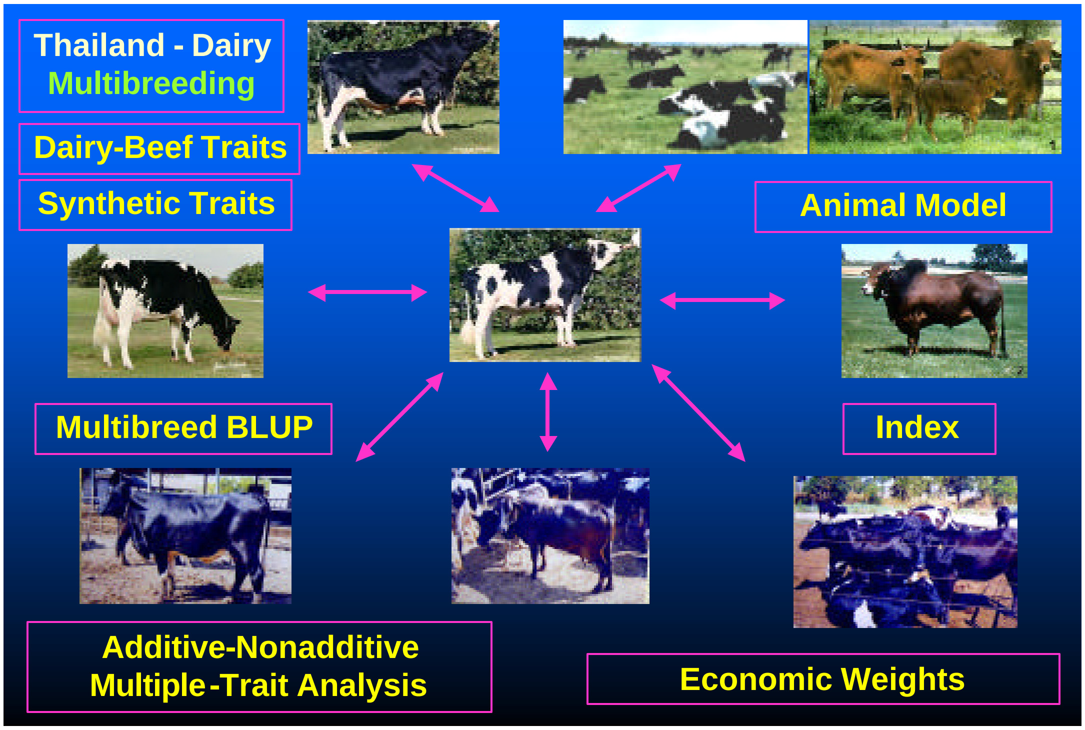
Multibreed BLUP

Index

Additive-Nonadditive
Multiple-Trait Analysis

Economic Weights

Figure 8. Future dairy cattle genetic evaluation strategy in Chile.



Thailand - Dairy
Multibreeding

Dairy-Beef Traits

Synthetic Traits

Animal Model

Multibreed BLUP

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Additive-Nonadditive
Multiple-Trait Analysis

Economic Weights

Figure 9. Future dairy cattle genetic evaluation strategy in Thailand.

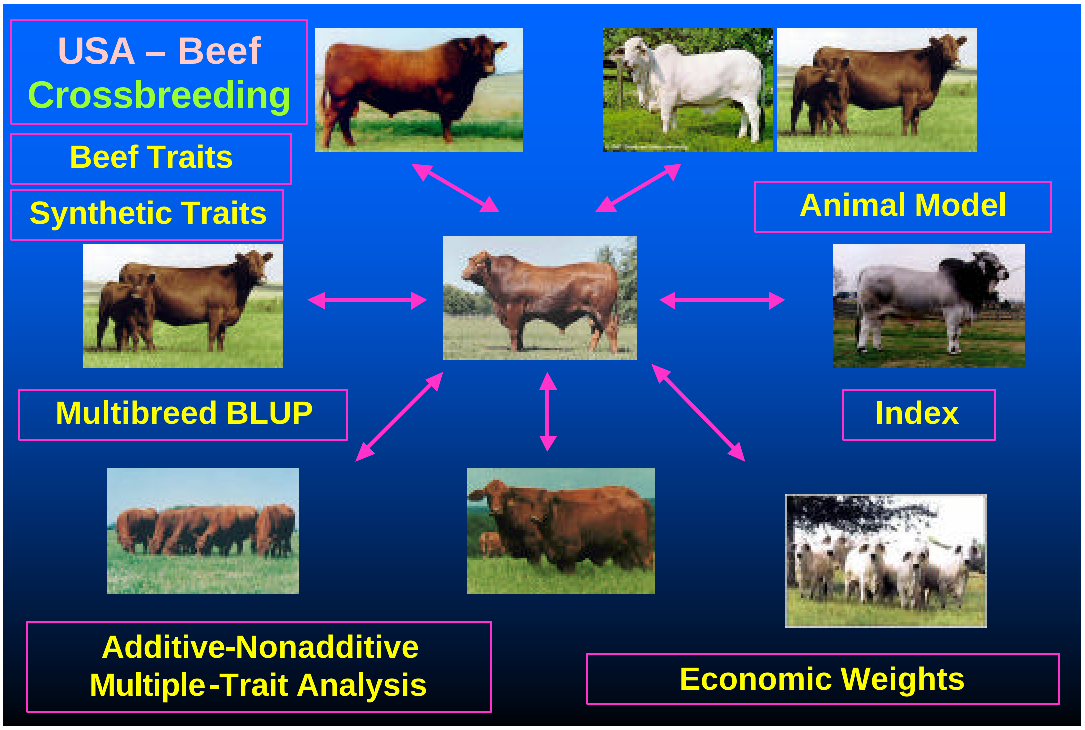


Figure 10. Future beef cattle genetic evaluation strategy in the USA.

Multibreed information collected by some breed associations in the USA together with genomic and proteomic information generated microarray technology will likely be major contributors to the continued improvement of the accuracy of multibreed genetic evaluations. In the more distant future this biological information will likely be used to engineer cattle that not only fit local environmental conditions better, but also are economically superior to less improved genotypes.

Factors Contributing to the Development of New Genetic Evaluation Procedures

New Traits. Genomic sequencing of plants and animals, and structural and functional genomics have opened new doors for the understanding and prediction of the biological functions of individual genes and of groups of genes. Products of individual genes or of groups of genes create specific environmental conditions within their specific tissues and across other tissues inside the body of an animal. A trait of economic importance (e.g., milk yield, yearling weight) could be viewed as the outcome of the actions of many of these groups of biochemically interrelated genes (functional groups of genes) acting at one or more specific times in the life of an animal. In addition, these functional groups of genes will interact with external environmental conditions to produce the outwardly visible phenotype of an animal for a given trait.

When a fully automated biochip technology or a similarly massively parallel biochemical characterization technology becomes inexpensive, fast, and efficient in the future, it will be possible: 1) to characterize the genetic material of *individual animals* for its DNA content, 2) to measure the activity of specific groups of genes whose connection to a specific trait or traits is previously known, 3) to evaluate the activity of the products of these genes, and 4) to assess their influence on the activity of other relevant groups of genes. *All of this will be done at a specific point in the life of an animal*. If this type of analysis is done at various times over specific segments of the productive life of an individual (e.g., for growth traits or milk traits), a substantially better prediction of the genetic and phenotypic potential of an animal for a traditional trait of economic importance could be obtained (**Figure 11**). A logical next step could be the production of animals with bioengineered-enhanced traits followed by the dissemination of their genetic material into the population by artificial insemination, embryo transfer, and cloning.

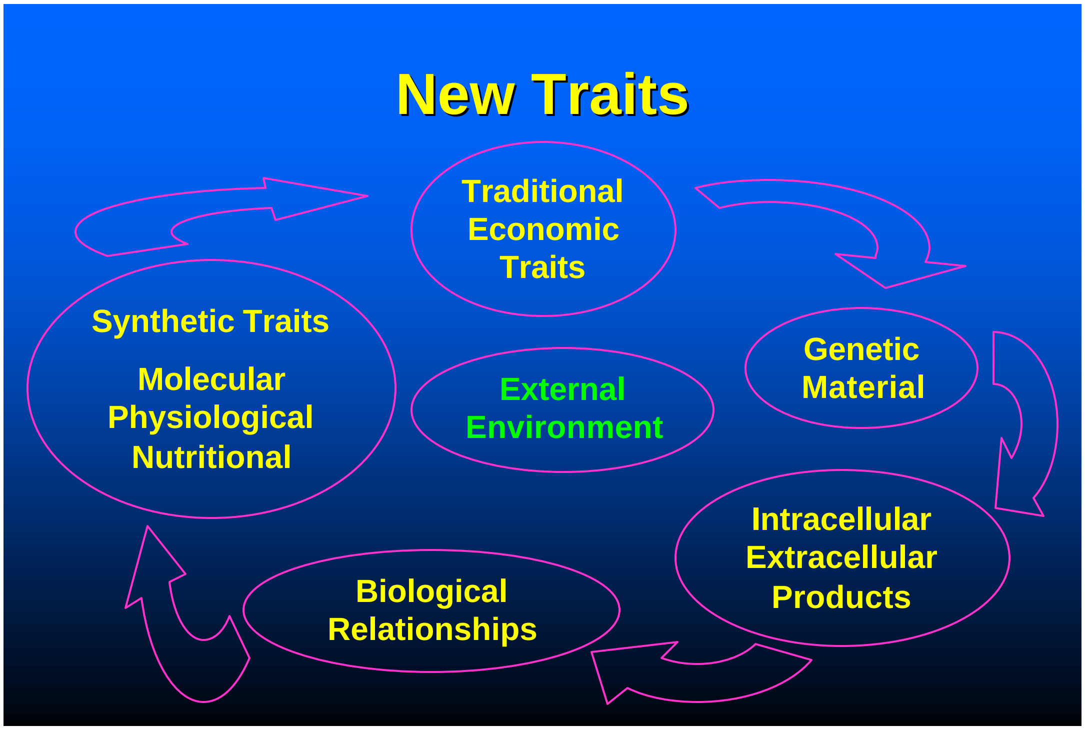


Figure 11. New traits for future genetic evaluations

New Models. With the advent of new, more accurate biological subtraits (i.e., traits responsible for parts of traditional economic traits such as milk yield), genetic evaluation models will need to be revised and adapted to account for interrelationships among all relevant subtraits. The new genetic-statistical models will need to make substantially larger use of biological relationships to maximize the benefits of the vast amounts of biological information that will be available. The resulting genetic-statistical models should be able to predict individual genetic values with substantially higher accuracy than production trait models. However, the increased level of complexity of the new genetic-statistical models will probably require a systems approach and enormous computing resources. This may severely limit their usability and even make them impractical for repeated genetic predictions. Thus, until hardware and software capabilities make complex genetic-statistical models of practical use, these models will need to be simplified, and compromises between biological accuracy and computational feasibility will need to be implemented. The more accurate future genetic evaluation models become the more comprehensive they are likely to be, with modules ranging from heavily biological to heavily statistical. Both linear and nonlinear statistical approaches are likely to coexist in such models (**Figure 12**).

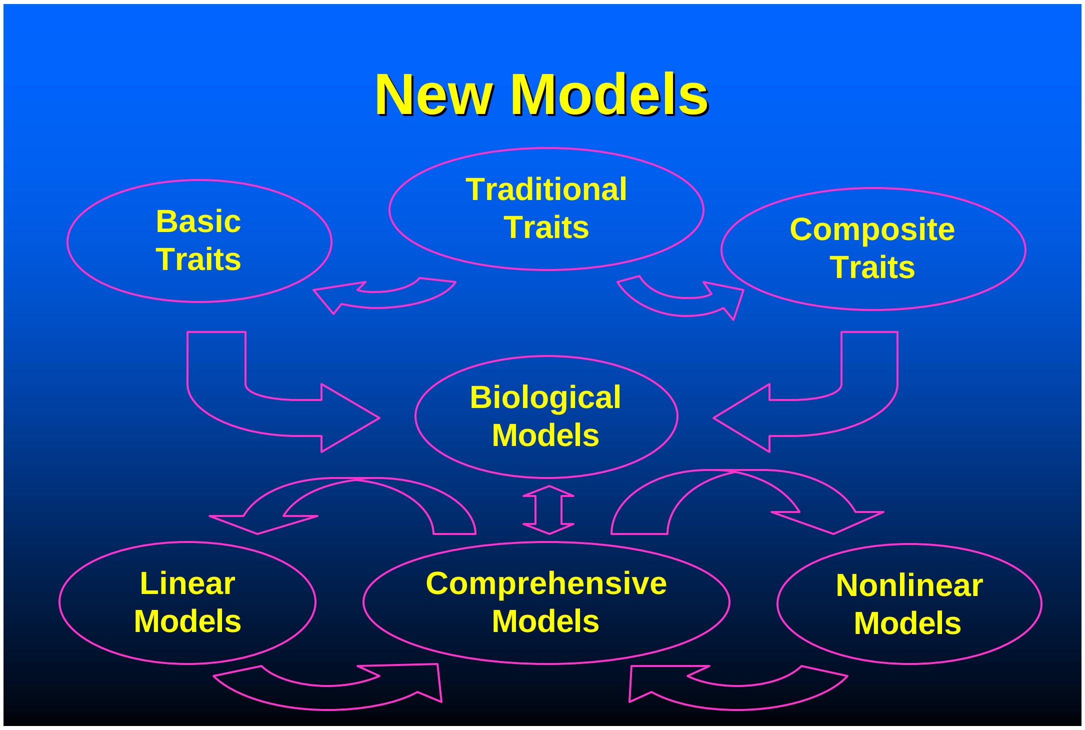
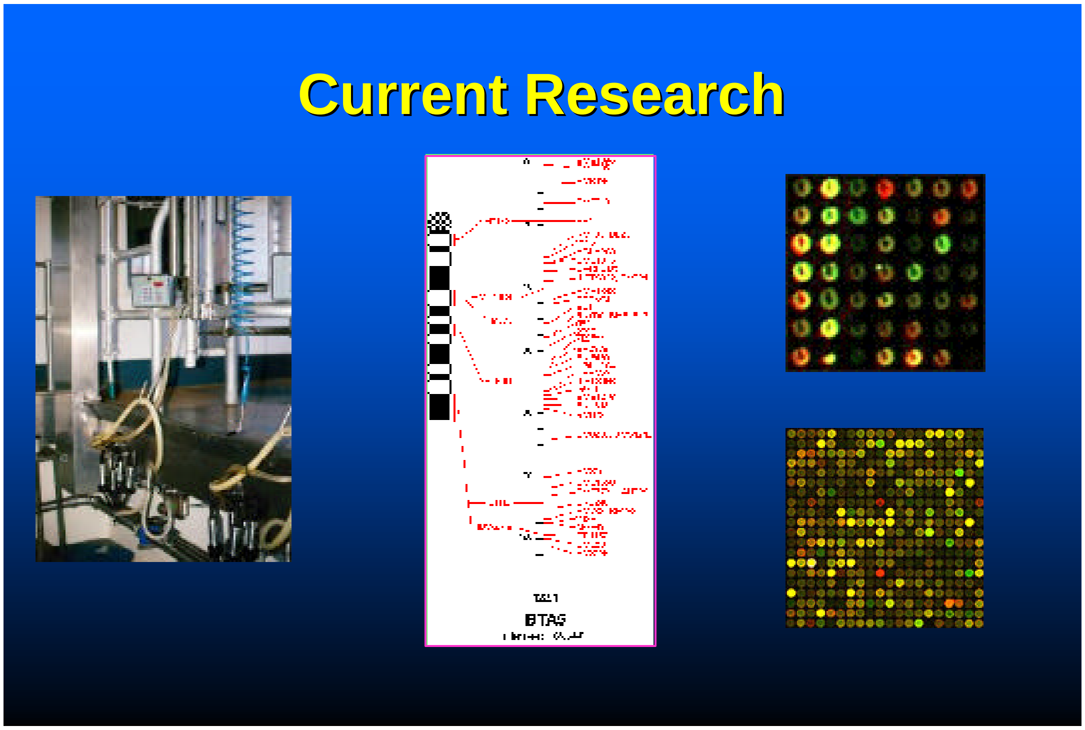


Figure 12. New models for future genetic evaluations

Current Genetic Research and Mainstream Adoption of New Sampling Technologies. Currently the majority of the data collected by beef and dairy cattle breed associations in the USA is on traditional economically important traits. The cattle genome sequencing effort plays no role in national sire evaluations. Markers for single genes or groups of genes of economic relevance will continue to be found at an increased rate in the future. However, marker research will probably have little impact on quantitative traits determined by large number of alleles. Quantitative biotechnological systems (e.g., biochips) hold a much larger promise for the characterization and genetic improvement of quantitative traits in cattle and other domestic animal species (**Figure 13**).



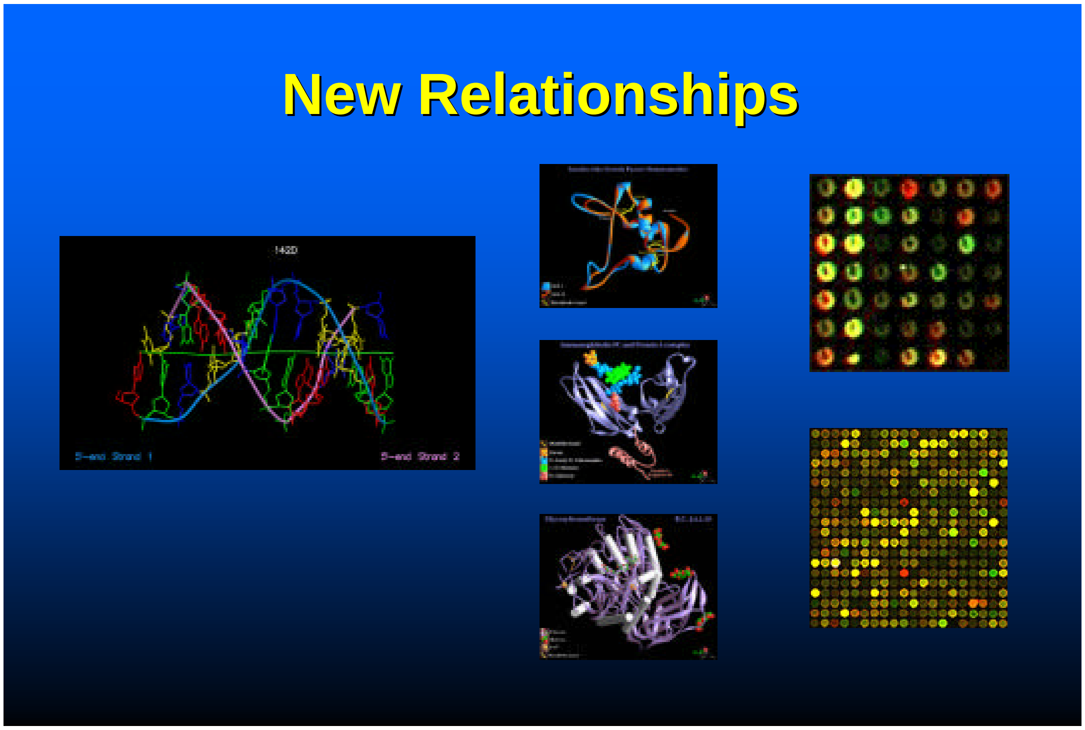
Current Research

Figure 13. Current research on new sampling technologies

Adoption of biochip technologies for the characterization of individual animals on a large scale will help characterize unibreed and multibreed populations to a substantially more accurate degree than it is possible today. Measurements of internal products of subtraits will enable genetic prediction for components of a traditional economic trait, thus substantially increasing the power and accuracy of the selection process. In addition, the accuracy of prediction of the outcome of matings to produce progeny with specific characteristics should also be greatly enhanced, both in single-breed and in multibreed populations.

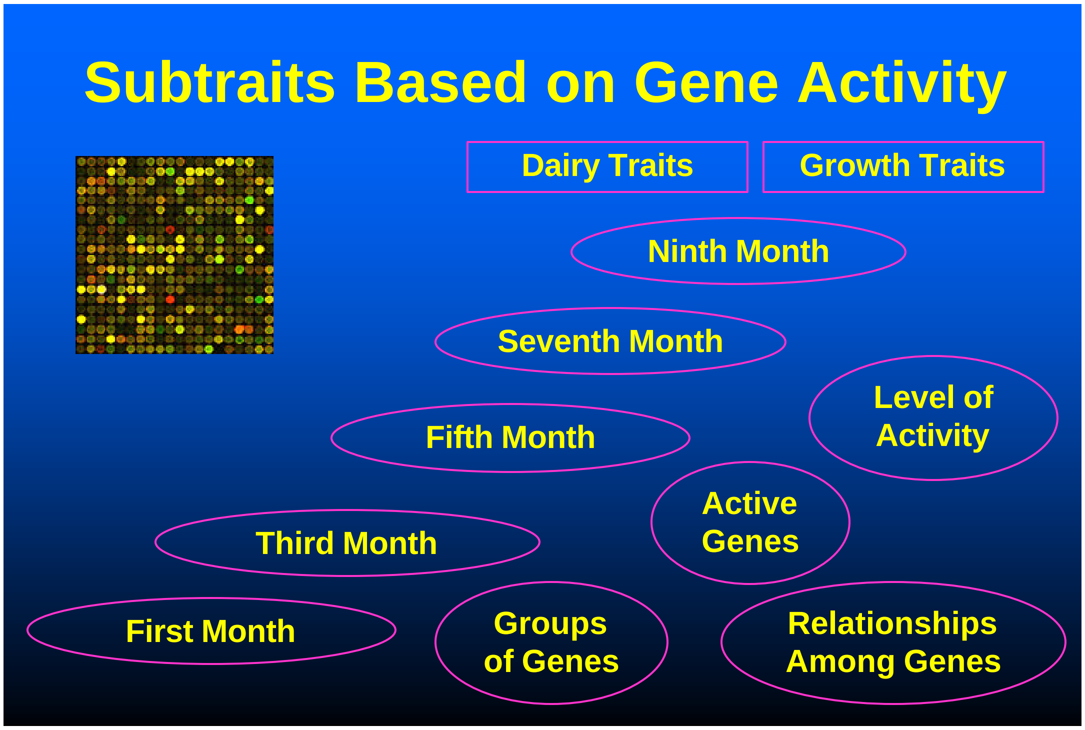
Analysis of biological data sets in complete populations will permit the generation of extremely accurate databases on biochemical relationships among individual genes and groups of genes. This data bank should tremendously improve our understanding of genetic associations among traits, the generation of subtraits amenable for genetic improvement, and our capability for generating increasingly more complete (and complex) genetic-statistical models (**Figure 14**).

As an example of genetic-statistical modeling possibilities for the new biological information, consider the following case. Suppose that biochip measurements of batteries of genes associated with a traditional economic trait (e.g., milk yield) were made on a large number of animals at *various specific times* (e.g., monthly). Biochips could have been created for various purposes: i) to determine whether a gene was active at a specific time, ii) to measure the level of activity at that time, and iii) to determine the level of influence of some genes on others (subtraits within traditional economic traits).



New Relationships

Figure 14. New subtraits measured by biological technologies



Subtraits Based on Gene Activity

Dairy Traits

Growth Traits

Ninth Month

Seventh Month

Level of Activity

Fifth Month

Active Genes

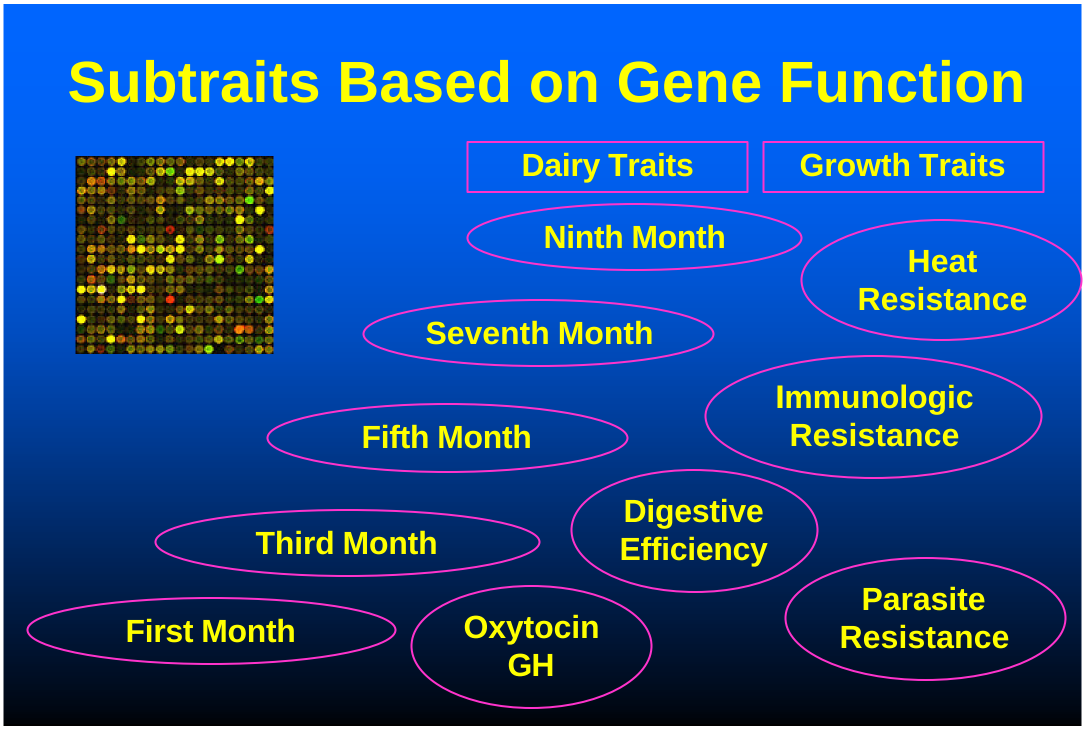
Third Month

First Month

Groups of Genes

Relationships Among Genes

Figure 15. Subtraits for traditional economic traits based on gene activity



Subtraits Based on Gene Function

Dairy Traits

Growth Traits

Ninth Month

Heat Resistance

Seventh Month

Immunologic Resistance

Fifth Month

Digestive Efficiency

Third Month

Parasite Resistance

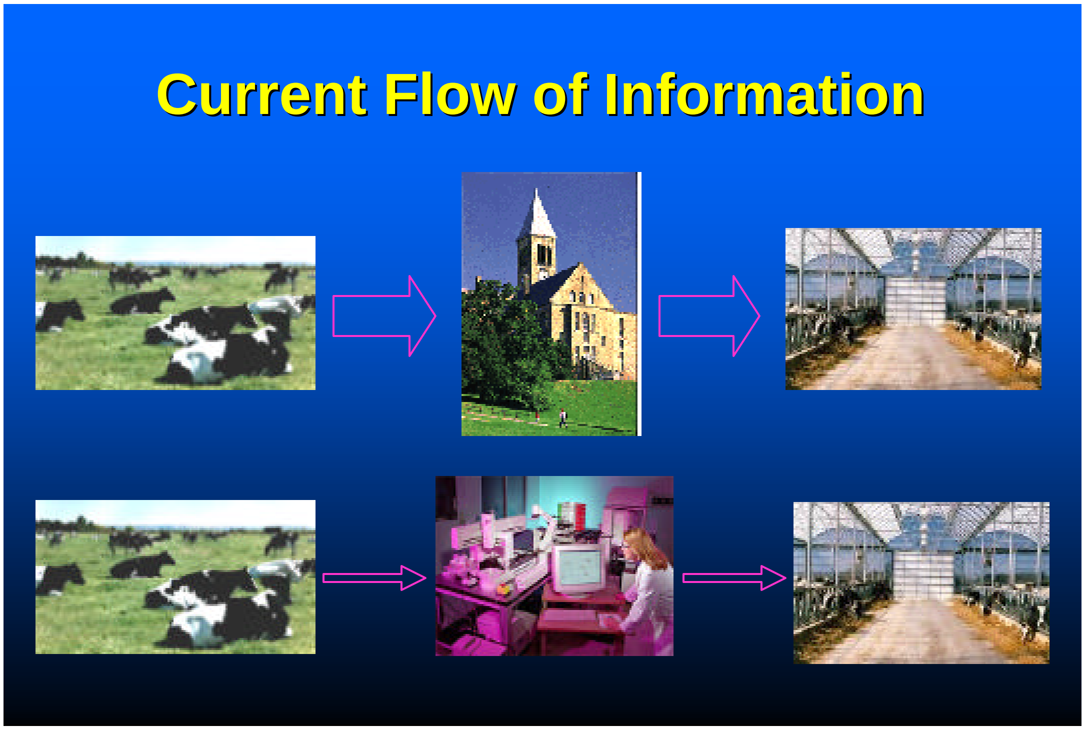
First Month

Oxytocin GH

Figure 16. Subtraits for traditional economic traits based on gene function

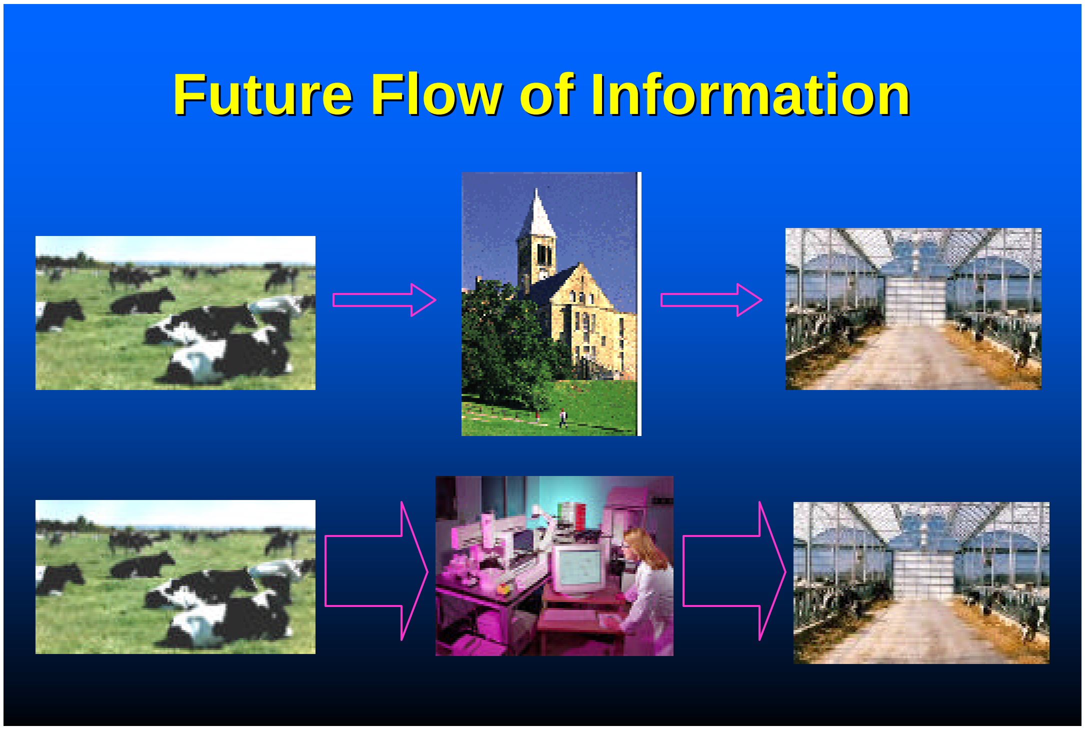
Assume that the association of genes to organs or tissues is also known. At least two types of analyses are possible: 1) analysis based solely on the level of activity of the genes involved (**Figure 15**), and 2) analyses based on the association of groups of genes to specific functions (**Figure 16**). In both instances it would be possible: a) to predict the effect of each subtrait at each time, b) to measure variation and covariation among subtraits, and c) to predict genetic values of animals for all subtraits and the associated traditional economic traits. The level of activity of the various sets of genes at various times in the life of an animal will also depend on the external environment. Thus, future genetic-statistical models will be a multidimensional problem that will need to account for: a) changes in gene activity over the lifespan of an animal, b) changes in the internal environment of an animal over time, and c) changes in the external environment around an animal over time. Because of the dynamism of and the interrelationships among these three sets of factors, genetic-statistical evaluation models in the future are likely to become genetic-statistical evaluation systems requiring complex and powerful software and hardware.

Flow of Information. The success of the research, development, and implementation of beef and dairy national animal evaluation systems in the USA has relied on the unrestricted flow of information from producers to breed associations to universities or government organizations involved in genetic animal evaluation and vice versa. Raw data was collected by producers and stored at breed association headquarters, genetic evaluations were computed at universities and government institutions, and finally producers received predictions, animal rankings, genetic trends, and other relevant



Current Flow of Information

Figure 17. Current flow of information.



Future Flow of Information

Figure 18. Future flow of information.

information by electronic or paper means. Most of the data collected was for traditional economic traits. Only a minor fraction was for biological analyses (**Figure 17**).

The current form of the flow of data for genetic animal evaluation may change drastically in the future as biological analytical techniques become faster, more efficient, and more affordable. If biological techniques are adopted by the cattle industry as one more tool for genetic improvement, the vast majority of the information generated for genetic animal evaluation purposes will be biological (**Figure 18**). Several issues are likely to arise if, or when, this scenario becomes a reality: 1) what types of animal tissue samples will be needed (blood ?, hair ?), 2) who will collect these samples (producers ?, breed associations?, private companies ?), and 3) who will own the rights over the information and the outputs (genetic evaluations, biological products) produced by the biological and genetic-statistical analyses of the tissue samples.

New Informatics and New Research Structures. If the current status of biological sampling collection and analysis is an indication of what will happen in the future, most sampling will be done by the producer, samples will be sent to private laboratories, which will create their own private databases. This is likely to generate (at least initially) a large number of private databases. The question of ownership again arises here. Who will own the data, the tissues sampled, and the products generated in the laboratory analysis ?, Producers ?, Private companies ?, Co-ownership ? These issues will need to be satisfactorily resolved in the context of the new informatics structure if cattlemen are to receive appropriate compensation for their involvement in this new era of biotechnology and bioinformatics (**Figure 19**).

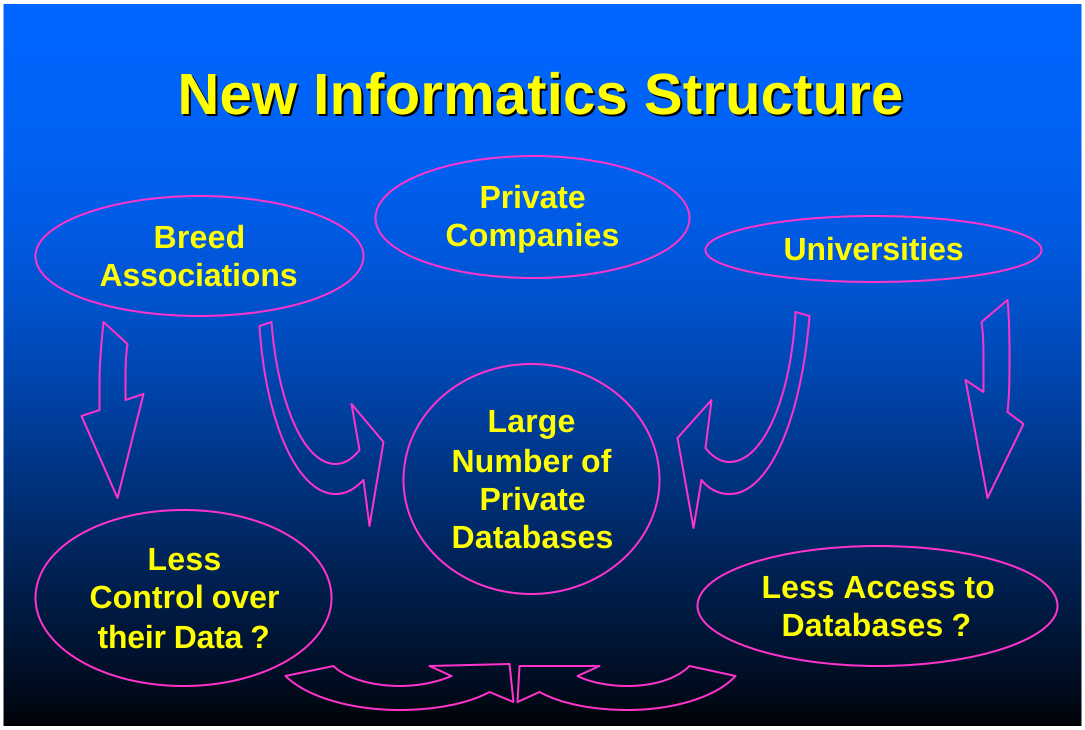
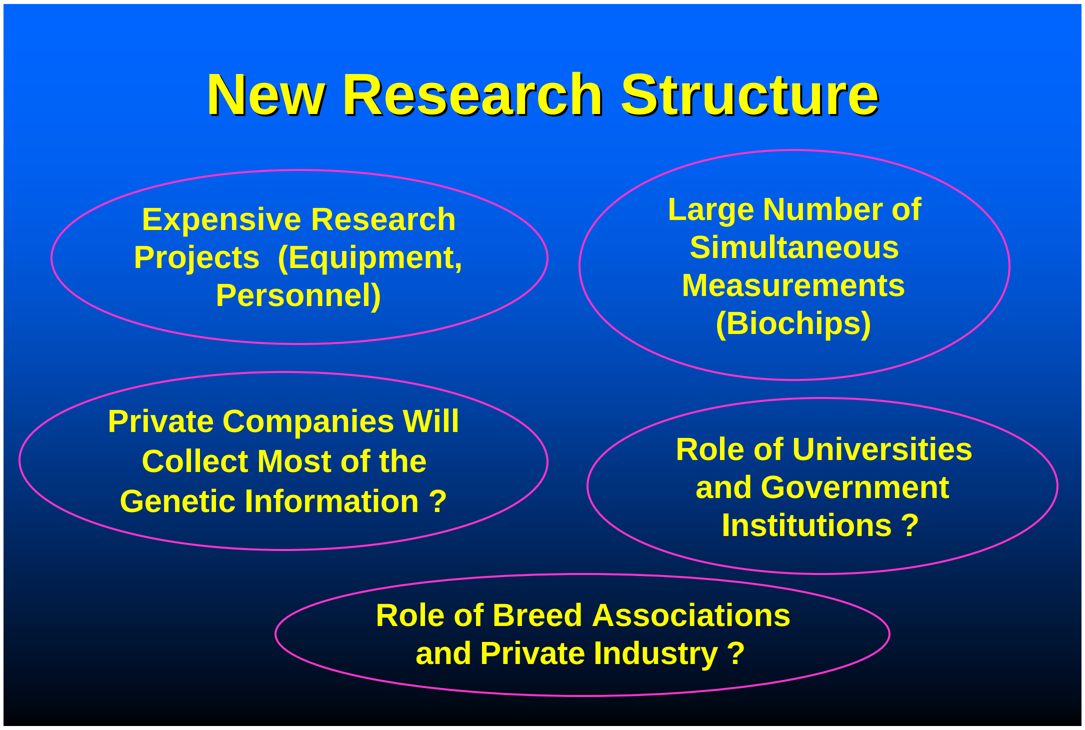


Figure 19. Future informatics structure.

University researchers involved in national animal genetic evaluation will need access to the new biological data sets to develop and test new genetic prediction procedures. If private companies control these databases, a) will universities have access to them for research purposes or to conduct national cattle genetic evaluation systems (**Figure 20**) ?, or, b) will private companies develop their own genetic evaluation systems and procedures for the new biological traits, and provide them to producers as an additional service (as it has happened with poultry and swine)?



New Research Structure

Expensive Research Projects (Equipment, Personnel)

Large Number of Simultaneous Measurements (Biochips)

Private Companies Will Collect Most of the Genetic Information ?

Role of Universities and Government Institutions ?

Role of Breed Associations and Private Industry ?

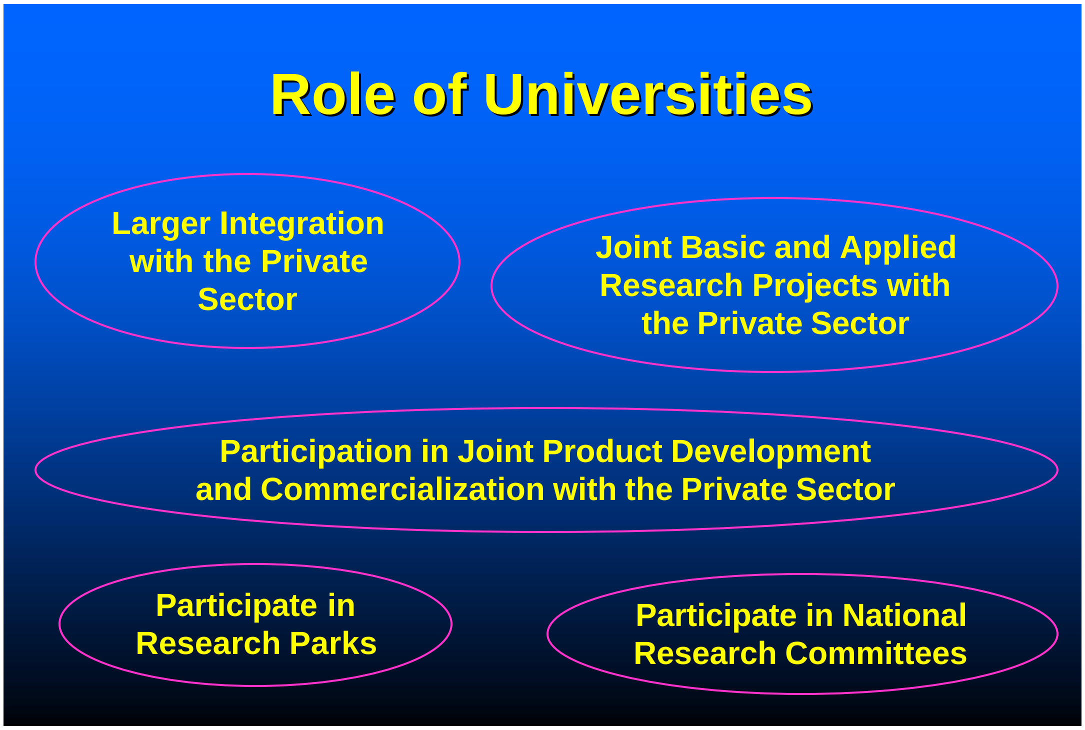
Figure 20. Future field research structure.

Role of Universities, Government Institutions, and Private Industry in Future Genetic Improvement Systems

Assuming a massive influx of biological information available for a large portion of the cattle population, what will be the role of universities, government institutions, breed associations, and private companies in future national animal genetic evaluations ?

The role of government institutions in the development of the agriculture and livestock industries will probably remain an important one in many countries for years to come. Assuming a continued progression towards a worldwide market economy, well-established semi-private or private organizations are likely to eventually take over some of the tasks that these government institutions perform today. One such task is the organization of an economically viable dairy and beef cattle industry, and within it, the task of developing and maintaining a dynamic and up-to-date cattle genetic improvement program whose flexibility allows it to react appropriately to internal and external market fluctuations.

Universities are likely to become even more integrated to the private sector in the future. Budgetary constraints have already caused most agricultural universities to look at the private sector for a large portion of their research and development funding. University faculty will increase their level of participation in joint research and development projects with the private sector. Research parks will likely be the primary place of university-industry collaborative research and development (**Figure 21**). Non-profit research parks will facilitate communication and integration of research, development, and marketing objectives among faculty involved in national animal evaluations and private companies dedicated to the analysis of biological samples and the creation of biological databases.



Role of Universities

Larger Integration with the Private Sector

Joint Basic and Applied Research Projects with the Private Sector

Participation in Joint Product Development and Commercialization with the Private Sector

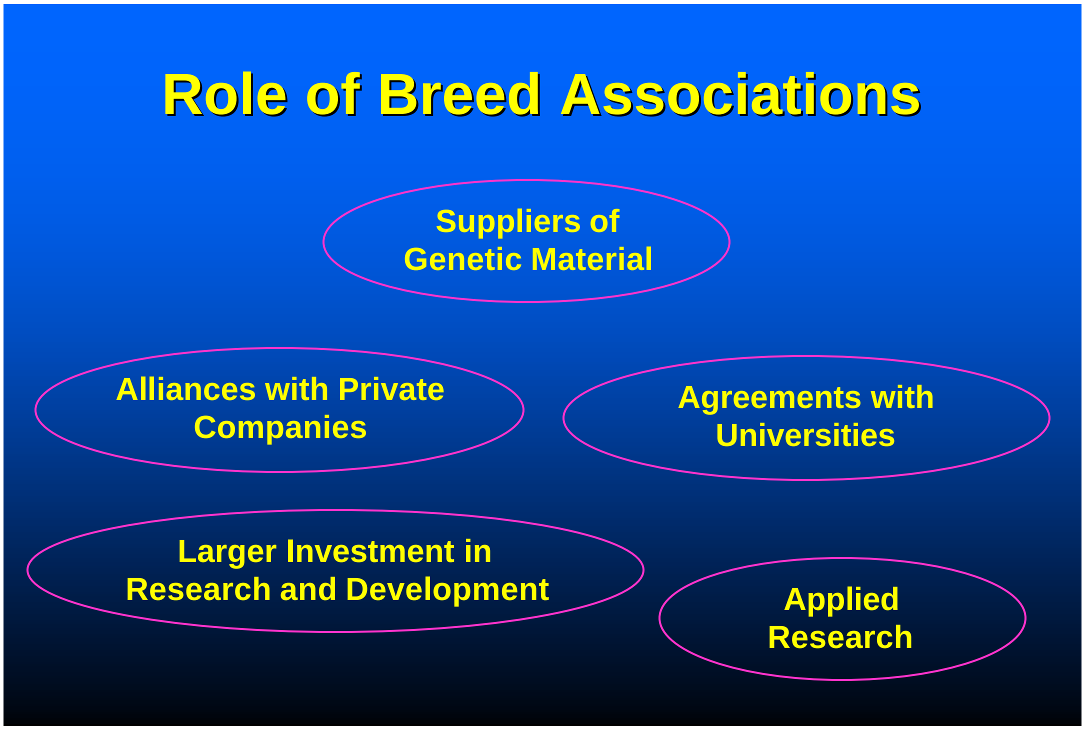
Participate in Research Parks

Participate in National Research Committees

Figure 21. Future trends in university activities.

Breed associations are likely to continue to be one of the main cattlemen organizations in the USA in the near future. As such, they will probably continue to be the entity that will organize and channel the biological sampling of cattle at a national level, set the standards for sampling procedures, and represent producers in dealing with laboratories dedicated to the analysis and generation of biological databases. Breed associations could establish alliances with certain private laboratories to use a uniform protocol for all laboratory analysis and database structure. To achieve these goals breed associations will probably need to make substantially larger investments in research and development than current levels.

Breed associations will also probably continue to establish agreements with university researchers, particularly those working at universities involved in national animal genetic evaluations. The focus of these joint breed-association-university research efforts is likely to continue to be primarily applied research (**Figure 22**). These collaborations will facilitate the incorporation of new genetic evaluation methodologies to national genetic evaluation systems. National research and coordinating committees will continue to provide a forum for the establishment of uniform genetic-statistical procedures across breed associations. Their role will need to be expanded to account for biotechnological procedures if adopted by the breed associations.



Role of Breed Associations

Suppliers of Genetic Material

Alliances with Private Companies

Agreements with Universities

Larger Investment in Research and Development

Applied Research

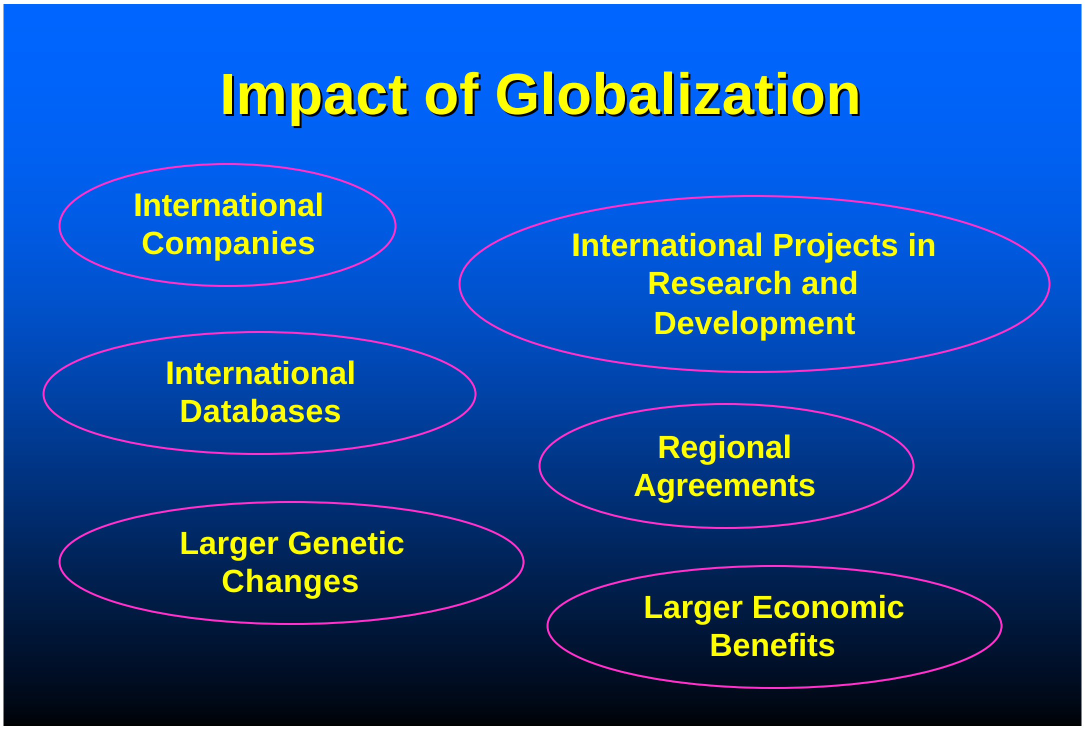
Figure 22. Future trends in breed association activities.

The role of private industry will continue to expand in the future. Vertical integration of the beef industry (e.g., alliances) has become a popular alternative to the usual average marketing strategy in the USA in recent years. The main reason behind this change is the loss of beef market share to pork and, primarily, poultry. There are currently over forty branded beef products in the USA (e.g., Certified Angus Beef and Nolan Ryan's Natural Tender Aged Beef). Their goal is strictly an economic one (to produce a consistent product for which the consumer is willing to pay a premium price). Genetic evaluation of the participating cattle populations is not currently one of their objectives. However, if they expand and become as large and influential as similar organizations in the pork and poultry industries, then genetic evaluation and mating strategies are likely to become an integral part of their structure in the future.

Impact of Globalization on Research and Development of Genetic Improvement Procedures

Collaboration among researchers across countries and the development of international companies have been the norm rather than the exception for a number of years. The globalization of research, development, and business practices has been largely driven by global marketing strategies, and it has been greatly facilitated by enormous developments in communication and information hardware and software. The pace of development of communication and information technologies will continue to accelerate in the future. This, in turn, will continue to facilitate the integration of research, development, and marketing efforts of global bioinformatics and biotechnological companies, thus increasing the speed of service and product development.

International research and development collaborations in basic and applied sciences will certainly continue to increase and expand in the future (**Figure 23**). This will be enormously advantageous for quantitative genetics research that requires large data sets that may already exist in other countries, or that may be created much more rapidly and cheaply if an appropriate number of countries are involved.



Impact of Globalization

International Companies

International Projects in Research and Development

International Databases

Regional Agreements

Larger Genetic Changes

Larger Economic Benefits

Figure 23. Effect of globalization on genetic evaluation

These international collaborations will accelerate the creation of reliable international databases, decrease costs, and by judicious coordination, minimize duplications of efforts. Because of the larger size of the data sets and the larger populations they are likely to be represented, larger genetic trends, and potentially larger economic benefits might be achieved. Clear rules for the ownership, distribution, and use of these databases and of their products will need to be established, particularly if they contain biological data.

Implications

Future genetic animal evaluation, selection, and mating strategies are likely to be impacted more by changes in the nature of traits being evaluated and selected for than by changes in genetic-statistical models and procedures. The realization of these changes will rely heavily on the development and adoption of cost-effective tissue sampling techniques and laboratory analyses of more precisely measured biological traits. The total cost of these new genetic evaluation systems is likely to be higher than current ones. However, these higher costs will decrease over time as biological technologies improve, and they will be eventually offset by larger economic benefits derived from using the new biological traits for prediction and selection of animals in unibreed and multibreed populations.

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