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Applied to animal breeding for disease resistance

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ABSTRACT

Animal diseases cause significant losses to livestock's and breeders, resultant in direct damages to animals, reduced productivity and cost of treatment. One of the promising additional methods to control diseases is breeding animals for disease resistance. The resistance of animals to diseases is related to their ability to withstand pathogens and harmful environmental influences.

For the planned control of hereditary diseases in domestic animals, it is required not only an accurate knowledge of their inheritance but also an accurate and monotonous description and designation of the disease. Therefore, in order to avoid misunderstandings in identifying hereditary anomalies in domestic animals, an international nomenclature has been created for their description and designation. According to this nomenclature, hereditary diseases of each species of animals are designated by a certain letter of the alphabet. Specific diseases peculiar to this species are characterized by numerical indexes.

Developments in technologies, such as genomic selection, may help overcome several of the limitations of traditional breeding programmes and will be especially beneficial in breeding for lowly heritable disease traits that only manifest themselves following exposure to pathogens or environmental stressors in adulthood. The current paper provides a brief overview of the present-day application of microsatellites markers in animal breeding and make a significant contribution to the overall farm animal health and resistance to disease.

Keywords:*Disease resistance, Animal Breeding, Animal health, Quantitative genetics, Molecular markers.*

1. REVIEW METHODOLOGY

We searched web of science and used the following terms: model breeding disease; model breeding disease selection; selection disease model; breeding disease livestock; genetics disease poultry; evolution disease; Epidemiol gen disease; Epidemiol gen livestock.

2. INTRODUCTION

Genetically determined resistance with an unknown mechanism of inheritance against diseases caused by bacteria, viruses,and parasites has been found in many species of domestic animals.

many hundreds of years cattle with the greatest resistance to disease have probably survived to leave more offspring in succeeding generations than those less resistant to disease. Resistance to disease also may have increased indirectly through a favorable association with other characteristics, such as growth rate or milk yield, which have received major emphasis in genetic improvement programs in cattle. However, except for some selection against mastitis in dairy cattle, genetic resistance to disease has not received direct emphasis in genetic improvement programs. Greater understanding of biological mechanisms involved in disease resistance could lead to more effective sélection of breeding stock.

When studying the resistance of diseases in crop production, it was revealed that individual diseases have the most vivid and diverse picture of their manifestation. This leads to the fact that in the following generations it is necessary to again conduct complex measures for selection for resistance. In animal husbandry, this problem has not been studied well enough, but the research is very intensive. Such an assessment in livestock farming is in the initial state and there is no characteristic for one breed or line. However, conducted studies have shown that in a particular group of animals there is reliable resistance to certain diseases. It should be borne in mind that such stability arose not as a result of breeding, but in the natural selection of individual breeds or related groups. Thus, to identify the resistance and susceptibility of the breed to various diseases. Such rocks can serve as a basis for solving the problem under consideration.

The problem is no longer whether to breed for disease resistance but how. Selective breeding does pose specific problems not found in selection for production traits. For example, the traits used to determine resistance to many diseases are not normally distributed and require different statistical procedures (15-17). The problem is less the statistical procedures than the fact that genetic theory assumes that the underlying liability to disease is normally distributed and it can be difficult to reconcile clearly non-normal distributions with quantitative genetic theory.

Selective breeding to reduce the incidence of a disease is likely to have profound consequences for animal health, welfare and farming profitability. However, most reviews written are not readily accessible for those with little background in quantitative genetics. The inadvertent exclusion of many stakeholders has had the unfortunate consequence that much of the debate over selective breeding for disease resistance has been conducted at two levels. Quantitative geneticists and professional animal breeders have embraced the idea of selective breeding for disease resistance and the debate is about methods to achieve this goal and encourage uptake by breeders. In contrast, many outsiders are still concerned about the wisdom of selective breeding.

Improved animal health is a major objective in current animal breeding strategies, but is difficult to achieve by traditional breeding methods. Thus, selection for genetic disease resistance provides a potential avenue for improving the health status of farm animals, increasing productivity and reducing the need for pharmaceutical intervention, in this way reducing costs and delaying the appearance of resistant pathogens. The achievement of such improvement is one of the most important applications of molecular genome research.

Individuals vary in their susceptibility to disease and much of this susceptibility is genetic in origin. Farmers and breeders can exploit this genetic variation to identify and use animals that are relatively resistant to disease. Of course, breeding for disease resistance is not a universal panacea; there is little point in selective breeding for resistance to a disease where effective and sustainable alternative control measures, such as vaccination are effective. Similarly, there seems little point in selective breeding for resistance to exotic diseases that require infected animals to be identified and culled when the disease is imported into the country. Nonetheless, selection for disease resistance is a useful tool for the control of many diseases and is most effective as part of an integrated disease control strategy.

This review will introduce some of the key concepts in animal breeding then describe the process of breeding for disease resistance. Most of the published work is in sheep and cattle and the emphasis will be on the lessons those species have for other systems.

A further concern was that as parasites and pathogens are capable of more rapid evolution than their hosts, selection of hosts might be overwhelmed by the response of the pathogen or parasite. Again, there is no evidence that this happens (10-11). Another exaggerated concern was the possibility of trade-offs between disease resistance and production traits. In some circumstances, disease resistant animals are less productive (12); in other circumstances disease, resistant animals are more productive (13;14). In themselves, trade-offs are not fatal to selection for disease resistance. Many traits in selection schemes have negative genetic correlations and selection indices maximize the responses to traits that are unfavorably correlated.

3. FACTORS OF BREEDING OF AGRICULTURAL ANIMALS FOR RESISTANCE TO DISEASES

Diseases cause enormous damage to livestock. Therefore, it is necessary to address the issue of breeding animals that are resistant to various diseases, is a very urgent problem of modern livestock. However, the selection of animals for disease resistance is hampered by a number of factors:

•Complex genetic conditioning of resistance.

•The complex genetic nature of pathogens.

•Inability to make extensive use of contagion to detect resistance.

•The absence of reliable indirect criteria of stability or susceptibility.

•Rapid variability of pathogens and the emergence of new strains that overcome animal resistance.

•A large interval between generations, which leads to a long selection and loss of achievements obtained in the previous generation.

•The presence of a negative correlation between stability and signs of productivity.

•Stability of many types of pathogens is not accompanied by resistance and other species.

4. HERITABILITY AND REPEATABILITY OF RESISTANCE TO DISEASES

The proportion of variability, determined by the genotype of the animal. The higher the coefficient of heritability, the more effective the selection of animals that are resistant or susceptible to the disease.

For each farm, there is a value for this coefficient, in connection with which it must be calculated and used in a particular herd. This parameter is widely used in zoo technology to increase the development and productivity indicators from generation to generation.

In veterinary science, he is still not paid due attention, so it is determined only by scientific research.

Modern computer technologies make it possible to determine all selection-genetic parameters, incl. The coefficient of heritability and repeatability. Repetition indicates the stability of the change in the value of the studied trait with the age of a group of animals or in different parts of the body. In veterinary medicine, repeat can be used to assess the resistance to disease of the same group of animals. This allows you to organize a selection of susceptible to diseases at an early age and to discard them in a timely manner.

5. MASS SELECTION FOR RESISTANCE

Animals during their economic use undergo a series of assessments, the results of which are used to decide whether animals will be allowed to continue reproduction. Three stages of evaluation:

1) By origin. When they want to get more descendants.

2) According to the animal's own indicators, i.e. By the degree of manifestation of resistance or susceptibility to diseases. This evaluation is a mass selection for resistance and its effect is determined by the degree of heredity to a particular disease.

3) On the quality of offspring. In the selection plan, it is of the greatest value, since the quality of offspring can be judged on the ability.

To ensure selection for sustainability, it is necessary to carry out measures to identify individuals characterized by the traits under study. To infectious diseases, resistance can be determined only in disease-prone herds. At the same time, the difficulty lies in the fact that the disease manifests itself through the phenotypic manifestation of the signs of the disease (2;5).

6. RESISTANCE TO COCCIDIOSIS

One of the basic features, as a criterion, is the resistance of chickens of different ages to survival for more than 10 days after infection with a certain number of helminths. Measures to increase resistance to diseases:

•Diagnostics.

•Genealogical analysis of the herd.

•Selection for sustainability.

•Evaluation of producers.

•Cultivation of sustainable producers.

•Transplantation of embryos.

•The inclusion of relevant sections in the plans of the breeding work.

•Using a personal computer.

•Methods of biotechnological use

With the transfer of livestock production to industrial production technologies, the need to prevent infections and invasions, to create types, lines and breeds of animals that are resistant to stress and non-contagious diseases, capable of prolonged exploitation in conditions of complexes with preservation of high productivity and fertility, has increased Every year the productivity of livestock and poultry in highly developed countries is reduced by 20% due to diseases. To reduce these losses is one of the main tasks in the intensification of the industry. It is established that some breeds, populations within the rocks, individual animals are characterized by complete immunity to certain diseases or become extremely ill. These distinctive pedigree features are passed down from generation to generation. Thus, the animals of the Kostroma and Bestuzhev breeds steadily transmit immunity to leukemia to their offspring. Zebu and zebuvidny cattle are resistant to pyroplasmosis, gastrointestinal diseases, leukemia Differences in susceptibility to diseases are found between lines and families, offspring of different producers. This indicates that heredity plays a decisive role in the resistance and susceptibility of animals to diseases. Resistance to diseases is inherited most often as a polygenic trait. To display such a sign, it is necessary to accumulate in the genotype of animals a certain number of alleles with an additive (total) effect, which increases the resistance of the organism to pathogenic factors (viruses, bacteria, etc.). Susceptibility to the disease manifests itself only in the presence of relevant factors (viruses, bacteria) and the absence of genes that determine the resistance of the organism.

Prospects of breeding for increasing the resistance of animals to diseases. Since the molecular bases of diseases and the mechanisms of their genetic determination have been established, it is necessary to conduct a purposeful work to eradicate hereditary pathology. Already, the prevention of certain diseases and anomalies is based on the use of biochemical, cytological

and direct genetic markers. Thus, the prevention of mannosidosis of cattle is carried out by selecting (rejecting) animals heterozygous for the level of the mannosidase enzyme. VLUD and CVM-syndromes in Holstein are revealed on the basis of PCR diagnostics. Stress resistance and stress sensitivity in pigs are determined by the reaction to halothane anesthesia. The cytogenetic analysis reveals carriers of chromosome aberrations, which makes it possible to increase the fertility and viability of animals. The development of genetic engineering opens new opportunities in the fight against diseases. There is an opportunity to eradicate some diseases by isolating and cloning the genes that determine the formation of immunity, regulating the immune response, controlling the presence of antigenic components of diseases and parasites. A special role is assigned to genes controlling the main complex of histological compatibility, protein-mediators,and antibodies. It has been established that such diseases as sheep pruritis, Marek's disease and chicken leukaemia and some others are associated with the main complex of histological compatibility.

Studies on prurigo have shown that in sheep of different breeds the severity of the disease is not the same. Some breeds of chickens are highly resistant to the development of lymphoma; others are not very resistant. Immune breeds have a certain complex of histological compatibility, which makes it possible to select for increased resistance to diseases of this kind.

Lymphocytes in the process of immune reaction are able to release peptides that stimulate or suppress antibody production and division in cells. Such mediators, or hormones, are called lymphokines. One of them - interleukin-2 - promotes the replication of lymphocytes, the other interferon is widely used in medicine and in the treatment of respiratory diseases of animals. Now the necessary amounts of interferon are obtained with the help of genetic engineering by cloning the genes encoding this protein. In the near future, lymphokines will find wide application in the prevention of stress.

The detection of T-cell function in antibody coding makes it possible to prevent viral diseases of livestock such as leukemia, blue tongue syndrome, malignant biliary fever, false rabies, African swine fever, sheep prurigo, Marek's disease, leukemia, and influenza in birds.

Knowledge of the nature of immune reactions of the organism when certain pathogenic factors influence it allows creating effective vaccines. Specially designated monoclonal antibodies are used to identify products produced by pathogens. With their help, the genes encoding the protein envelopes of viruses are identified and cloned, which makes it possible to create highly targeted and harmless vaccines. However, individual pathogens have the ability to alter or mask their antigens, making it difficult to use vaccines. In these cases, biological agents will be created to fight the pathogens, so-called vectors, which can be mosquitoes, mites, aphids, mosquitoes that destroy disease vectors. Only with one enumeration of modern achievements in molecular genetics, immunogenetics, cytogenetics,and genetic engineering are it difficult to cover the possibilities of using them in veterinary medicine (20). However, there is no doubt that prevention and therapy of diseases are entering a new era; the era of immunogenoprophylaxis and immunogene therapy.

The possibilities of such immunogenotherapy were demonstrated, in particular, in the treatment of newborn piglets and calves using monoclonal antibodies specific for the so-called pili antigens on the enterotoxigenic form of E. coli causing diarrhea.

The use of genetically engineered specific vaccines against diarrhea of calves, foot-and-mouth disease of cattle significantly reduces the incidence of animals. However, the vaccinated animals proved to be resistant only to one specific strain of the virus. In this regard, there is a need to create new variants of serums.

Scientists associate further successes in the fight against animal diseases:

•With the study of the genetic basis of susceptibility to diseases;

•Studies in the molecular structure of genes that regulate the immune response;

•The development of tests of molecular diagnostics using monoclonal antibodies, which requires the study of the structure of the genetic material and the antigenic composition of pathogens - viruses, bacteria, parasites, etc.;

•The creation of a technology for the production of "subunit" vaccines and the use of other antigenic components;

•Researching the possibilities of strengthening the immune response to vaccines, etc.

7. RESISTANCE TO DISEASES AND ITS TYPES

Resistance is the hereditarily conditioned immunity of the organism to certain pathogenic factors. Some authors the notion of resistance to infectious diseases is replaced by the concept of nonspecific resistance (resistance) as opposed to specific stability (immunity), in which specific antibodies play a protective role in the body. Nonspecific resistance is due to the action of active and passive defense mechanisms. Active mechanisms include phagocytosis and antibacterial action of certain nonspecific factors contained in the blood. Of the passive mechanisms should be mentioned protective barriers of the body, such as the skin and its derivatives, lymph glands, connective tissue and metabolic processes. Stability is the first protective barrier of the body, often determining the outcome of the lesion. There are the following types of stability:

Species (for example, cows,and horses);

•Pedigree (for example, sheep of the Kent breed are less sensitive to trichostrongylosis than other breeds).

•individual, in which in the case of the appearance of the disease in the herd, a part of the individuals do not develop the disease.

Resistance to a particular disease can be absolute if the organism under any conditions is immune to this pathogen, and conditional when the disease develops in certain environmental conditions. The opposite of resistance to disease is the predisposition, or susceptibility, of animals to diseases. Susceptibility of the animal to this disease can be determined by the absence of some of the above-mentioned nonspecific defines systems.

Resistance to harmful influences of the environment also depends on the activity of active defines mechanisms and certain qualities due to the anatomical structure and functioning of the neurohumoral system. Adverse factors of the environment can cause a stressful reaction of the body, which is effectively countered by an adaptation syndrome controlled by the pituitary-adrenal system.

The inheritance of resistance to diseases has not been studied in detail. In some cases, resistance to certain diseases is determined by one or two pairs of genes, sometimes it is caused by a polygenic system, which, with strong interaction of factors such as sex, age, and level of productivity, different conditions of content leads to high variability in the manifestation of resistance in the animal population (8-9-11-12-16).

8. STABILITY AND SUSCEPTIBILITY TO INFECTIOUS AND PARASITIC DISEASES

The mechanism of inheritance of resistance to such viral diseases in animals, like galloping in sheep, leukaemia in cows, Marek's disease in chickens, has not yet been deciphered.

Galloping in sheep (scrapie) is a dangerous infectious disease caused by a little-known virus-like factor. It is difficult to flow and appears in the itching and disturbance of movement coordination. Movements of sick animals resemble gallop. Sheep are infected with this disease at the age of 2-4 years. The disease leads to the death of animals. Infection, apparently, occurs with direct contact. The method of treatment is absent. It turned out that only certain sheep are affected. According to Parry's hypothesis, susceptibility to infection shows homozygous for gene s, while its normal allele 5, even in the heterozygous state, guarantees complete resistance to the disease. From the studies of the author mentioned, carried out on sheep with genotypes known from this gene, it follows that the offspring from crosses SS $_X$ SS, SS $_X$ Ss and SS $_X$ ss did not develop scrapie until the age of 4.5 years, but among 12 sheep from the parents Ss $_X$ Ss 10 were healthy, and two fell from this disease. Among 38 descendants from crossing Ss $_X$ ss 23 were healthy, and 15 patients. In the case of sheep susceptibility to scrapie, there is a special case of infectiousness, which apparently binds to certain parts of the DNA that make up the s gene. The pathogenic activity of this gene is realized with the help of an infectious factor that forms a complex with it. This factor is realized together with the genetic material of the host organism. Darlington suggested that such an infectious factor, by analogy with the prophage, be called a provirus.

It is believed that leukaemia (leukemia) in cattle should be determined by a provirus that, in conjunction with a particular gene designated by the letter r, causes the disease, while the R allele with incomplete dominance is a repressor to leukaemia provirus. A similar action is possessed by oncogenic viruses, which on the basis of their RNA synthesize DNA sequences. These molecules are then incorporated into the DNA of the host chromosomes, creating a specific complex in them, replicating as a whole and causing the transformation of the host cells into cancerous ones.

A completely different protection system is responsible for the resistance of chickens to white diarrhea (pullorosis). In the first days of life, chickens do not yet have the established mechanisms of thermoregulation and behave like cold-blooded animals. The Hutt and Crawford based on body temperature measurements for the first time after hatching received two hen lines with "high" and "low" body temperatures during this life cycle period. After two generations of selection, the line with a "high" temperature differed by 5 ° C from the line with a "low" temperature. Artificially infecting chickens of both lines with identical doses of Salmonella pullorum bacteria, the researchers showed that the lines vary very much in resistance to disease. The mortality of infected chickens by the 3rd day of life in a line with a high temperature was 8.6%, and from "low" -40.7%. The mechanism of resistance to white diarrhea is based on the ability to respond to infection by rapid and strong temperature increase, as a result of which the disease does not develop.

9. PROTECTIVE MECHANISMS OF THE BODY

The ability of an organism to resist diseases or protective power, can be nonspecific (resistance) and specific (immunity). Resistance and immunity are divided into congenital and acquired. Congenital resistance means that pathogenic factors (viruses, bacteria) are unable to reproduce in the cells and tissues of the animal. Intracellular replication of certain pathogenic bacteria and viruses is almost not controlled by humoral antibodies so that a high antibody titer in the serum can not protect the host organism from the harmful effects of the pathogenic factor. To protect against infections such as brucellosis, salmonellosis, listeriosis and other diseases, a second vaccination is necessary to develop an immune response. The immune response depends on the breed and the species of the animal, as well as on the nature of the pathogenic factor.

The body has a number of protective devices against infectious diseases. The most important role among them is played by external protective factors - skin, body secretions, and numerous components of blood serum. Skin performs mainly the role of a mechanical barrier. Mucus, secreted by the nasal cavity, upper respiratory tract, gastrointestinal tract, catches and detains bacteria in their progression.

Recently, the mechanisms of the immune system have been intensively studied. Schematically they are represented as follows. There is a group of undifferentiated stem cells of the bone marrow, of which certain types of blood and lymphatic cells develop: red blood cells, lymphocytes, granulocytes, etc. Lymphocytes are activated in specialized tissues: T-lymphocytes in the thymus; B-lymphocytes - in birds in the factory bag; in mammals, the location of their location is not established. B-lymphocytes

determine in the body humoral, and T-lymphocytes; cellular immunity. All immune responses are subordinated to the central nervous system. If it refuses, then lymphocytes can produce antibodies against their own cells, resulting in autoimmune disease. In the normal state, the immune system reacts only to substances that get into the body from the outside. The protective capacity of the body is formed already in the fetal period - part of the gamma globulin during pregnancy through the transplacental barrier is transferred from the mother to the fetus. Therefore, immunity, partly congenital, is acquired without including the genetic apparatus of the fetus. A newborn animal receives antibodies from the mother colostrum until its own immunity is formed.

The strength of the body's immune response is under genetic control. Such substances as leukomitogenes, leukoretrhines, leukokinesins, leukotoxins,andangiotropins, are responsible for the function of leukocytes and are controlled by the corresponding gene locus. One of the achievements of immunogenetics in recent years is the discovery of a gene that codes for the structure of an immunoglobulin. Genetic concentrations of immunoglobulin in various breeds of cattle have been established. High heritability of the concentrations of this protein (0.52-0.69) makes it possible to select for increasing the specific resistance of animals. Another important achievement of immunogenetics is the discovery of a major histocompatibility complex (MHC). Leukocyte antigens localized on the membranes of nuclear cells not only determine the compatibility of tissues and organs during transplantation but also determine the genetic resistance of animals to certain diseases. The system of the main histocompatibility complex is characterized by pronounced polymorphism, which makes it possible to use it to control the origin of animals. Types of leukocyte antigens are controlled by allelic groups of genes and inherited by an autosomal codominant type. The role of the leukocyte system of antigens in the immune response and susceptibility or resistance of the organism to diseases is proved. It is emphasized that the complementary content of serum depends on the system of leukocyte antigens. There are a number of examples that characterize the genetic conditioning of animal resistance and immunity. The participation of the genotype in the realization of the general and specific protection of the animal organism against diseases has been established. The presence of hereditary conditionality of the level of natural resistance in cattle is determined. The coefficient of heritability of bactericidal activity is 14%, lysozyme - 24, total serum protein - 48, gamma globulins - 60%. The coefficient of heritability of the level of lysozyme activity of milk and the titer of normal blood antibodies is established. The indicator of the first sign is 0.403, the second indicator is 0.414. These characteristics have a wide variability in herds (from 6 to 50%) and differ significantly in some related groups of animals (lines, families). The data on the genetic resistance of pigs to neonatal enteritis caused by E. coli have been published. Due to the natural immunity associated with specific intestinal secretions, in some pigs, the E. coli bacteria cannot attach to the intestinal wall and multiply. Isolation of the surface of the body, internal cavities and glands can wash out bacteria and prevent their penetration into the body. The bactericidal properties of the secretions are determined by the content of lysozyme in them. Inter-breed and individual features of lysozyme activity of tear fluid have been established. The higher the activity of lysozyme, the more resistant the animal is to the infection with infectious keratoconjunctivitis. Thus, purebred import animals of the Aberdeen-Angus breed and their descendants are more predisposed to keratoconjunctivitis than carnivorous animals obtained on the basis of an absorbent crossing of Kalmyk cattle. In studying the pathogenesis of allergic lung disease in horses, the relationship between this disease and the system of leukocyte antigens is established. A reliable relationship was also determined between the ability of a horse to produce antibodies and leukocyte antigens. The connection between the disease and the system of leukocyte antigens is also found in cattle. It has been established that some animals do not develop babesiosis. They are resistant to ticks of the Vorhilus genus, carrying the causative agents of pyroplasmosis. These tick-resistant individuals show definite leukocyte antigens, which are not found in susceptible animals. Particular attention should be paid to diseases of blood systems and metabolism. This category of diseases is divided into five groups: anomalies of amino acid metabolism, anomalies of carbohydrase metabolism, a violation of the metabolism of dehydration, congenital hormonal disorders,and abnormalities of blood metabolism.

In Holstein cattle, hereditary blood coagulation disorder (factor XI deficiency) occurs. To study the nature of the inheritance of this factor, an analyzing crossing was carried out involving carriers of a coagulation disorder of normal and factor XI deficient animals. It is established that the defect is inherited by the recessive type. The frequency of the mutant gene in one of the populations of Holstein cattle ranged from 7.0 to 16.9%. In the same breed, hereditary immunodeficiency, called the VLUD syndrome, was identified. Calves - homozygous carriers of the recessive BL-gene die at the age of 4-6 months due to the inability to withstand viral and bacterial infections affecting the respiratory system and gastrointestinal tract. A similar syndrome - combined immunodeficiency - was found in horses of the Arabian breed. To prevent this defect, a method is developed for detecting

10. ESTIMATED BREEDING VALUE

The Estimated breeding value (EBV) is the second key concept. If there is only a single record on one animal and no information on any of his relatives, then the estimated breeding value is the heritability multiplied by the difference between the individual observation and the population mean. For example, selection for nematode resistance in sheep uses faecal egg counts. Faecal egg counts are typically log transformed to normalize the distribution. If a lamb has a faecal egg count 2 log units (100 eggs per gram) above the flock mean and the heritability is 0.3, then the EBV = 0.3 x 2. This corresponds to an EBV of +0.6 log transformed units.

A single record is not particularly useful because the accuracy and the reliability are relatively low. In practice, additional information is used. This might take the form of repeated records and information on relatives, especially siblings, offspring or parents. In practice, EBV is usually calculated by specialized computer programs, such as ASReml or VCE. These programs can take all available information into account. The more information that is available, then the more reliable and accurate will be the results. These programs also adjust the phenotypic observations to allow for known effects such as sex, herd, year and season. Herd, year and season are often grouped together to form a single source of environmental variation that affects herd means.

The accuracy of the estimated breeding value is the correlation between the true and the predicted breeding value. For a single measurement, the accuracy is the square root of the heritability. In the above example, the accuracy is the square root of 0.3 which is 0.55. The reliability of the estimated breeding value is the square of the accuracy. In this example, the reliability is equal to the heritability and is 0.3.

11. REPEATABILITY

The third key concept is the repeatability. Sometimes, it is possible to take repeated records from the same individual, e.g. milk yield in successive lactations. The usefulness of repeated records depends upon the repeatability. The repeatability is the variance between individuals (Vb) divided by (Vb + Vw) where Vw is the variance within individuals.

When most of the variation is among individuals, then the repeatability is high. It decreases as the amount of variation within individuals increases (i.e. as the repeated records become less similar). When there are only two records with equal variances, then the repeatability is equal to the correlation.

The repeatability can be thought of as Vg (genotypic variance) + Vpe (permanent environmental variance) divided by the total (phenotypic) variance. In other words, the similarity between observations depends upon the genotypic component plus the permanent environmental component. The repeatability should be equal to or greater than the heritability. As the repeatability can be quickly estimated even without pedigree records, it provides a convenient way to estimate the upper limit of the heritability.

12. GENETIC CORRELATION

The fourth key concept is the genetic correlation. As this is the correlation between the additive genetic effects, it is also known as the additive genetic correlation and is the correlation between the breeding values. If two traits are genetically correlated this means that their breeding values are correlated and the value for one trait can be predicted from the other. Selection for one trait would also produce a change in the genetically correlated trait. If both traits are measured, then selection can increase one trait while leaving the other unchanged or achieve more rapid progress in both traits. If the genetic correlation is negative, as with milk production and milk protein percentage, it is possible to increase both traits but progress is slower. For example, milk production is positively correlated with the incidence of mastitis (18;19). Selecting for increased milk production alone obviously increases milk production. This selection regime also increases the incidence of mastitis.

Indicator traits are those traits that are relatively unimportant in themselves but are genetically correlated with economically important traits. Indicator traits can be used to select for traits that are difficult to measure or have low heritability. Somatic cell scores are an indicator of mastitis incidence and they are now being measured in many dairy cows. Future selection indices will incorporate somatic cell scores. Selection will then either reduce the incidence of mastitis or prevent it rising(17-18).

13. PREDICTING THE RESPONSE TO SELECTION FOR A SINGLE TRAIT

The breeders' equation states that the response to selection (R), the expected improvement in a trait in the offspring, can be predicted by the selection differential (S) multiplied by the heritability (h^2). This applies to a single generation of selection for a single trait, where the response is measured in generations and the population is large enough to ignore the effects of inbreeding and drift. As selection proceeds, genes change in frequency; unfavorable genes may disappear while favorable genes may become fixed. Changes in the extent of genetic variation will influence the heritability. The heritability is the variance in breeding values divided by the phenotypic variance (V_a/V_p) and the selection differential is the selection intensity multiplied by the phenotypic standard deviation $i\ \sigma_p$. Rearranging terms gives the response to selection as $\sigma a\ h\ i$, where σ_a is the variation in breeding values, h is the accuracy of selection and i is the intensity of selection.

$R = h^2S$
$R = (V_a/ V_p)\ i\ \sigma_p$
$R = \sigma_a\ h\ i$
Response to selection on multiple traits.

The response to selection on multiple traits depends upon the additive genetic variances and covariance of the traits (49). The equation is

$R = G\beta$

Where R is the change in the multivariate phenotype, G is the additive genetic variance-covariance matrix and β is the selection gradient which is estimated from the partial regression coefficients. As with selection for a single trait, this index is best for production traits and may not capture the full benefits of selective breeding for disease resistance. Mathematical modeling is required to capture the response to selection (19-20)

14. MATHEMATICAL MODELING

Quantitative genetic theory can accurately predict the response to selective breeding of production traits but is less effective at predicting the response to selection for resistance to infectious diseases because selecting resistant animals and culling susceptible animals can alter the rate of disease transmission. In other words, the genetic theory assumes that the environment remains unchanged but culling heavily infected or diseased animals can reduce the contamination of the environment with transmission stages. This is particularly true for terrestrial livestock. For example, selective breeding for nematode resistance on the basis of

egg count reduces the number of parasite eggs shed into the environment (44-46). Selective breeding may also reduce contamination in marine environments but this may vary with the disease.

There are a large number of epidemiological models that have explored variation among individuals in their contribution to infectious disease dynamics, especially for parasite infections (50). However, surprisingly few have explicitly incorporated genetic variation and even fewer have modeled the epidemiological and genetic response to selection for disease resistance (51).

The production of transmission stages is more persistent and predictable for endemic metazoan parasitic infections than microbial infections. Consequently, modeling the response to selection for parasite resistance is easier than for resistance to microbial infections. To our knowledge, there are only two published models that predict the response to parasite resistance. The first models the response to selection against nematode infection of lambs (46). The lamb model predicts relatively rapid responses to selection for lower faecal egg counts following natural nematode infection with predominantly Teladorsagia circumcincta. The responses observed in practice were less rapid (3). One possible explanation is that selection in practice involves multiple traits. Another is that the model did not attempt to capture immune responses. It essentially assumed that reduced parasite numbers due to immune responses were counterbalanced by increased larval intake. However, the immune response may play a stabilizing role in nematode infection as reduced levels of infection generate reduced immune responses (52).

The overall goal of a program to define relationships between simple genetic markers and diseases in cattle has a major difference if compared to a similar program in humans. That is, very rare diseases and those occurring after products e age are of minor concern in cattle but are very important m humans. Thus, we feel that our research efforts should be directed toward overall immune responsivenesssincethe most common denominator in many cattle losses is opportunistic infections brought about by stresses. Unfortunately, this dice- tats that we will not have a large data base from laboratory species or humans from which to work. Our current and future efforts are to combine the disciplines of molecular biology, immunogenetics, and epidemiology to define simple genetic markers and their relationships to disease resistance.

15. TO INCREASE THE RESISTANCE OF ANIMALS TO DISEASES, VETERINARIANS AND BREEDERS SHOULD CARRY OUT THE FOLLOWING ACTIVITIES

1) Organize the diagnosis of diseases. All data on the diseases and reasons for the disposal of animals should be taken into account in pedigree cards. All anomalies are taken into account and described;

2) Conduct a genealogical analysis of the herd and provide a comprehensive assessment of the gene pool of families. Identify families that are resistant and susceptible to disease.

3) To select the young for the tribe, if possible, from mothers who are resistant to diseases and the duration of productive use;

4) Constantly evaluate the producers in terms of resistance and susceptibility of offspring to diseases and signs of productivity, etc.

5) To receive producers of the next generation from highly productive mothers from families with complex resistance, and fathers evaluated for resistance to offspring;

6) Use embryo transplantation as one of the methods for increasing the efficiency of selection for disease resistance.

7) Include in the plans for breeding work sections on the issues of increasing the resistance of animals to diseases and measures to prevent the spread of hereditary anomalies;

8) Include in breeding indexes information on animal resistance to diseases;

9) Use direct and indirect selection in the complex, including mass selection, selection of families and within families, assessment of producers for the resistance of the offspring to diseases, use markers;

10) Process information on diseases and causes of animal culling using computers;

11) Use in the future methods of biotechnology, including genetic and cellular engineering, which will allow successful selection of disease resistance, stress resistance and the duration of productive use of animals.

16. CONCLUSIONS

It should be expected that limiting the spread of some infectious and parasitic diseases through the use of genetic resistance will find wide application in practice if it is possible to identify resistant animals not only in case of disease or infection. Great hopes are relegated to the use of markers that would signal the existence of such stability without contact of the animal with pathogenic agents.

In connection with the impossibility of breeding absolutely resistant animals, an integrated approach to disease control is needed, including methods of veterinary medicine, breeding and ensuring optimal levels of feeding and maintenance. The relative hereditary resistance of animals creates favorable conditions for obtaining a greater effect from vaccination.

The development of molecular markers for genetic analysis has led to a great increase in our knowledge of livestock genetics and our understanding of the structure and behavior of animal genomes.

Breeding for disease resistance is desirable and feasible. The practical methods are similar to existing breeding schemes but determining the optimal weighting to give disease resistance can be challenging. It is difficult to estimate the relative economic value of disease traits because this depends upon the prevalence of infection and disease as well as the effectiveness of treatment. In addition, predicting the response to selection for resistance to infectious disease requires mathematical models. Few models exist and these models require additional development before they can accurately predict the response to infection.

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