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Discussion on the Current Situation of Animal Genetic Improvement and Its Prospects for the Future

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Introduction

Quantitative genetic evaluation of domestic animals for economically important traits has undergone enormous changes in the last 30 years. However, these changes will pale in comparison with the changes that will arise from the new quantitative biotechnologies that are currently emerging. These quantitative biotechnologies are the result of new and expanding associations between areas such as physical sciences, engineering, material sciences, computer sciences, physiology, molecular genetics, genomics, functional genomics, robotics, and nanotechnology.

As a result the merging of interests and interdisciplinary research and development collaborations, the time lapse between research and application has been dramatically reduced. These collaborations have occurred across universities and research institutions, as well as in large private companies. The involvement of private funds and private industry has probably been the major force behind this trend. Universities have become active participants in research-for-profit endeavors. This trend is likely to continue and expand in the future.

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

The objectives of this discussion are: 1) to briefly describe the problem of quantitative genetic evaluation as it is understood today, 2) to relate current genetic evaluations to those used in the past, 3) to envision genetic evaluation practices in the future, and 4) to project potential roles of universities, breed associations, and private industry in future genetic evaluations.

Current View of Quantitative Genetic Evaluation

The problem of evaluating animals quantitatively can be organized in the following segments: 1) definition of the population, 2) identification of a set of economically important traits, 3) identification of the set of relevant genetic and environmental effects for each trait, 4) development of appropriate genetic-statistical models for genetic evaluation and estimation of genetic and environmental parameters, 5) development of appropriate computational algorithms to obtain estimates of genetic

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[1] Invited Seminar, University of Chile, Santiago, January 24, 2001.

parameters and predictions of genetic effects, 6) use of genetic predictions to select future parents in the population, and 7) development of appropriate within subpopulations and across subpopulations 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 Angus, Brahman, Brangus, 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 have 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 assumed to be determined by a large number of alleles of small effect. The types of information collected on economically important traits in beef cattle (weights at various ages) and in dairy cattle (milk yield, fat percent, protein percent) have changed little over the last fifty 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 the 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 internal environment of the body of an animal could potentially be subdivided into several environmental regions, complicating potential genetic analyses even further.

Development of appropriate 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. In this regard, the vast majority of genetic-statistical models 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). However, multitrait linear models are still the most prevalent models used for genetic evaluation in the world today. Furthermore, probably the vast majority of models still assume a single population, and a common set of genetic and environmental parameters, even though the population being analyzed is composed of several known subpopulations with potentially different means and variances (e.g., several breeds and crossbred groups). Multibreed models have been used to compute genetic covariances and to predict genetic values for straightbred and crossbred animals in several small multibreed populations (USA, Colombia). The only national multibreed model currently in place in the USA is the one for the Simmental-Simbrah-Canadian Simmental multibreed population.

Development of appropriate computational algorithms to obtain estimates of genetic parameters and predictions of genetic effects. Computational algorithms will be determined by the type of population (unibreed, multibreed), the type of trait (continuous, categorical), the size of the population (small, large), and the number of traits to be simultaneously analyzed. Computational algorithms used in genetic evaluations can be broadly classified into two types: direct and iterative. Most national genetic evaluation systems have traditionally been programmed as iterative systems, and have used a variety of transformations to improve computational efficiency. Direct computational systems have traditionally been used to obtain predictions of genetic values in small data sets and to estimate variance components using restricted maximum likelihood procedures. However, with the dramatic increase in microcomputer speed and memory in recent years, direct computational systems using sparse matrix algorithms have become a feasible alternative to iterative procedures, except for extremely large national data sets.

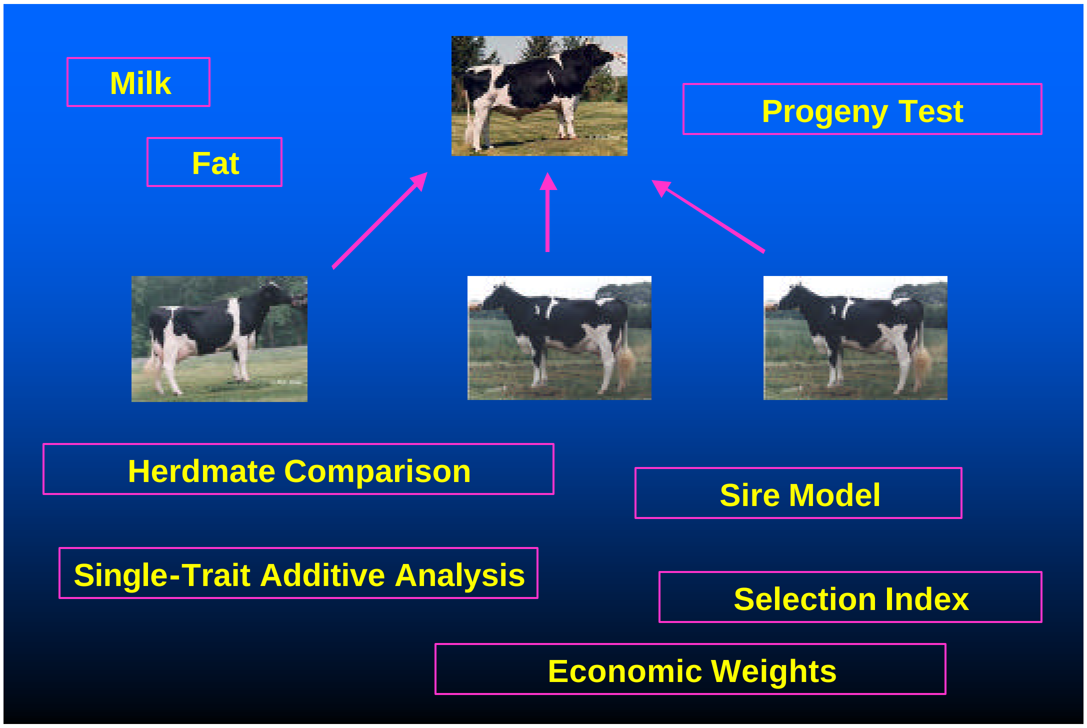
Use of genetic predictions to select future parents in the population. Genetic predictions have been used somewhat differently in beef and in dairy cattle. Indexes have been supplied in dairy cattle sire summaries for decades in addition to predicted genetic differences. Contrarily, beef cattle summaries have traditionally published genetic predictions only. 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. Genetic predictions have been successfully used both in dairy cattle and in beef cattle to 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 subpopulations and across subpopulations 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 is economically disadvantageous. Thus, the upgrading process has frequently been stopped at somewhere between 62% and 87% Holstein. In short, the mating scheme applied to a particular population will primarily depend on the net economic advantage over competing mating systems.

Early Genetic Animal Evaluation Procedures

Genetic evaluation procedures for large unbalanced data sets have traditionally been a compromise between accuracy of prediction given status 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. These systems were used in both beef and dairy cattle. The last implementation of such systems in dairy cattle was probably the herdmate comparison. The main objective of these 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. Dairy cattle sire evaluation strategy using BLP or early BLUP procedures.

Typical traits of economic interest were milk yield, fat percentage, and protein percentage. Analyses were 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 systems followed a strategy similar to 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.

Later on, some dairy cattle systems switched changed their genetic evaluation procedures from BLP-based to BLUP-based. The first BLUP models used were sire models. Later on, sire-maternal grandsire models were implemented. During this period, 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

Most of the progress in national genetic evaluation programs over the last 20 years have been the result of improved database storage and management and modeling and statistical methodologies. 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 evaluations of multiple traits dramatically improved the accuracy of prediction of genetic values. Thus, larger number of truly superior animals (especially sires) were identified, and with the help of artificial insemination large numbers of progeny of these animals were produced. Consequently, steeper genetic trends were observed in both beef and dairy cattle populations for economically important traits. Sire summaries today publish not only genetic predictions for a large number of traits, but also tables of percentiles to help locate the 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 are aimed at providing a succinct picture of the various forms of genetic evaluation and mating programs today. 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 versions of the dairy animal model is the test-day model that uses random regression to predict milk production traits at any 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

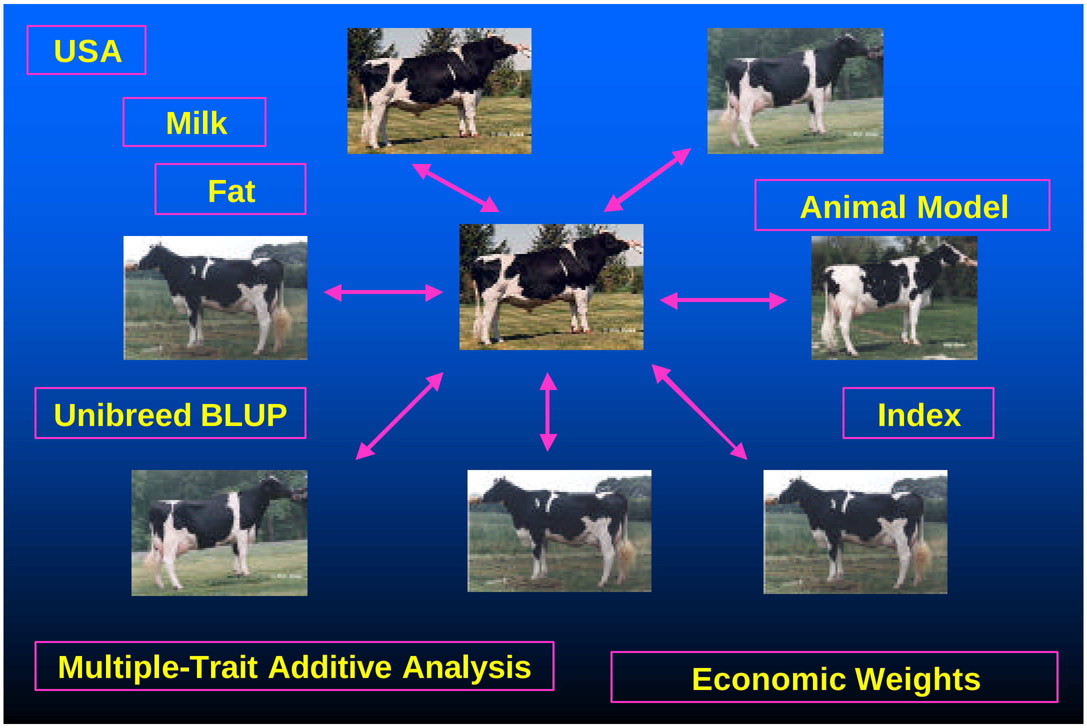
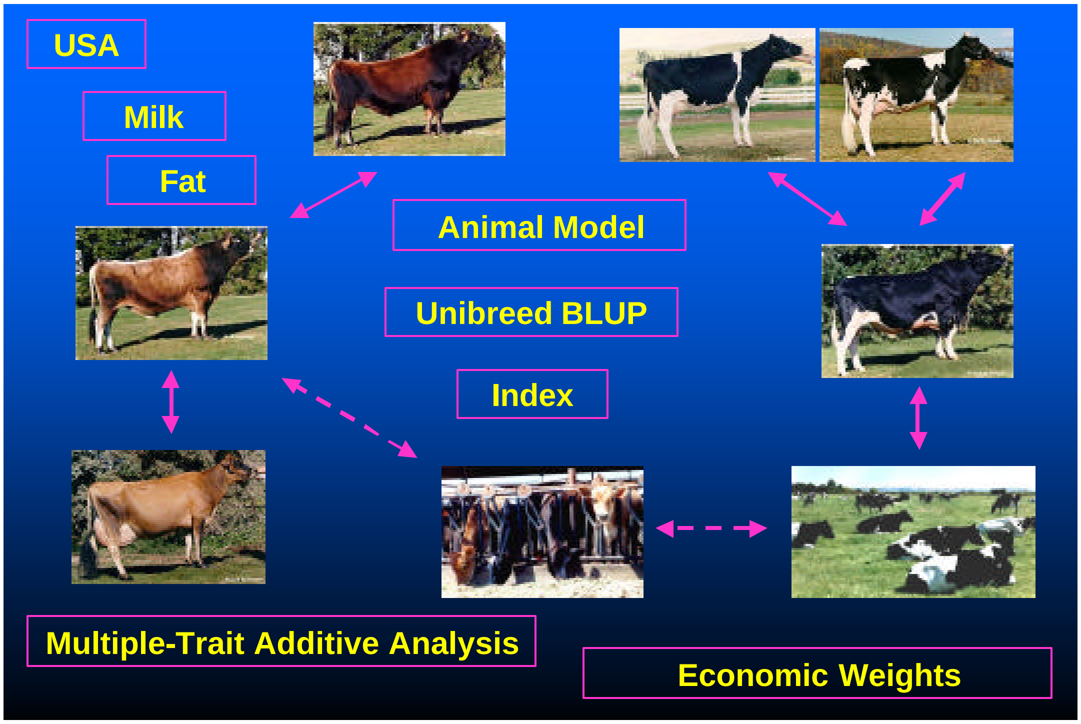


Figure 2. Dairy cattle genetic evaluation strategy in the USA.

(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. However, all dairy breeds (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 imported Holstein semen from USA, Canada, Great Britain, and New Zealand during the last 20 years. The local breed was European Friesian. Sires from all these countries were used to upgrade the local population. Crossbred sires of various Holstein fractions (.25, .50, .75) were also used a parents. The 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 (Figure 3). A sizable and well-kept recording system is in place. This recording system should facilitate the migration to a more current genetic evaluation system.



USA

Milk

Fat

Animal Model

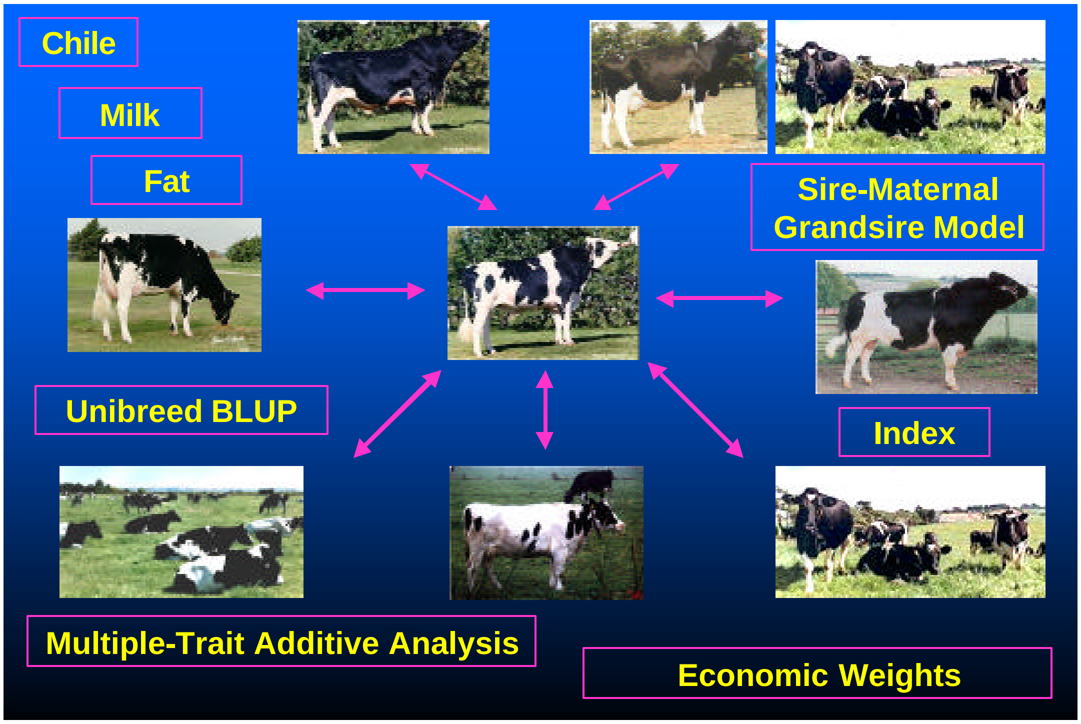
Unibreed BLUP

Index

Multiple-Trait Additive Analysis

Economic Weights

Figure 3. Dairy cattle crossbreeding in the USA.



Chile

Milk

Fat

Sire-Maternal Grandsire Model

Unibreed BLUP

Index

Multiple-Trait Additive Analysis

Economic Weights

Figure 4. Dairy cattle genetic evaluation strategy in Chile.

The situation in Thailand is 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, groups animals according to their Holstein fraction, and 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.

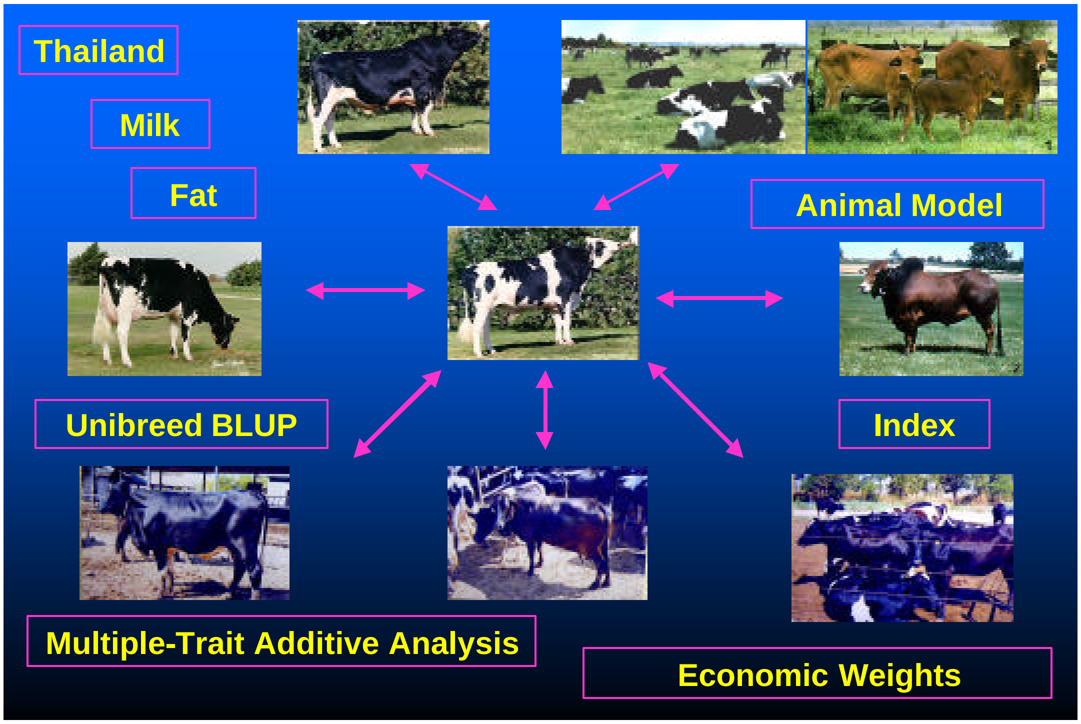
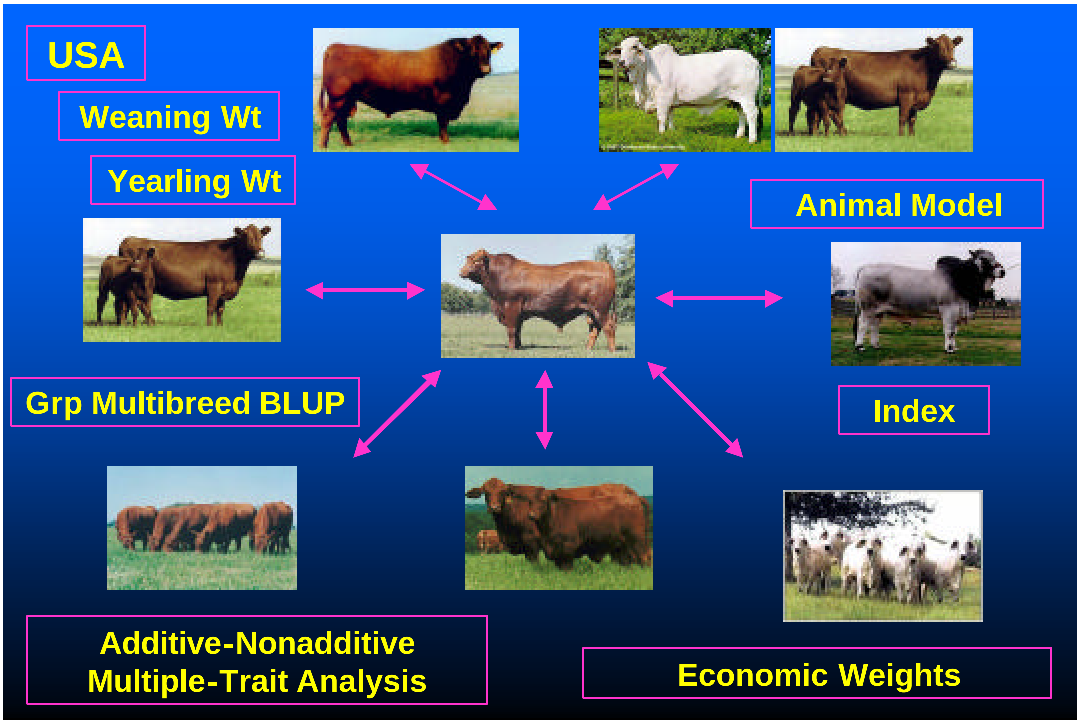


Figure 5. Dairy cattle genetic evaluation strategy in Thailand.

National beef cattle 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). Other universities in the

USA involved in national beef cattle genetic evaluations currently use intrabreed genetic evaluation procedures.



USA

Weaning Wt

Yearling Wt

Animal Model

Grp Multibreed BLUP

Index

Additive-Nonadditive Multiple-Trait Analysis

Economic Weights

Figure 6. Beef cattle genetic evaluation strategy in the USA.

Future Genetic Animal Evaluation Procedures

General Overview of Future National Genetic Evaluation Systems

Changes to national beef and dairy genetic animal evaluation procedures will continue to be evolutionary rather than revolutionary. Field data retrieval is likely to continue to be the most important factor when deciding what traits to collect information for genetic evaluation and for selection purposes. In the near future (5 to 10 years), 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, calpastatin in beef cattle). In the more distant future however, when massively parallel biochemical characterization techniques (biochips or microarrays) 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 dramatically enhanced. However, the random aspect of 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.

Unless there is a major change in the composition of the dairy and beef cattle population structures, genetic evaluation systems in the USA will be similar to 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 on be added to 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). These new traits will probably be composites generated from microarray analyses.

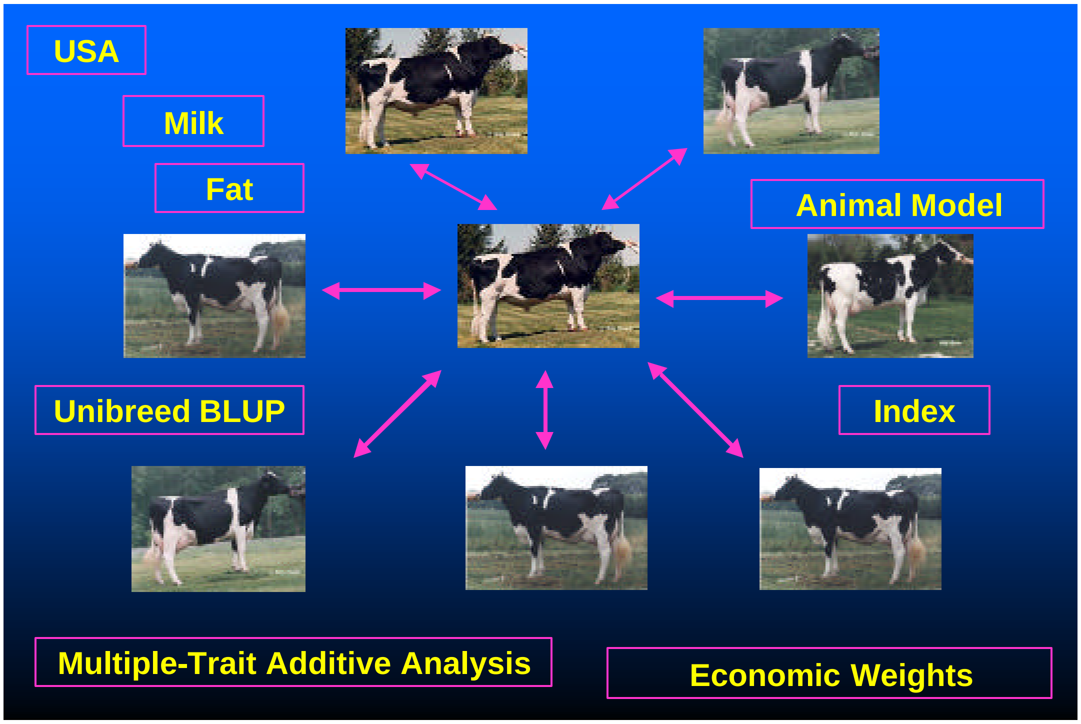
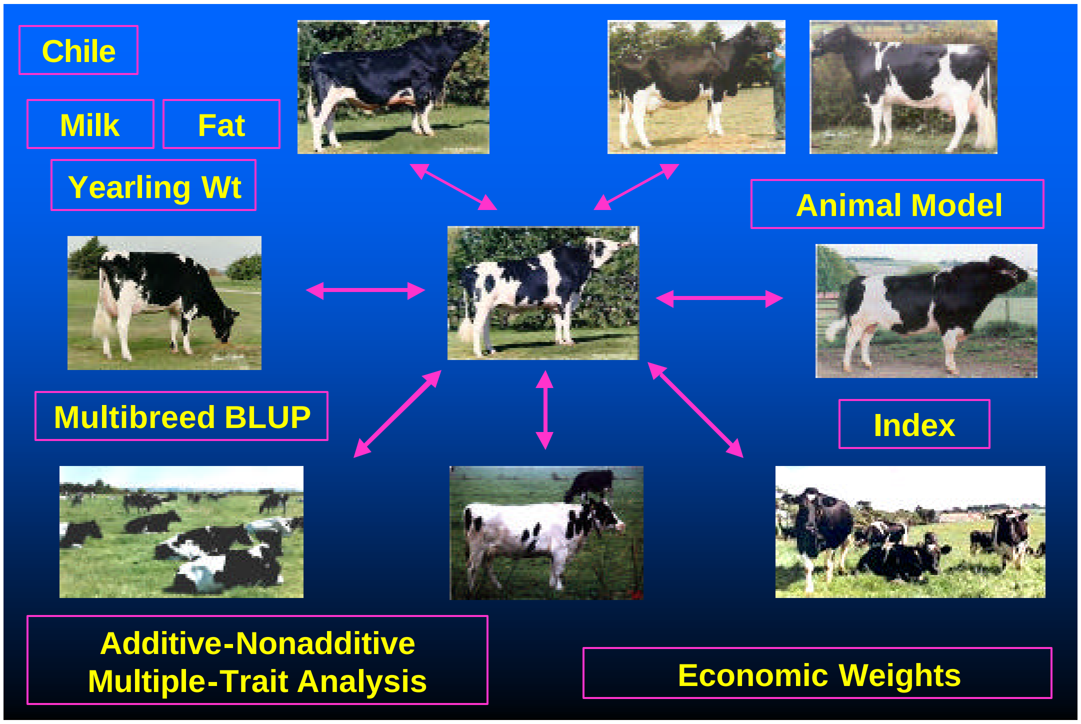


Figure 7. Future dairy cattle genetic evaluation strategy in the USA.

Crossbreeding in the USA is likely to continue to be used as a management tool to control calving difficulties in Holstein heifers. If the level of inbreeding in the Holstein breed continues to increase, using crossbreeding as a means of counteracting the negative effects of inbreeding (Holstein with Brown Swiss and Jersey), is likely to continue to increase in the future. Some dairy cows will also continue to be introduced in beef crossbreeding schemes as a way of increasing milk production or milk quality in beef cows. In such cases, it would be advantageous to incorporate information from straightbred dairy animals in the beef multibreed genetic analysis.

The situation of Holstein-importing countries like Chile and Thailand with a Holstein-*Bos indicus* or Holstein-*Bos taurus* multibreed population is substantially



Chile

Milk

Fat

Yearling Wt

Animal Model

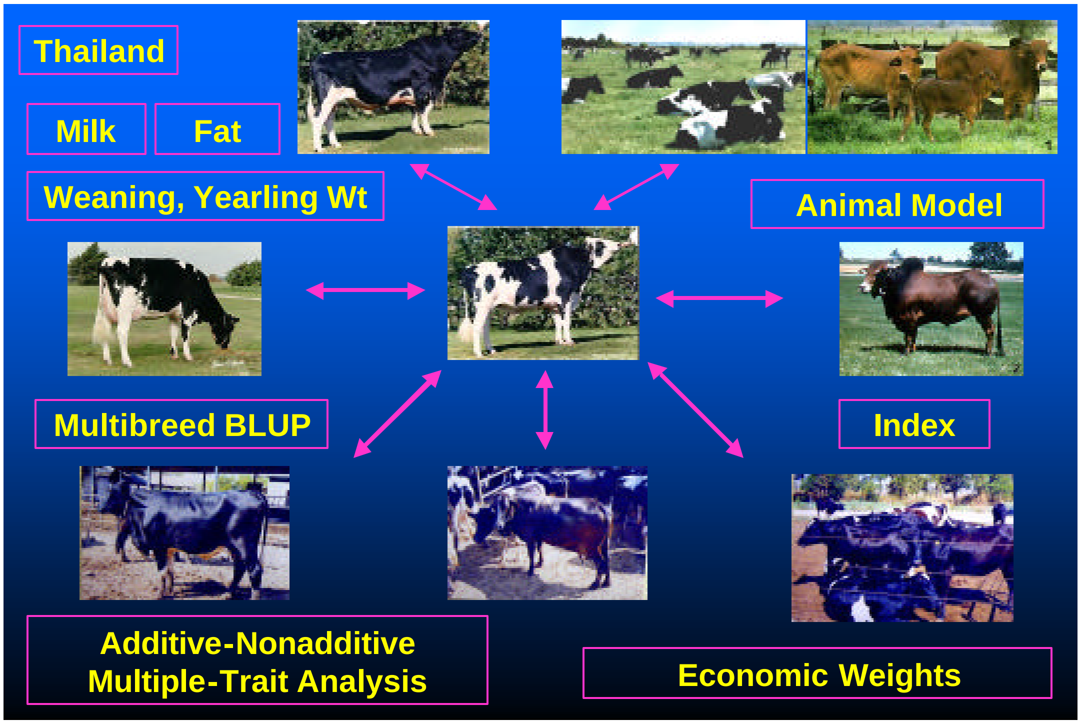
Multibreed BLUP

Index

Additive-Nonadditive
Multiple-Trait Analysis

Economic Weights

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



Thailand

Milk

Fat

Weaning, Yearling Wt

Animal Model

Multibreed BLUP

Index

Additive-Nonadditive
Multiple-Trait Analysis

Economic Weights

Figure 9. Dairy cattle genetic evaluation strategy in Thailand.

different. The main issue is whether the ongoing upgrading mating scheme will 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 Holstein animals are better suited to the local tropical environment. A similar situation may exist in temperate countries like Chile, where some producers may not be willing to adopt the highly controlled management, nutritional, and environmental conditions required by high-producing Holstein cows. As a result of the variety of goals and interests of dairy farmers, it is likely that multibreed populations of some form involving Holstein will exist in these countries, at least in the near future. Under these circumstances, some form of a multibreed animal model will be needed both in Chile (Figure 8) and in Thailand (Figure 9). Unless the beef market changes in Chile, straightbred and crossbred animals will be genetically evaluated only for dairy related traits (traditional and new). In Thailand, however, beef traits are likely to become an integral part of any national genetic animal 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). 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 sequence of these genes will permit the identification of the breed of origin of these alleles.

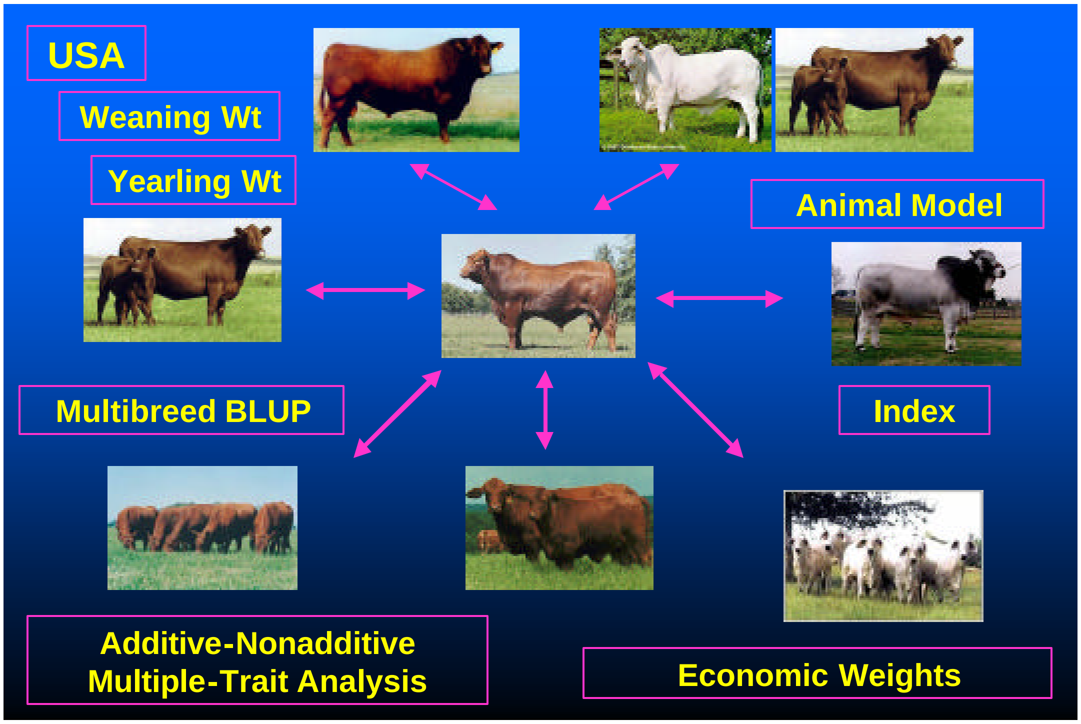


Figure 10. Future beef cattle genetic evaluation strategy in the USA.

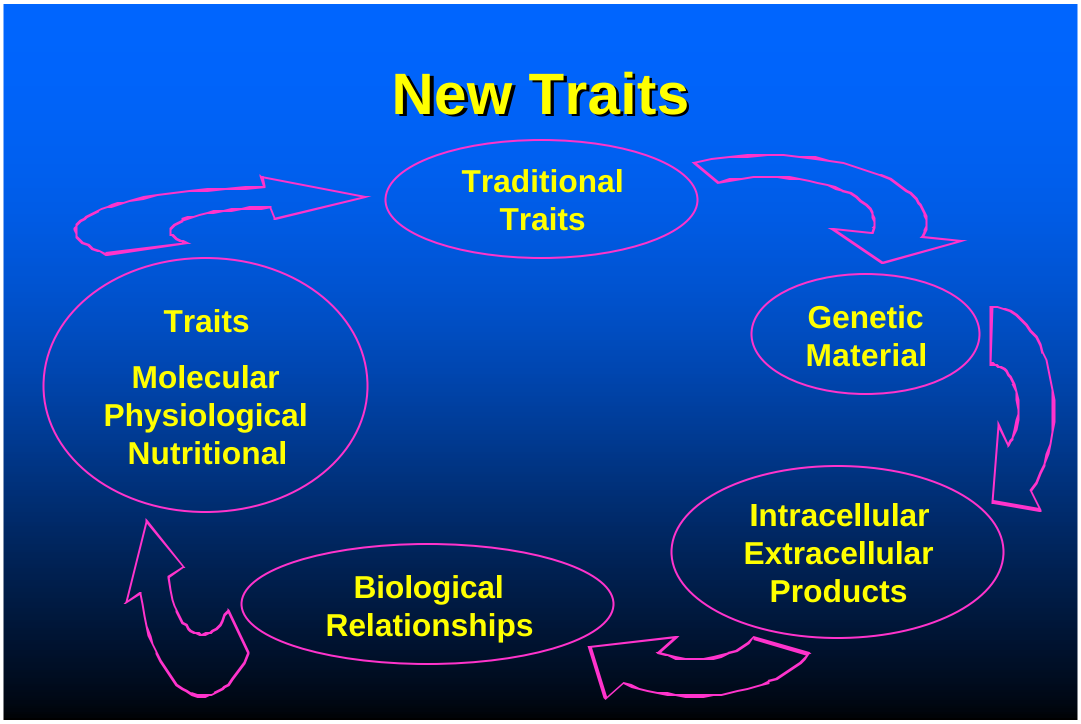
Furthermore, measurement of the level of activity of genes responsible for these subtraits in straightbred and in crossbred animals will permit the generation of dramatically more accurate multibreed genetic predictions and estimations of multibreed genetic and environmental levels of variation. Multibreed information collected by some breed associations (e.g., Simmental) together with genomic and proteomic information generated microarray technology will likely be major contributors to the continued improvement of multibreed genetic evaluations.

Factors Contributing to the Development of New Genetic Evaluations

New Traits. Genomic sequencing of plants and animals 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 related 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.

If biochip technology or similarly massively parallel biochemical characterization technology becomes fully automated, inexpensive, fast, and efficient in the future, it might be possible to characterize the genetic material of *individual animals* for its DNA content, the activity of specific groups of genes whose connection to a specific trait or traits is previously known, evaluate the activity of the products of these genes, and their influence on the activity of other relevant groups of genes, all of it 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 animal (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).

New Models. With the advent of new, biologically more accurate subtraits (i.e., traits responsible for part of a traditional economic trait such as milk yield), genetic evaluation models will need to be revised and adapted to account for interrelationships among all relevant subtraits. New genetic-statistical models will probably make substantially larger use of biological models to account for the increased degree of accuracy brought by the new biological information. However, the level of complexity of biological models will probably require a systems approach and enormous computing resources that will severely limit its usability and make it impractical for repeated genetic predictions. Thus, a compromise between biological accuracy and computational feasibility will have to be reached. The more accurate future genetic evaluation models become the more systemic they are likely to become, with modules that range from heavily biological to heavily statistical. Both linear and nonlinear compromises are likely to coexist in such models (Figure 12).



New Traits

Traditional Traits

Genetic Material

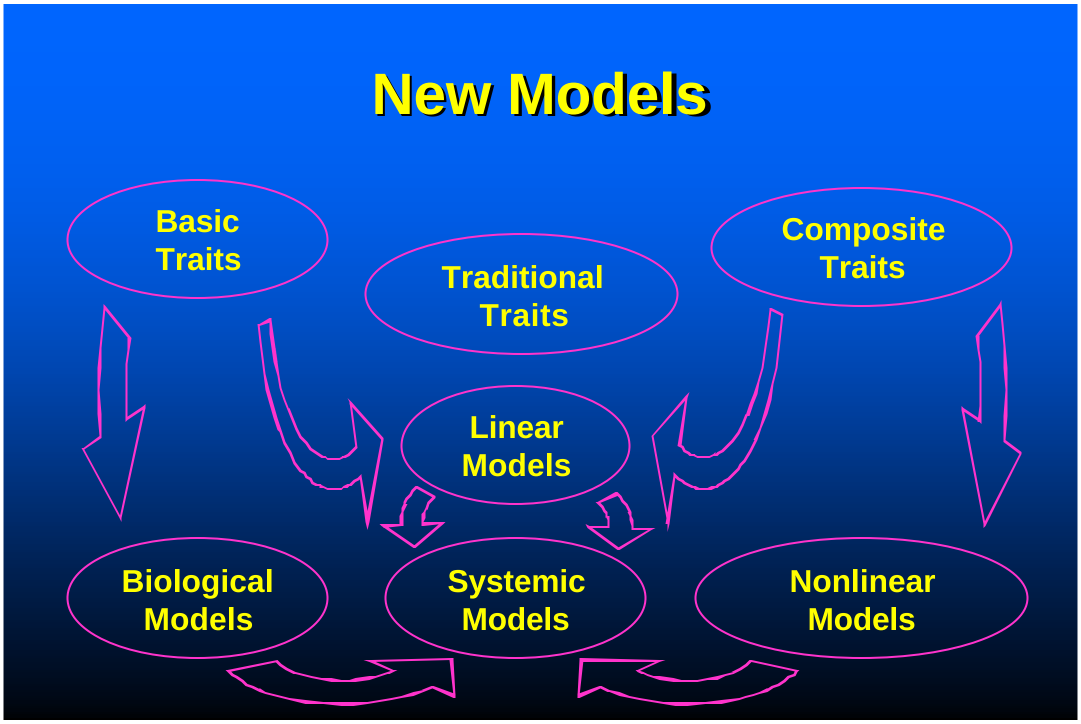
Intracellular Extracellular Products

Biological Relationships

Traits

Molecular
Physiological
Nutritional

Figure 11. New traits for future genetic evaluations



New Models

Basic Traits

Traditional Traits

Composite Traits

Linear Models

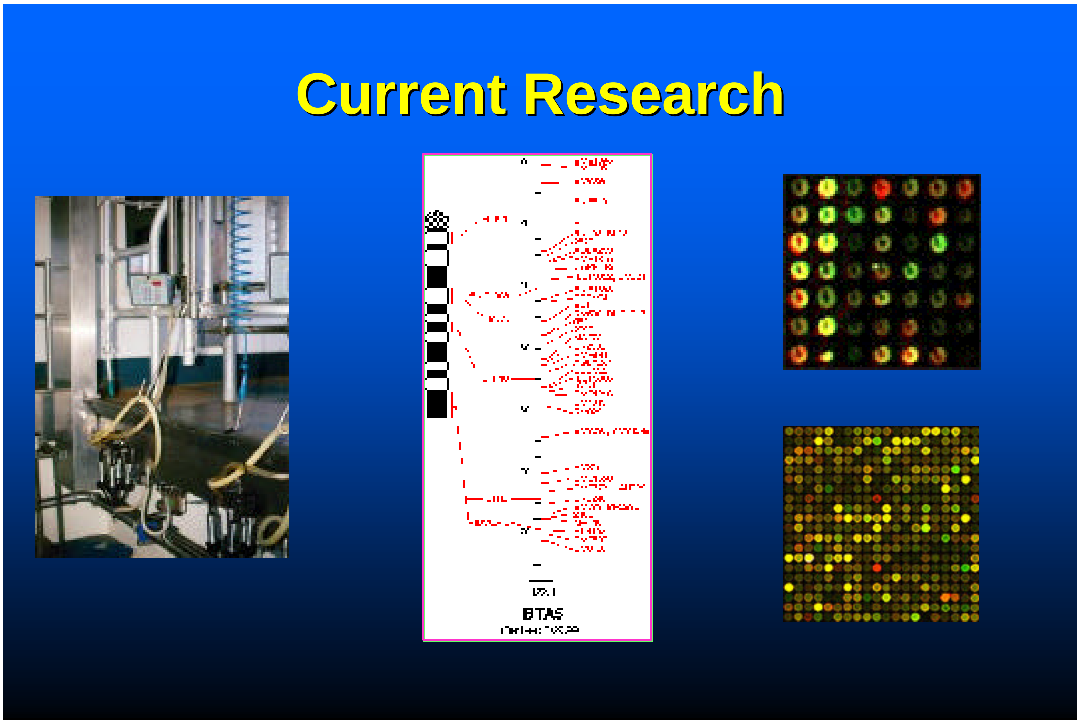
Biological Models

Systemic Models

Nonlinear Models

Figure 12. New models for future genetic evaluations

Current Genetics Research and Mainstream Adoption of New Sampling Technologies. Currently the majority of the data collected by beef and dairy 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, this type of research will have little impact on traits determined by a large number of alleles. Quantitative biotechnological systems (biochips) hold a much larger promise for the characterization of quantitative traits (Figure 13).



Current Research

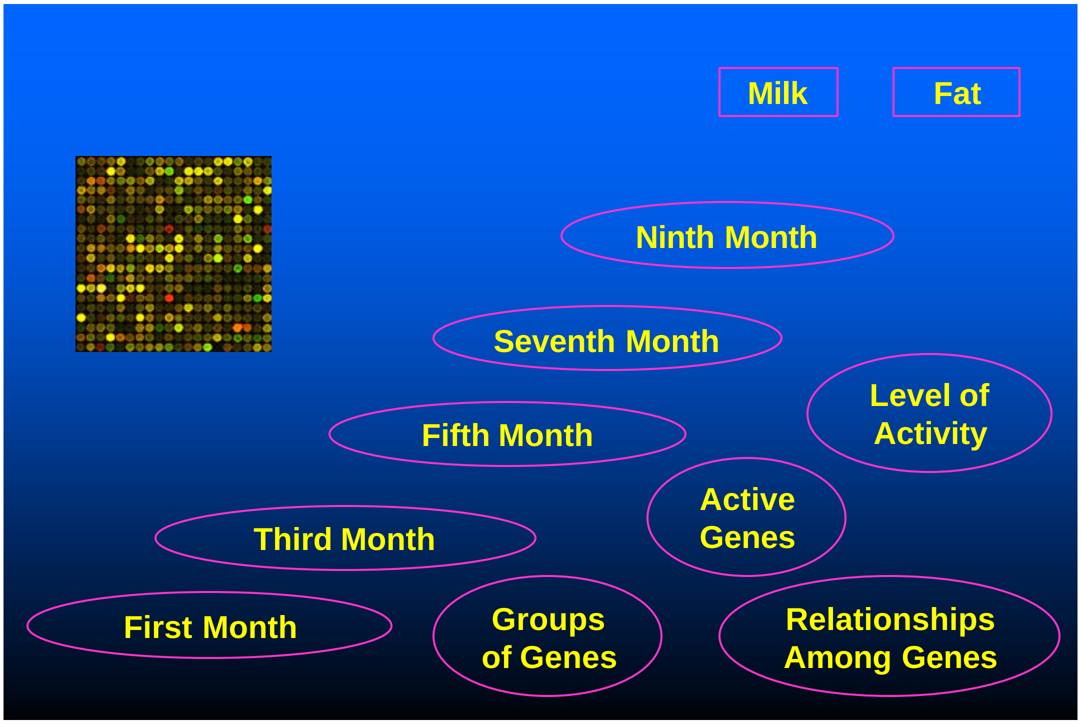
Figure 13. Current research on new sampling technologies

Adoption of biochip technologies for the characterization of individual animals on a large scale will help characterize unibreed and multibreed populations to a substantially better degree than possible today. Measurements of internal products of subtraits will enable prediction for components of a traditional economic trait, substantially increasing the power and accuracy of the selection process. In addition, mating animals to produce progeny with specific characteristics will be greatly enhanced, both within a 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 dramatically improve the explanation (causality) of genetic associations among traits, the generation of new subtraits, and our capability for generating increasingly more complete (and complex) genetic-statistical models (Figure 14).

New Groups of Traits

Figure 14. New subtraits measured by biological technologies



Milk

Fat

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 two traditional economic traits based on gene activity

As an example of genetic-statistical modeling possibilities of the new biological information, consider the following case. Suppose that biochips 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 with 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). 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), 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.

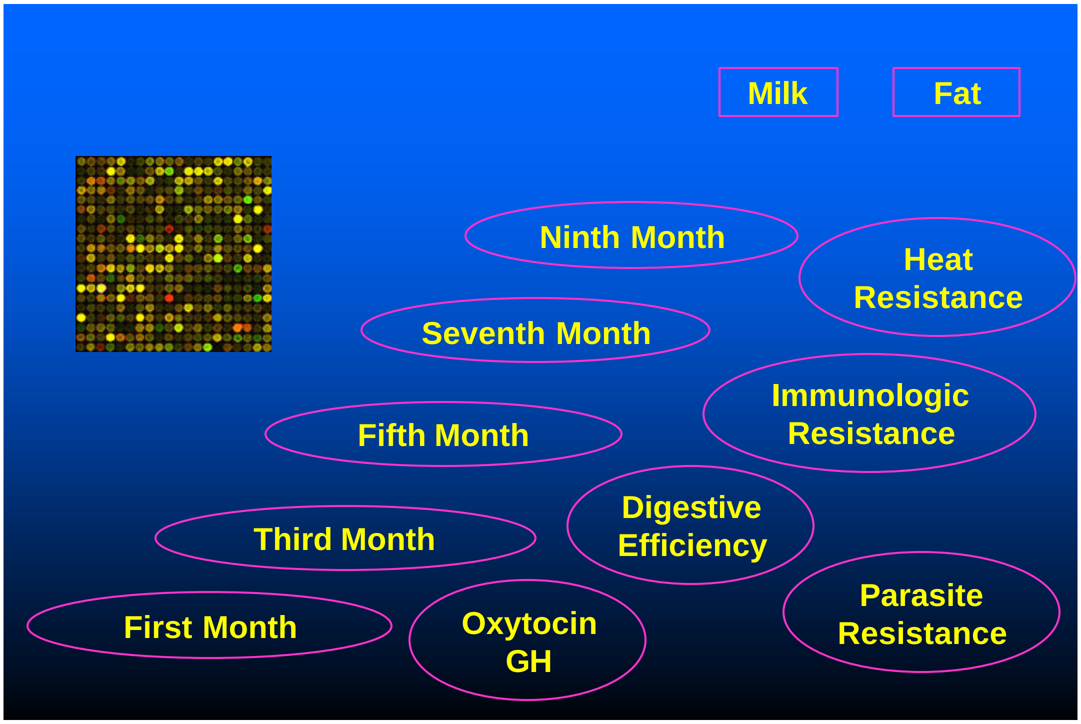
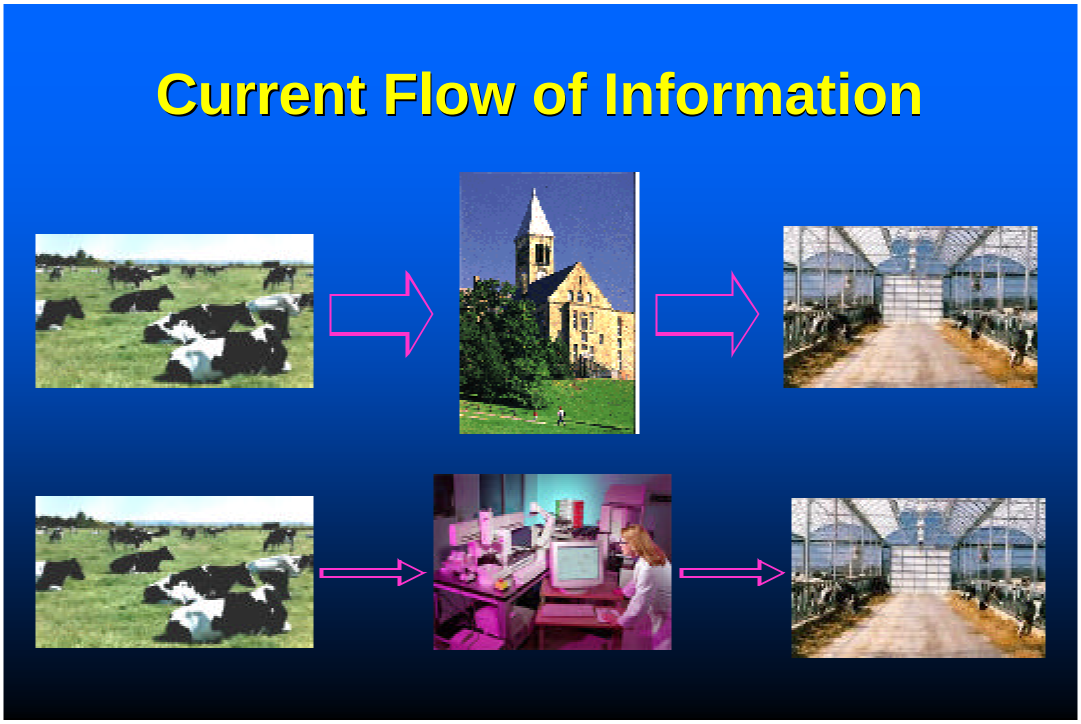


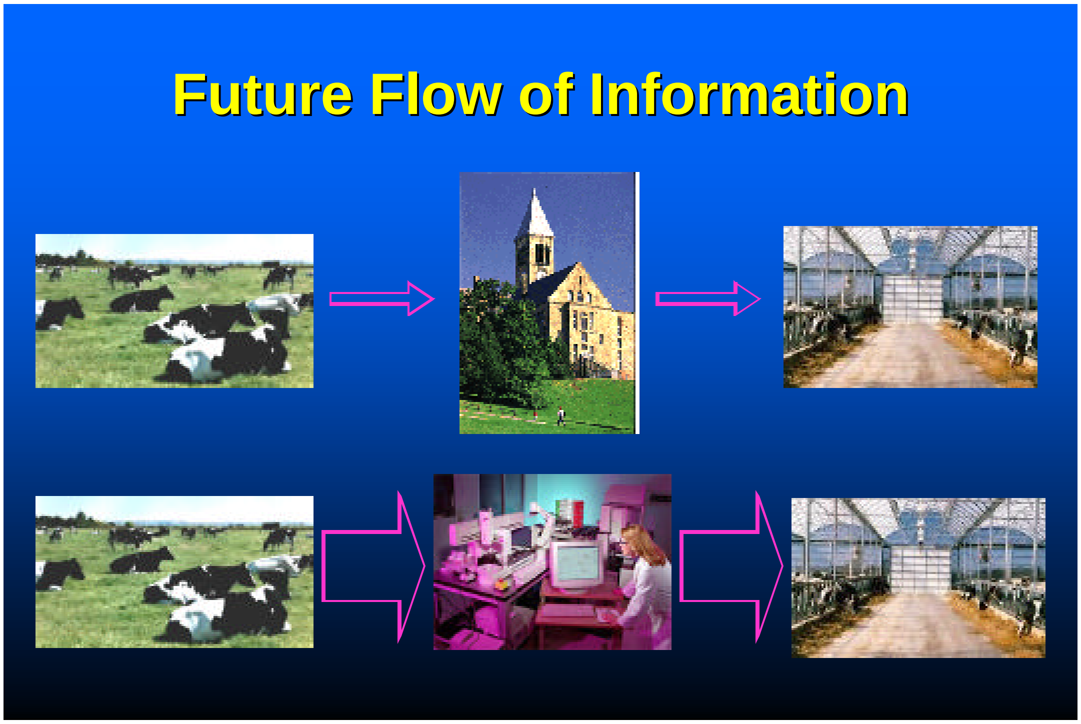
Figure 16. Subtraits for two traditional economic traits based on gene function

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 unimpeded 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, stored in breed associations, genetic evaluations obtained at universities and government institutions, and finally producers received predictions, animal rankings, genetic trends, and other relevant 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).



Current Flow of Information

Figure 17. Current flow of information.



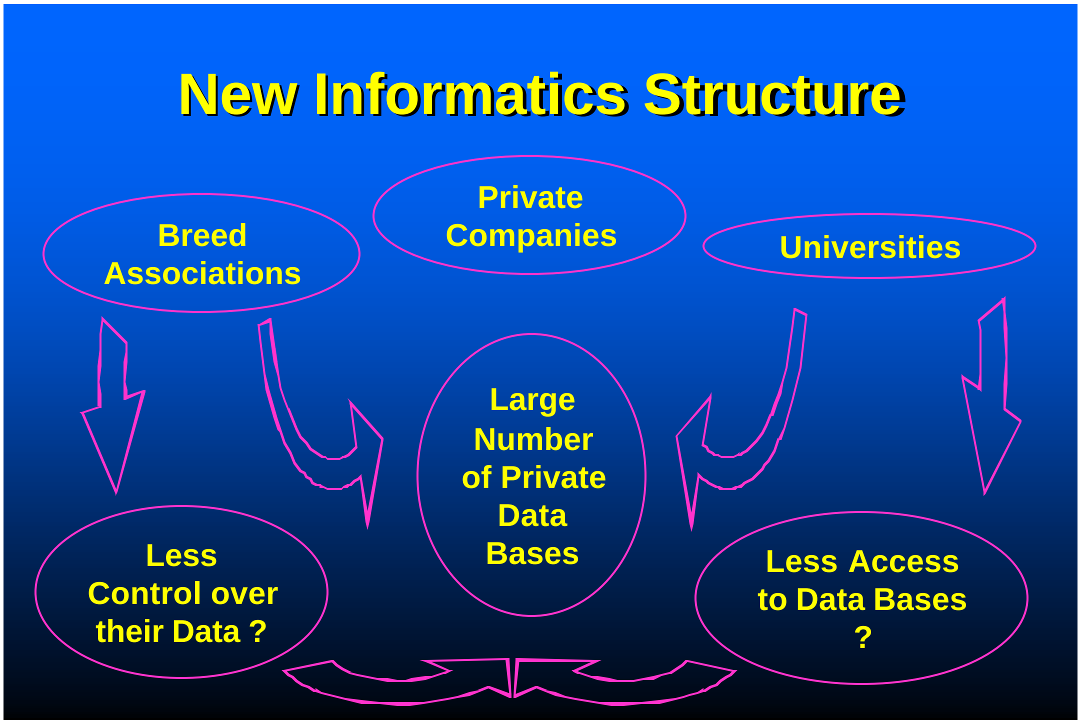
Future Flow of Information

Figure 18. Future flow of information.

The current form of the flow of data for genetic animal evaluation may change drastically in the future if biological analytical techniques become fast, efficient, and affordable. If this happens, and 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 this scenario became 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 numerical analysis of the tissue samples.

New Informatics and New Research Structures. If the incipient 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. Again, questions to be resolved here is who will own the data, the tissues sampled, and the products generated in the laboratory analysis ?, the producer ?, the private company ?, co-ownership ? These issues will need to be satisfactorily resolved in the context of this newly generated informatics structure if cattlemen are to receive all the benefits from their investment in these new sources of information (Figure 19).



New Informatics Structure

Breed Associations

Private Companies

Universities

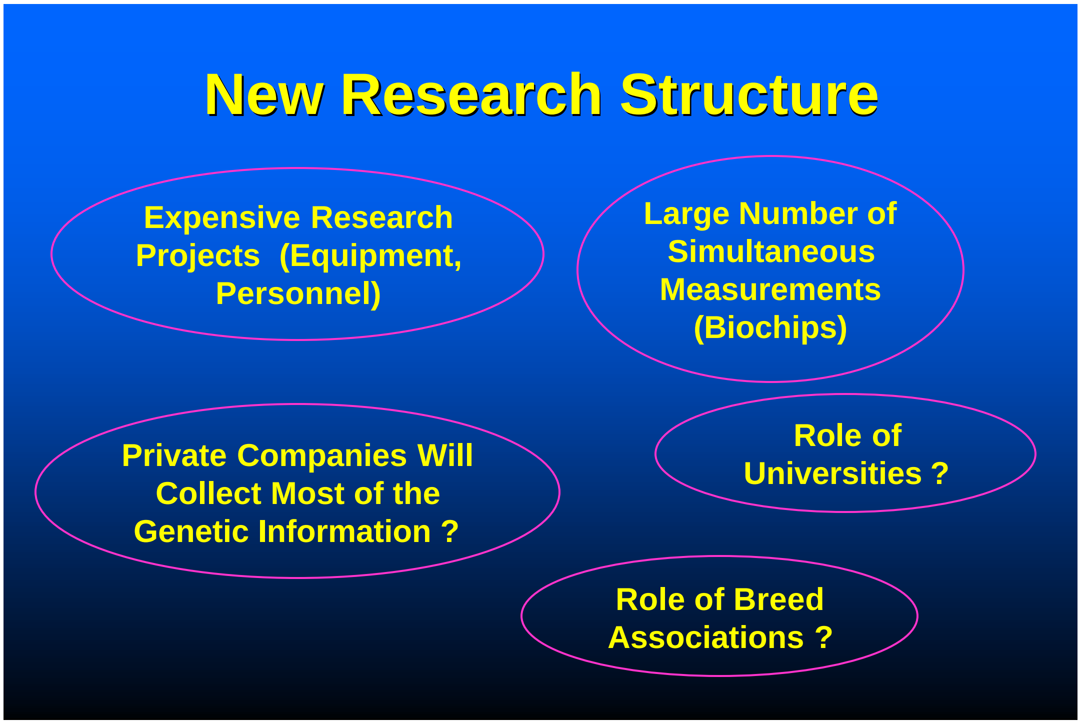
Large Number of Private Data Bases

Less Control over their Data ?

Less Access to Data Bases ?

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, will universities have access to them for research purposes or to use this information in national cattle genetic evaluation systems (Figure 20) ?, or, will private companies also be involved in genetic evaluation systems and procedures for the new biological traits, and provide them to producers as an additional service ?



New Research Structure

Expensive Research Projects (Equipment, Personnel)

Large Number of Simultaneous Measurements (Biochips)

Private Companies Will Collect Most of the Genetic Information ?

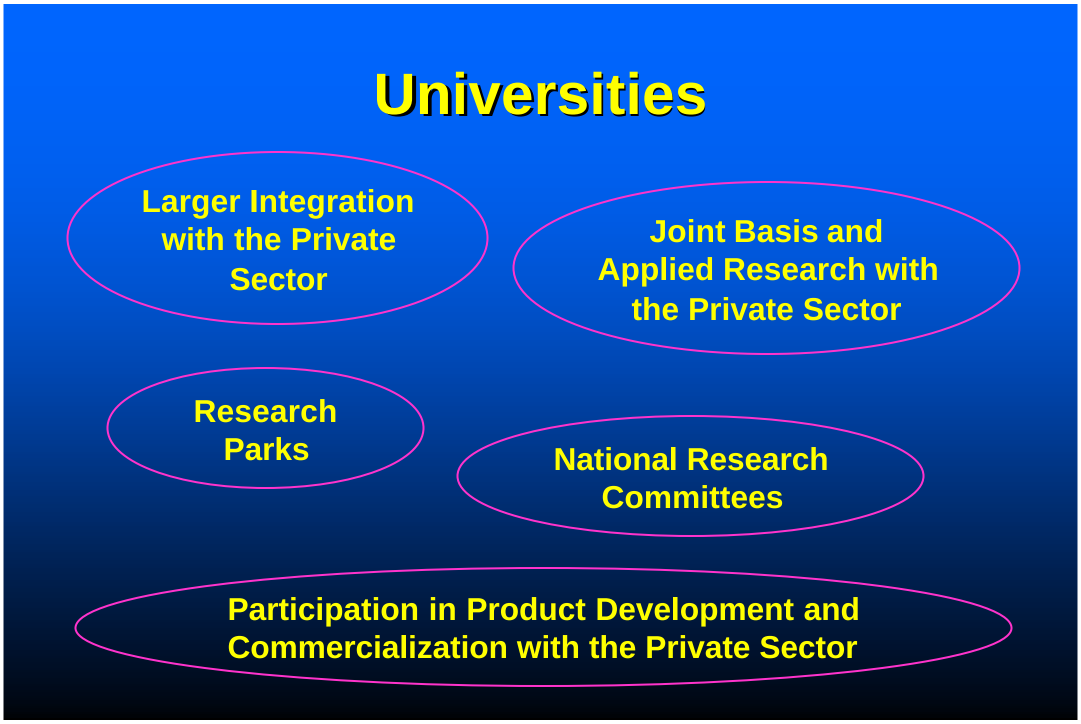
Role of Universities ?

Role of Breed Associations ?

Figure 20. Future field research structure.

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

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.



Universities

Larger Integration with the Private Sector

Joint Basis and Applied Research with the Private Sector

Research Parks

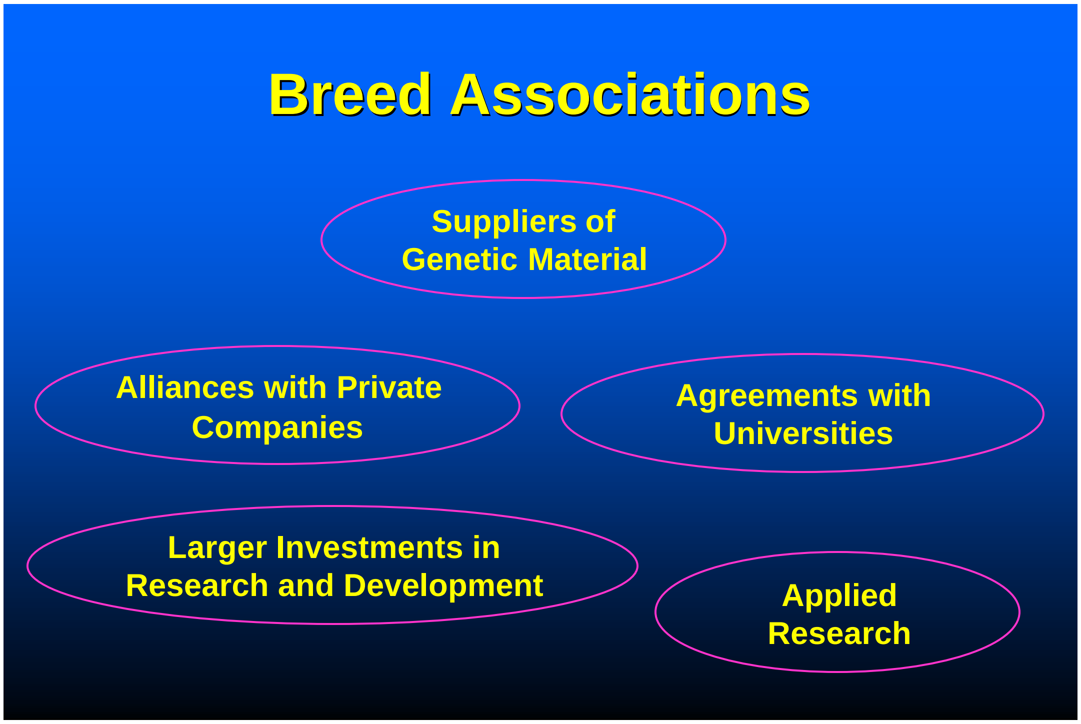
National Research Committees

Participation in Product Development and Commercialization with the Private Sector

Figure 21. Future trends in university activities.

Breed associations are likely to continue to be the main cattlemen organization in the USA in the future. As such, it will probably 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 ends breed associations will probably need to make substantially larger investments in research and development than the current levels.

Breed association will also probably continue to establish agreements with university researchers, particularly those working in 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.



Breed Associations

Suppliers of Genetic Material

Alliances with Private Companies

Agreements with Universities

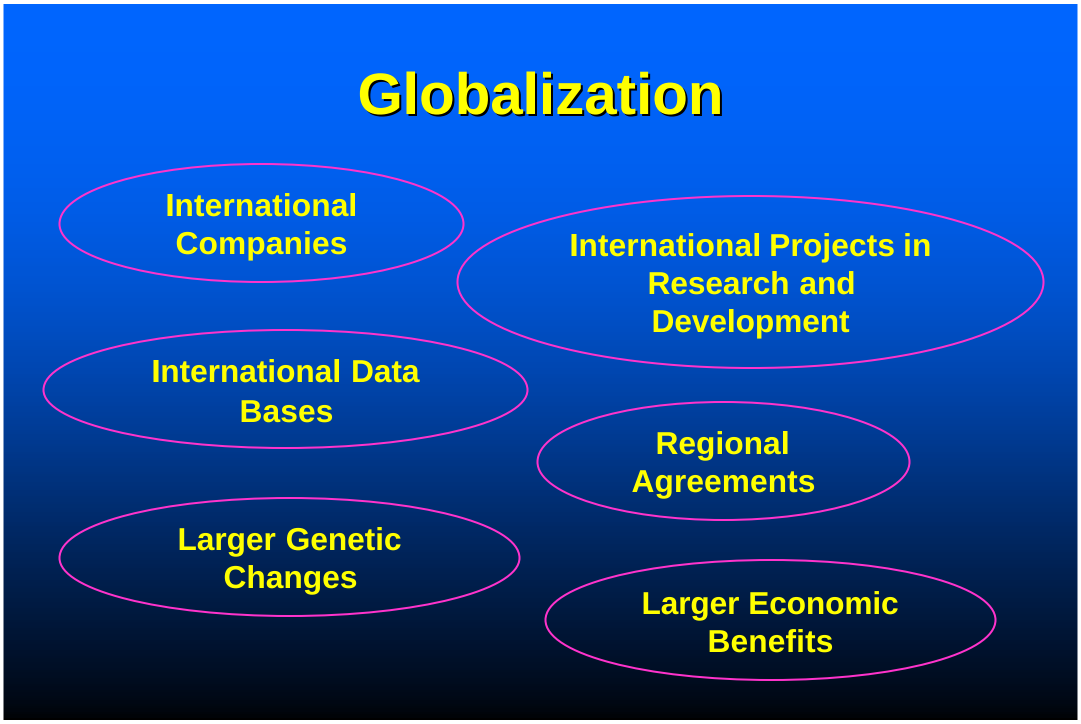
Larger Investments in Research and Development

Applied Research

Figure 22. Future trends in breed association activities.

Globalization. Collaboration among researchers across countries and the development of international companies have increased dramatically in number in recent years. These globalization of research, development, and business practices has been greatly facilitated by enormous developments in communication, particularly the Internet. The pace of development of communication and information technologies will continue to accelerate in the future. This in turn will 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. 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. 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 represent, larger genetic trends, and potentially larger economic benefits might be achieved (Figure 23). 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.



Globalization

International Companies

International Projects in Research and Development

International Data Bases

Regional Agreements

Larger Genetic Changes

Larger Economic Benefits

Figure 23. Effect of globalization on genetic evaluation

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 because of 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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