

Some reviews that may be of interest:

Abstracts only are reproduced here.

Ordered by publication date, most recent first.

Title: Application of DNA markers in animal industries

Author(s): [Jeon JT](#), [Lee JH](#), [Kim KS](#), [Park CK](#), [Oh SJ](#)

Source: [AUSTRALIAN JOURNAL OF EXPERIMENTAL AGRICULTURE 46 \(2\): 173-182 2006](#)

Document Type: Article

Language: English

Abstract: The current animal industry is both technology-intensive and globalised. Efficient molecular tools, such as DNA markers, are in demand to strengthen competitive power by maximising the improvement of livestock and obtaining the trust of customers by the verification of product origins. This review describes the present techniques applying DNA markers in the animal industry, with a focus on beef cattle and pigs. Preliminary data from an individual traceability assay for Hanwoo (Korean cattle) using 20 microsatellite markers is described. The potential uses of the assay are demonstrated for several key markers of different traits: for the porcine stress syndrome gene using the RYR mutation; for acid meat using the PRKAG3 mutation; for intramuscular fat using the FABP3 mutation and for fixing the Dominant white allele using KIT duplication. In addition, a possible strategy is suggested to discriminate between pig breeds using mutations of KIT, MC1R, ND2 and the 11-bp insertion in the D-loop of mitochondrial DNA. The industrial application of DNA techniques is limited at present, however, it is expected that DNA markers originating from trait genes, especially those of low-heritability and difficult-to-measure traits, may contribute to maximising the improvement of the major economic traits of animals in the future.

Author Keywords: DNA markers; DNA techniques; industrial application; traceability

KeyWords Plus: INTRAMUSCULAR FAT-CONTENT; BINDING PROTEIN GENE; DOMINANT WHITE COLOR; MEAT QUALITY TRAITS; MYOSTATIN GENE; BELGIAN BLUE; DOMESTIC PIG; LITTER SIZE; CATTLE; MUTATION

Addresses: Oh SJ (reprint author), Rural Dev Adm, Natl Livestock Res Inst, Dept Anim Genom & Bioinformat, Suwon 441250 South Korea

Title: Successes and failures of small ruminant breeding programmes in the tropics: a review

Author(s): [Kosgey IS](#), [Baker RL](#), [Udo HMJ](#), [Van Arendonk JAM](#)

Source: [SMALL RUMINANT RESEARCH 61 \(1\): 13-28 JAN 2006](#)

Document Type: Review

Language: English

Abstract: Despite the large numbers and importance of adapted indigenous sheep and goats in the tropics, information on sustainable conventional breeding programmes for them is scarce and often unavailable. This paper reviews within-breed selection strategies for indigenous small ruminants in the tropics, highlighting aspects determining their success or failure. The aim is to better understand opportunities for genetic improvement of small ruminants by the resource-poor farmers in traditional smallholder and pastoral farming systems. Dismal performance of programmes involving breed substitution of exotics for indigenous breeds and crossbreeding with temperate breeds have stimulated a recent re-orientation of breeding programmes in tropical countries to utilize indigenous breeds, and most programmes are incipient. The success rate of some breeding programmes involving native breeds is encouraging. Definition of comprehensive breeding objectives incorporating the specific, immediate, and long-term social and economic circumstances of the target group as well as ecological constraints was found lacking in some projects that failed. To achieve success, it is necessary to look at the production system holistically, and involve the producer at every stage in the planning and operation of the breeding programme, integrating traditional behaviour and values. (c) 2005 Elsevier B.V. All rights reserved.

Author Keywords: small ruminants; breeding programmes; tropics; review

KeyWords Plus: ANIMAL GENETIC-RESOURCES; SUBHUMID TROPICS; DJALLONKE SHEEP; LIVESTOCK; GOATS; MANAGEMENT; RESISTANCE; SELECTION; GAMBIA; EWES

Addresses: Van Arendonk JAM (reprint author), Egerton Univ, Dept Anim Sci, POB 536, Njoro 20107 Kenya

Title: Discovery, validation and delivery of DNA markers

Author(s): [Nicholas FW](#)

Source: [AUSTRALIAN JOURNAL OF EXPERIMENTAL AGRICULTURE 46 \(2\): 155-158 2006](#)

Document Type: Article

Language: English

Abstract: Early attempts at finding markers for quantitative trait loci (QTL) in the 1950s and 1960s involved searching for associations between production traits and polymorphisms at loci encoding blood groups, milk proteins and blood proteins. Overall, this work identified many small and/or non-significant associations, insufficient to warrant their use in marker-assisted selection. It was not until the discovery of microsatellites in the early 1990s that a really useful form of DNA marker became available. By the mid-1990s, linkage maps comprising mainly microsatellites covered most regions of most chromosomes of the cow, and it was then possible to hunt for QTL using a mapping approach first proposed in *Drosophila* back in 1961. Fine-mapping of QTL has eventually resulted in the identification of markers in or near particular genes. Some of these markers have been commercialised. In most cases, the actual causative quantitative trait nucleotide (QTN) remains elusive. The recent development of technologies for large-scale detection and genotyping for single nucleotide polymorphisms (SNPs) and for placing the entire genome on a chip have opened up exciting possibilities for the future: geneticists should begin contemplating how best to use SNP and genome chips, which will surely become a reality. Just as one must estimate genetic and phenotypic correlations for every new quantitative trait that is introduced into a genetic evaluation scheme, so must the correlated effects of new DNA markers be evaluated before their commercial use. Researchers and their funders must resist the temptation to cut corners in getting markers to market.

KeyWords Plus: GENETIC-LINKAGE MAP; DAIRY-CATTLE; BOVINE; POLYMORPHISMS; GENOME; LOCI

Addresses: Nicholas FW (reprint author), Univ Sydney, Fac Vet Sci, Sydney, NSW 2006 Australia

Title: Use of DNA technologies for the conservation of animal genetic resources: A review

Author(s): [Talle SB](#), [Chenyabuga WS](#), [Fimland E](#), [Syrstad O](#), [Meuwissen T](#), [Klungland H](#)

Source: [ACTA AGRICULTURAE SCANDINAVICA SECTION A-ANIMAL SCIENCE 55 \(1\): 1-8 MAY 2005](#)

Document Type: Review

Language: English

Abstract: Awareness of the value of genetic resources has stimulated the study of the genetic diversity of indigenous breeds, which can be characterized using phenotypic and genotypic information to prioritize for conservation. The observed genetic variation of the population is influenced by the biology and circumstances of the individuals through which it passes, including migration, population size and selection. Therefore, selection of appropriate genetic analysis is vital to the success of diversity studies. Neutral and non-neutral genetic markers are both used to characterize breeds for conservation purposes; selection depends on the availability, applicability and objectives of the study, as markers are highly variable in their information content. The application of DNA based markers in diversity studies is valuable for filling gaps in documentation and confirming its accuracy. However, selection of breeds for conservation should also consider more criteria including degree of endangerment, traits of economic or scientific importance, ecological, historical and cultural values.

Author Keywords: genetic diversity; livestock resources; molecular technology; selection criteria

KeyWords Plus: EUROPEAN CATTLE BREEDS; POPULATION-STRUCTURE; MICROSATELLITE LOCI; PHYLOGENETIC TREES; MOLECULAR MARKERS; FREQUENCY DATA; DIVERSITY; DISTANCES; EVOLUTIONARY; INDIVIDUALS

Addresses: Talle SB (reprint author), Norwegian Univ Life Sci, Dept Anim & Aquacultural Sci, Box 5003, NO-1432 As Norway

Title: Inbreeding - lessons from animal breeding, evolutionary biology and conservation genetics

Author(s): [Kristensen TN](#), [Sorensen AC](#)

Source: [ANIMAL SCIENCE 80: 121-133 Part 2 APR 2005](#)

Document Type: Review

Language: English

Abstract: Increased rates of inbreeding are one side effect of breeding programmes designed to give genetic progress for traits of economic importance in livestock. Inbreeding leads to inbreeding depression for traits showing dominance, and will ultimately lead to a decrease in genetic variance within populations. Here we review theoretical and experimental literature from animal breeding, evolutionary biology and conservation genetics on the consequences of inbreeding in terms of trait means and genetic and environmental variance components. The genetic background for these effects is presented and the experimental literature interpreted in relation to them. Furthermore, purging of deleterious alleles and the variable nature of effects of inbreeding on populations are discussed. Based on the literature, we conclude that inbreeding in animal breeding must be controlled very efficiently to maintain long-term sustainable livestock production in the future. The tools to do this efficiently exist, and much can be learnt on inbreeding from the literature in fields only distantly related to animal breeding.

Author Keywords: animal breeding; genetic variance; inbreeding; sustainability

KeyWords Plus: DROSOPHILA-MELANOGASTER; POPULATION BOTTLENECKS; ARTIFICIAL SELECTION; INBRED LINES; ENVIRONMENTAL-STRESS; PHENOTYPIC VARIANCE; COVARIANCE-MATRIX; ADDITIVE VARIANCE; FOUNDER EVENTS; DAIRY-CATTLE

Addresses: Sorensen AC (reprint author), Danish Inst Agr Sci, Dept Genet & Biotechnol, POB 50, DK-8830 Tjele Denmark

Title: Biotechnologies and their potential impact on animal breeding and production: a review

Author(s): [Raadsma HW](#), [Tammen I](#)

Source: [AUSTRALIAN JOURNAL OF EXPERIMENTAL AGRICULTURE 45 \(7-8\): 1021-1032 2005](#)

Document Type: Article

Language: English

Abstract: Recent developments in mammalian biotechnologies that have been driven largely by medical bioscience, offer new opportunities for livestock industries. Major impacts may be expected in the area of reproductive, genomic and cell technologies that could lead to improved animal breeding strategies or animal production and health applications. In particular, the use of advanced reproductive technologies to select animals at very early stages of life, possibly as early as a 4-day embryo, combined with genomic technologies to predict genetic merit, could lead to significantly increased rates of genetic gain. Such advanced animal breeding technologies will depend strongly on conventional quantitative genetic evaluation systems. Genetic modification in the near future will offer targeted animal improvement options for control of health and production. Long-term impact of genetic modification on animal production systems will depend on consumer acceptance, and its perception by social, environmental and animal welfare groups. However, the opportunity to develop animal products beyond conventional boundaries may prove too attractive with genetic modification eventually being accepted as the norm. The naturally synergistic effect of ex vivo transgenic modification of embryo stem cell or somatic cell lines, combined with nuclear transfer present potentially high value propositions for development of novel and high value products. Opportunities for the mass production of elite males for use in extensive animal production systems will be possible.

KeyWords Plus: QUANTITATIVE TRAIT LOCI; OF-THE-ART; GENETICALLY-MODIFIED FOODS; GERM-CELL TRANSPLANTATION; DAIRY-CATTLE; GENE-THERAPY; IN-VITRO; ARTIFICIAL-INSEMINATION; NUCLEAR TRANSFER; GM FOODS

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Title: Applications of linear models in animal breeding - A review

Author(s): [Singh B](#)

Source: [INDIAN JOURNAL OF ANIMAL SCIENCES 75 \(8\): 999-1007 AUG 2005](#)

Document Type: Review

Language: English

Abstract: Brief descriptions of linear models having applications in animal breeding are given. Methods for estimation of fixed effects, prediction of breeding values and estimation of variance components from linear models in animal breeding are reviewed. Non-negative estimates and optimal designs for estimating variance components are briefly discussed.

Author Keywords: BLUP; breeding value; linear models; variance components

KeyWords Plus: VARIANCE COMPONENT ESTIMATORS; RESTRICTED MAXIMUM-LIKELIHOOD; UNBIASED PREDICTION; MIXED MODELS; CATEGORICAL DATA; UNEQUAL NUMBERS; VALUES; CLASSIFICATIONS; DESIGNS

Addresses: Singh B (reprint author), Indian Vet Res Inst, Div Livestock Econ & Stat, Izatnagar 243122 Uttar Pradesh India

Title: Sustainability in farm animal breeding: a review

Author(s): [Gamborg C](#), [Sandoe P](#)

Source: [LIVESTOCK PRODUCTION SCIENCE 92 \(3\): 221-231 MAR 2005](#)

Document Type: Article

Language: English

Abstract: The paper examines the notion of sustainable farm animal breeding. A brief explanation of why sustainability matters is offered first. After this, the historical development of the concept of sustainability is charted. The authors then turn to review published literature with a bearing on sustainable farm animal breeding. Little has been written directly on the subject: the requirements of sustainable farm animal breeding await serious clarification. The paper looks at SEFABAR (Sustainable European Farm Animal Breeding and Reproduction), a project designed to identify sustainable practices in farm animal breeding which ran for nearly 3 years from 2000. In this project commercial breeders and breeding scientists were required, with the professional assistance of bioethicists, economists, social scientists and NGO representatives, to develop a definition of sustainable farm animal breeding. The authors describe initial attempts to carry out this task. They then describe a general method of building a definition of sustainability-the so-called concern-criteria-indicators method-that was used in SEFABAR to good effect. They note the progress that was made once this method was introduced. Finally, the importance of communication is explained. The authors suggest that the concept of sustainability can be effectively used to organise and facilitate dialogue between stakeholders, including the breeding industry and society as a whole. (c) 2004 Elsevier B.V. All rights reserved.

Author Keywords: farm animal breeding; communication; criteria; ethics; stakeholders; sustainability

KeyWords Plus: PRODUCTION SYSTEMS; WELFARE; AGRICULTURE; MANAGEMENT; LIVESTOCK; GOALS

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Title: An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds

Author(s): [Ollivier L](#), [Alderson L](#), [Gandini GC](#), [Foulley JL](#), [Haley CS](#), [Joosten R](#), [Rattink AP](#), [Harlizius B](#), [Groenen MAM](#), [Amigues Y](#), [Boscher MY](#), [Russell G](#), [Law A](#), [Davoli R](#), [Russo V](#), [Matassino D](#), [Desautes C](#), [Fimland E](#), [Bagga M](#), [Delgado JV](#), [Vega-Pla JL](#), [Martinez AM](#), [Ramos AM](#), [Glodek P](#), [Meyer JN](#), [Plastow GS](#), [Siggens KW](#), [Archibald AL](#), [Milan D](#), [San Cristobal M](#), [Laval G](#), [Hammond K](#), [Cardellino R](#), [Chevalet C](#)

Source: [CONSERVATION GENETICS 6 \(5\): 729-741 SEP 2005](#)

Document Type: Article

Language: English

Abstract: Genetic diversity within and between breeds (and lines) of pigs was investigated. The sample comprised 68 European domestic breeds (and lines), including 29 local breeds, 18 varieties of major international breeds, namely Duroc, Hampshire, Landrace, Large White and Pietrain, and 21 commercial lines either purebred or synthetic, to which the Chinese Meishan and a sample of European wild pig were added. On average 46 animals per breed were sampled (range 12-68). The genetic markers were microsatellites (50 loci) and AFLP (amplified fragment length polymorphism, 148 loci). The analysis of diversity showed that the local breeds accounted for 56% of the total European between-breed microsatellite diversity, and slightly less for AFLP, followed by commercial lines and international breeds. Conversely, the group of international breeds contributed most to within-breed diversity, followed by commercial lines and local breeds. Individual breed contributions to the overall European between- and within-breed diversity were estimated. The range in between-breed diversity contributions among the 68 breeds was 0.04-3.94% for microsatellites and 0.24-2.94% for AFLP. The within-breed diversity contributions varied very little for both types of markers, but microsatellite contributions were negatively correlated with the between-breed contributions, so care is needed in balancing the two types of contribution when making conservation decisions. By taking into account the risks of extinction of the 29 local breeds, a cryopreservation potential (priority) was estimated for each of them.

Author Keywords: biodiversity; conservation; genetic marker; pig

KeyWords Plus: GENETIC DIVERSITY; SUBDIVIDED POPULATIONS; CONSERVATION GENETICS; LIVESTOCK BREEDS; CATTLE BREEDS; MANAGEMENT; DISTANCE; PURPOSES; SIZE

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Title: QTL-based evidence for the role of epistasis in evolution

Author(s): [Malmberg RL](#), [Mauricio R](#)

Source: [GENETICAL RESEARCH 86 \(2\): 89-95 OCT 2005](#)

Document Type: Review

Language: English

Abstract: The extent to which epistasis contributes to adaptation and speciation has been a controversial topic in evolutionary genetics. One experimental approach to study epistasis is based on quantitative trait locus (QTL) mapping using molecular markers. Comparisons can be made among all possible pair-wise combinations of the markers, irrespective of whether an additive QTL is associated with a marker; several software packages have been developed that facilitate this. We review several examples of using this approach to identify epistatic QTLs for traits of evolutionary or ecological interest. While there is variability in the results, the number of epistatic QTL interactions is often greater than or equal to the number of additive QTLs. The magnitude of epistatic effects can be larger than the additive effects. Thus, epistatic interactions seem to be an important part of natural genetic variation. Future studies of epistatic QTLs could lead to descriptions of the genetic networks underlying variation for fitness-related traits.

KeyWords Plus: QUANTITATIVE TRAIT LOCI; GRAIN-YIELD COMPONENTS; PRIMARY GENETIC-BASIS; ORYZA-SATIVA L; ARABIDOPSIS-THALIANA; INBREEDING DEPRESSION; HYBRID STERILITY; SHIFTING BALANCE; COMPLEX TRAIT; RNA VIRUSES

Addresses: Malmberg RL (reprint author), Univ Georgia, Dept Plant Biol, Athens, GA 30602 USA

Title: Genetic evaluation for the beef industry in Australia

Author(s): [Graser HU](#), [Tier B](#), [Johnston DJ](#), [Barwick SA](#)

Source: [AUSTRALIAN JOURNAL OF EXPERIMENTAL AGRICULTURE 45 \(7-8\): 913-921 2005](#)

Document Type: Article

Language: English

Abstract: Genetic evaluation for beef cattle in Australia has been performed using an animal model with best linear unbiased prediction since 1984. The evaluation procedures have evolved from simple to more complex models and from few to a large number of traits, including traits for reproduction, growth and carcass characteristics. This paper describes in detail the current beef cattle genetic evaluation system 'BREEDPLAN' used for the Australian beef cattle industry, the traits analysed and underlying models, and presents a short overview of the challenges and planned developments of coming years.

Author Keywords: carcass; growth; phenotypes; reproduction; selection indexes

KeyWords Plus: MIXED-MODEL-EQUATIONS; MEAT QUALITY TRAITS; BREEDING VALUES; HEREFORD CATTLE; WEANING WEIGHT; ANGUS CATTLE; PHENOTYPIC CHARACTERIZATION; ANIMAL-MODEL; CARCASS; PARAMETERS

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Title: Uncovering cryptic genetic variation

Author(s): [Gibson G](#), [Dworkin I](#)

Source: [NATURE REVIEWS GENETICS 5 \(9\): 681-U11 SEP 2004](#)

Document Type: Review

Language: English

Abstract: Cryptic genetic variation is the dark matter of biology: it is variation that is not normally seen, but that might be an essential source of physiological and evolutionary potential. It is uncovered by environmental or genetic perturbations, and is thought to modify the penetrance of common diseases, the response of livestock and crops to artificial selection and the capacity of populations to respond to the emergence of a potentially advantageous macro-mutation. We argue in this review that cryptic genetic variation is pervasive but under-appreciated, we highlight recent progress in determining the nature and identity of genes that underlie cryptic genetic effects and we outline future research directions.

KeyWords Plus: QUANTITATIVE TRAIT LOCI; PROTEIN-KINASE CASCADE; DROSOPHILA-MELANOGASTER; BRISTLE NUMBER; PHOTORECEPTOR DETERMINATION; NATURAL VARIATION; SELECTIVE SWEEPS; MODIFIER GENES; EVOLUTION; CANALIZATION

Addresses: Gibson G (reprint author), N Carolina State Univ, Dept Genet, Gardner Hall, Raleigh, NC 27695 USA

**Title: Genetic markers and their application in livestock breeding in South Africa:
A review**

Author(s): [van Marle-Koster E, Nel LH](#)

Source: [SOUTH AFRICAN JOURNAL OF ANIMAL SCIENCE 33 \(1\): 1-10 2003](#)

Document Type: Review

Language: English

Abstract: The development of molecular biological techniques has created new possibilities for the selection and genetic improvement of livestock. The discovery of the PCR had a major impact on the research of eukaryotic genomes and contributed to the development and application of various DNA markers. DNA markers have already found wide application in parentage verification, individual identification and control of genetic disorders. The ultimate use of DNA markers would be to identify quantitative trait loci (QTL) in order to practice genotypic selection. This paper reviews DNA markers (RAPD, DFP, RFLP AFLP, minisatellites, microsatellites, SNP) and provides a brief overview of the current application of these markers in animal breeding.

Author Keywords: DNA markers; molecular tools; genome mapping; QTL

KeyWords Plus: QUANTITATIVE TRAIT LOCI; AFFECTING CARCASS COMPOSITION; CHICKEN GENOME; MICROSATELLITE MARKERS; COMPOSITION MAPS; LINKAGE MAP; BOS-INDICUS; MILK-YIELD; CATTLE; POPULATION

Addresses: van Marle-Koster E (reprint author), Univ Pretoria, Dept Anim & Wildlife Sci, ZA-0002 Pretoria South Africa

Title: The use of genetic modification technologies in the discovery of genes affecting production traits and disease resistance in animals

Author(s): [Crawford AM](#)

Source: [NEW ZEALAND VETERINARY JOURNAL 51 \(2\): 52-57 APR 2003](#)

Document Type: Review

Language: English

Abstract: Genetic modification technologies, developed initially in laboratory strains of selected bacteria and viruses, are essential tools for understanding the genomes of livestock. These tools allow researchers to: isolate, sequence and characterise any livestock gene; locate genes on chromosomes; follow the inheritance of any gene and/or chromosomal region in any pedigree; detect phenotypic variation due to, or associated with, variation in the DNA sequence of a gene and identify the genetic alteration causing this.

Most of the many thousands of genes identified in livestock vary between individuals. Finding the best type of the key genes affecting animal productivity is an exciting and a daunting task. It is only possible with the use of laboratory-based genetic modification techniques. This review will briefly describe the technologies now in use and, using local examples, show how molecular geneticists are using these to help identify genetic alterations and breed healthier or more productive animals.

As with any new technology, a new language evolves to describe new products and processes. The new language makes communication easier between participants in the field but more difficult for others to understand the technology. A glossary of terms has therefore been added to this review to help readers less familiar with molecular genetics.

KeyWords Plus: BOORoola SHEEP; LINKAGE MAP; IDENTIFICATION; MUTATION; GENOMICS; CATTLE; QTL

Addresses: Crawford AM (reprint author), Univ Otago, Dept Biochem, AgRes Mol Biol Unit, POB 56, Dunedin, New Zealand

Title: DNA markers reveal the complexity of livestock domestication

Author(s): [Bruford MW](#), [Bradley DG](#), [Luikart G](#)

Source: [NATURE REVIEWS GENETICS 4 \(11\): 900-910 NOV 2003](#)

Document Type: Review

Language: English

Abstract: A series of recent genetic studies has revealed the remarkably complex picture of domestication in both New World and Old World livestock. By comparing mitochondrial and nuclear DNA sequences of modern breeds with their potential wild and domestic ancestors, we have gained new insights into the timing and location of domestication events that produced the farm animals of today. The real surprise has been the high number of domestication events and the diverse locations in which they took place - factors which could radically change our approach to conserving livestock biodiversity resources in the future.

KeyWords Plus: CYTOCHROME-B GENE; MITOCHONDRIAL-DNA; CATTLE BREEDS; EUROPEAN CATTLE; BOS-TAURUS; MULTILOCUS GENOTYPES; EMPIRICAL-EVALUATION; MODERN HUMANS; NEAR-EAST; D-LOOP

Addresses: Bruford MW (reprint author), Cardiff Sch Biosci, Main Bldg, Cathay Pk, POB 915, Cardiff CF10 3TL S Glam Wales

Title: The sustainability, feasibility and desirability of breeding livestock for disease resistance

Author(s): [Stear MJ](#), [Bishop SC](#), [Mallard BA](#), [Raadsma H](#)

Source: [RESEARCH IN VETERINARY SCIENCE 71 \(1\): 1-7 AUG 2001](#)

Document Type: Review

Language: English

Abstract: Selective breeding for disease resistance utilises proven animal breeding methods to improve animal health, welfare and productivity. Unsurprisingly, it is receiving more and more attention from livestock breeders. However, there are a number of largely theoretical arguments that have been raised as potential problems in selection for disease resistance. These can be classified under sustainability, feasibility and desirability. This review considers each of these areas in turn. Several examples show that enhanced resistance to disease is stable under natural selection and therefore deliberate selection for disease resistance should also be stable and sustainable. The feasibility of selective breeding depends in part upon the heritability of the trait or traits used to measure disease resistance, as well as the amount of variation among animals. The heritability of traits associated with resistance to many important diseases is often high and considerable variation among animals exists. Consequently, selective breeding for enhanced disease resistance is certainly feasible. The desirability of breeding for disease resistance depends upon whether there are trade-offs with other economically important traits. By and large these remain to be defined. However, even if unfavourable associations exist, breeders can create selection indices that include traits with unfavourable associations and maximise the desired responses while attempting to minimise undesirable effects. In conclusion, so long as one or more diseases exert a significant influence on livestock production, selective breeding will be a useful tool to assist in disease control.

KeyWords Plus: OSTERTAGIA-CIRCUMCINCTA INFECTION; MAJOR HISTOCOMPATIBILITY COMPLEX; FECAL EGG COUNTS; GASTROINTESTINAL NEMATODE PARASITES; HAEMONCHUS-CONTORTUS INFECTION; PERIPARTURIENT HOLSTEIN CATTLE; GENETIC-VARIATION; MERINO SHEEP; LYMPHOCYTE ANTIGEN; CLASS-I

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**Genetic variation can be changed under environmental and genetic stress.
Consequences for livestock breeding - a review**

Author(s): [Krausslich H](#)

Source: [JOURNAL OF ANIMAL BREEDING AND GENETICS-ZEITSCHRIFT FUR
TIERZUCHTUNG UND ZUCHTUNGSBIOLOGIE 117 \(4\): 275-280 AUG 2000](#)

Document Type: Article

Language: English

Abstract: Livestock breeding is exploitation of genetic variation in herdbook populations. Results of long term selection (domestication) experiments led to the assumption that some genes are normally silent and can be activated under genetic and environmental stress. RUTHERFORD and LINDQUIST (Nature 336: 336-342, 1998) provided the first evidence of a molecular mechanism which can activate silent genes. This article discusses this field of research with respect to the livestock breeding.

KeyWords Plus: DESTABILIZING SELECTION; MUSCLE MASS; IGF2 LOCUS; EVOLUTION; PIGS; MAPS; QTL

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Title: Applying breeding objectives to dairy cattle improvement

Author(s): [Dekkers JCM](#), [Gibson JP](#)

Source: [JOURNAL OF DAIRY SCIENCE 81: 19-35 Suppl. 2 SEP 1998](#)

Document Type: Article

Language: English

Abstract: Otherwise well-researched definitions of breeding objectives and selection criteria may never be used in practice if those definitions do not take into account the perceptions and wishes of the breeders for whom they are designed. Finding selection criteria that are widely accepted and implemented is a daunting task that requires considerable time and full interaction between the scientists and the industry. We review various aspects of this process and, in particular, how scientific principles can be used to ensure that the outcome best meets both the perceptions and needs of the users while remaining as close as possible to the technical economic optimum. Alternative methods of presenting and delivering selection indexes, such as index expression, index formulation, focus on response to selection rather than on index weights, construction of component indexes, and the use of direct accounting for costs of constraints rather than rescaling methods can all help in improving acceptance of an index. Development and implementation of selection criteria also involve consideration of the selective mating decisions that form an integral part of selection decisions in the field. The technical basis of factors that foster emphasis on individual mating decisions in the field are discussed in relation to formulation of the breeding goal and selection index and in relation to nonlinear economic and genetic parameters. Strategies that focus on use of a linear index for the selection of sires and dams followed by selective mating of selected parents have the greatest potential for implementation in the industry. We focus on examples taken from the Canadian dairy industry, but principles apply generally.

Author Keywords: breeding goals; selection index; profit; mating strategies

KeyWords Plus: LINEAR PROFIT-FUNCTIONS; SOMATIC-CELL SCORE; SELECTION INDEXES; ECONOMIC WEIGHTS; GENETIC EVALUATION; PRODUCTION TRAITS; MILK-PRODUCTION; SIRES; MODEL; YIELD

Addresses: Dekkers JCM (reprint author), Iowa State Univ, Dept Anim Sci, 201 Kildee Hall, Ames, IA 50011 USA

Title: Accounting for herd, year and season effects in genetic evaluations of dairy cattle: a review

Author(s): [van Bebber J](#), [Reinsch N](#), [Junge W](#), [Kalm E](#)

Source: [LIVESTOCK PRODUCTION SCIENCE 51 \(1-3\): 191-203 NOV 1 1997](#)

Document Type: Article

Language: English

Abstract: Contemporary groups, in genetic evaluations of dairy cattle commonly formed by fitting herd-year-season effects, can either be treated as fixed or random effects. For population structures that result in contemporary group subclass sizes of about 15 effective daughters or more, fitting contemporary group as a fixed effect to remove bias from genetic evaluations seems to be appropriate. For situations that result in contemporary group subclass sizes of about four effective daughters or less, the amount of information lost can be tremendous, and a compromise between accounting for bias and reducing prediction error variance should be found. Models that have been investigated to find such a compromise have in common that the amount of information lost is being reduced by either (i) fitting some HYS effect (or parts of it) as random, random and correlated, or random effects nested within a fixed effect or (ii) increasing the actual number of observations within subclasses by forming herd classes or by forming seasonal groups using clustering methods. The effectiveness of a model depends very much on the population structure, mainly on the average herd size, so no general statement about the appropriateness of a model can be made. The results of test-day (TD) models which, in contrast to 305-day yield models, allow a direct correction for effects specific to the time of recording of a cow's performance, clearly showed the importance of effects present at the day of test. Overall, it can be concluded that the definition of contemporary group effects is somewhat arbitrary and has often been a compromise between bias and the effective number of daughters. Therefore, methods, which allow a definition of cutoff points for contemporary groups only at points at which significant changes in environmental conditions actually occur, should be investigated. (C) 1997 Elsevier Science B.V.

Author Keywords: bias; prediction error variance; group size; level shifts; autocorrelation; Kalman filter; **BLUP**

KeyWords Plus: 1ST-ORDER AUTOREGRESSIVE PROCESS; MULTIPROCESS KALMAN FILTER; SOMATIC-CELL SCORE; TEST DAY RECORDS; TEST DAY MODEL; SIRE EVALUATION; CONTEMPORARY GROUPS; BREEDING VALUES; LONGITUDINAL DATA; LACTATION CURVE

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