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Advances in Genomics for Improving Cattle Health and Production

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Abstract

Recent advances in animal breeding and genetics that are pertinent to the prevention of disease in cattle can now be used as a component of an overall programme for enhanced cattle health. The role of genetic make-up to variations in resistance to several illnesses affecting cattle is summarised in this paper. There is substantial genetic heterogeneity in disease susceptibility among cattle, indicating that genetic selection for better disease resistance will be successful. However, the incorporation of health and disease resistance traits in national breeding goals is now hampered by a lack of good data on the individual animal susceptibility to disease. Developments in "omics" technologies, like genomic selection, may help traditional breeding programmes overcome some of their limitations. This is especially true for breeding for low-heritability disease traits that don't show up until an animal is an adult and has already been exposed to pathogens or environmental stressors. Nonetheless, it will still be important to have access to enormous databases of phenotypes related to health and disease. This review demonstrates unequivocally how important genetics are to cattle's general health and disease resistance. Hence, any comprehensive national disease management strategy should include breeding programmes for better animal health and disease resistance.

Background: With the potential for major performance and welfare improvements, efforts to reduce illness in cattle continue to make very significant strides. A better understanding of disease biology and epidemiology, as well as the creation of medications like antibiotics and anthelmintics for better disease control, are just a few examples of these advancements. In parallel, significant progress has been made in animal breeding and genetics, which is important for preventing animal diseases. Given that observable animal performance is the result of the interaction between the animal's genetic composition and the particular environment it was exposed to, these developments are of great interest to veterinarians. So, it makes sense that enhanced genetics could support present methods for preventing animal diseases. Because genetic gain is cumulative and permanent and because the genes introduced into a population can survive for many generations, it is profitable to improve animal health through genetic selection. Understanding the genetic basis of health and disease resistance not only makes it easier to establish breeding strategies for better health status, but it also produces knowledge for biomedical research in both humans and animals, with applications like vaccine creation.

Keywords: Biomedical research; Cattle health; Genomics; Production

Introduction

a. Genetic language

The terminology widely used by animal breeders to characterise the features of a population need to be defined before considering the genetics of animal health and disease resistance:

b. Phenotype

Simply put, an animal's phenotype is its behaviour as it is seen "in the field" (e.g., dystocia in cows or the presence or absence of infection as measured by a positive or negative diagnostic test result). A phenotype, or trait, can be discrete or continuous (also known as quantitatively; examples include milk yield and growth rate) (qualitative; e.g., did or did not succumb to disease). This review's goal is to provide an overview of research on the genetics of cattle disease resistance and animal health, with a focus on Irish cow studies. These findings have breeding implications for better animal health and disease resistance, which are described.

c. Genotype

There are various ways to define genotype. Breeders of animals frequently use genotype to characterise a certain strain of animal (e.g., animals of a given breed from a particular origin). To define the genetic variations (i.e., alleles) an individual contains at a certain location in its DNA, also known as a locus, molecular geneticists frequently use the term genotype.

Materials and Method

a. Genetic indicators

A genetic marker is a quantifiable variation in a population's DNA sequence. Microsatellites, indels (i.e., insertions or deletions of DNA fragments), single nucleotide polymorphisms (SNPs - pronounced "snips"), and copy number variants are examples of common polymorphic genetic markers (CNVs).

b. Locus of quantitative traits (QTL)

a chromosomal region that has been empirically shown to be statistically linked to variance in a complex or quantitative phenotypic variable.

c. Heritability

The percentage of phenotypic variation or differences within a

cohort of animals, that may be attributed to genetic diversity between individuals is known as heritability. Breeders of animals frequently refer to the narrow-sense heritability (h2), which is the percentage of phenotypic variation attributable to additive genetic variation (i.e., genes passed on from one generation to the next). Non-additive genetic variation is included in the numerator when calculating broad-sense heritability. We will only take into account narrow-sense heritability estimates in this review. The range of heritability is 0 (not heritable) to 1. (fully heritable). We can anticipate that a significant amount of the phenotypic differences between the parents will be handed down to the offspring if the heritability is high. Moreover, the manifested phenotype closely resembles the animal's genetic potential the more heritability there is.

d. Mother's genetic influence

The percentage of phenotypic diversity among offspring that is attributable to the genes expressed by the mother is known as maternal heritability. It is common to refer to a maternal heritability of calving difficulty, which takes into account factors like the dam's pelvic size. The direct heritability for problematic calves is the result of the dam's (and sire's) genes influencing factors like the size of the calf. Weaning weight has also been linked to maternal heritability, which takes into account the dam's hereditary traits including milk production [1-6].

e. Genetic diversity

A measurement of the variance or disparities within a population that are brought about by the animals' various genetic merits. The genetic standard deviation, or square root of the genetic variance, is a more popular way to express genetic variation within a population.

f. Biological connection

The strength of the linear association between two traits as a result of the genetic influences on each trait is referred to as their genetic correlation. It ranges from -1 (very adverse relationship), 0 (no relationship), and +1. (Strong positive relationship between two variables). Genetic correlations can result from a single mutation that affects both qualities (known as a pleiotropic impact) or from many mutations that influence both features but are typically inherited together (i.e., linked).

g. Breeding potential inferred (EBV)

According to an analysis of all the information on how well an animal and its close relatives perform for a trait, estimated breeding value is a determination of the genetic merit for an animal for a certain trait or set of qualities. The genuine breeding value (or true genetic quality) cannot be determined using conventional genetic evaluation techniques. The expected progeny difference (EPD), which is the EBV divided by two for beef cattle, or predicted transmitting ability (PTA), for dairy cattle, are the most common ways to evaluate the genetics of (i.e., an animal only passes half its genes to its progeny). The genetic gain for that trait will increase in proportion to the strength of the selection pressure. The heritability of the trait and the information available about the animal and its relatives both have an impact on the precision of selection. shows how, as the number of half-sib progeny with records rises across various heritability estimates, the accuracy of selection, ignoring pedigree contributions, increases. The accuracy will be greater for traits with a higher heritability for a given number of progeny. Accuracy levels close to unity are still possible, even for traits with low heritability, provided that there is enough data. So, if genetic diversity exists, genetic gain in low heritability variables is undoubtedly possible with the right breeding strategy and infrastructure for data collecting

and storage. Indirect selection for an associated characteristic may also improve the precision of selection for a particular trait (Figure 1). The generation interval is the average age of the parents at the time of the progeny's birth, while the genetic standard deviation is a measurement of the variation in the population. Irish dairy and beef cattle have a lifespan of roughly 6 years [3], which is consistent with estimates from other countries.

h. Cattle health and disease

i. Viral illnesses

Bovine viral illnesses are widespread in Ireland, including various respiratory viral infections and bovine viral diarrhoea (BVD) (infectious bovine rhinotracheitis [IBR], bovine parainfluenza-3 [PI-3] and bovine viral syncytial virus [BRSV]). There hasn't been any Irish research to yet that quantifies the genetic variation involved in bovine virus disease susceptibility. Nevertheless, breed variations in susceptibility to respiratory illness have been shown elsewhere [2-9]. Heritability estimates that are not zero have also been recorded, demonstrating the existence of genetic variations within breeds that affect susceptibility to respiratory disease. In Norwegian calves, Heringstad [5] calculated a respiratory illness heritability of 0.05 (SE = 0.018), with a genetic standard deviation of 2 percentage units. The most common agents causing respiratory disease in Norway are BRSV and PI-3 because the country is free of IBR and BVD.

j. Udder wellness

Mastitis is one of the most expensive diseases in dairy cattle production systems and is probably going to have a big impact on suckler beef production systems' profitability. Several international scientific investigations into the genetics of udder health have been conducted, including one that used Irish Holstein-Friesian dairy cows [8]. The heritability estimates for mastitis have varied between studies, reflecting variation in a wide range of factors including the person conducting the recording (e.g., farmer or veterinarian) and how they interpret the clinical signs, the completeness of data recording (e.g., some observations not recorded), as well as the pathogen and the environment, including exposure, which may influence how an animal's genotype expresses itself.
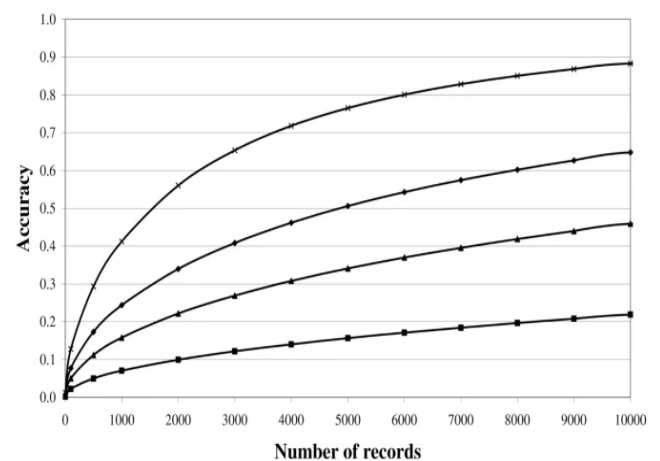

Figure 1: Accuracy of genomic selection for a trait between genotyped and phenotyped samples of animals with heritabilities of 0.03 (square), 0.15 (triangle), 0.35 (diamond), and 0.90 (x).

Discussion

a. Future investigation

Regular access to precise phenotypes—measurements of health traits—of animal health is one of the main obstacles to breeding for better animal health or disease resistance. Consequently, research must be done to create affordable and compassionate ways to either test animals for [10, 11] disease resistance to produce phenotypes (such as the tuberculin test) or to create precise biomarkers that can be easily detected in a lot of animals at a low cost. Achieving genetic gain also requires improved cooperation between veterinarians and animal breeders on the definition and collection of pertinent phenotypes as well as the most suitable statistical model, based on biological soundness.

Conclusions

The means for simultaneous selection on these qualities and other performance traits are available, and there is abundant evidence that genetics have a significant role in the health and resistance to disease in cattle. Additionally, the heritability estimates for health and disease resistance traits described in this review are probably an underestimate of the true heredity due to variances in exposure rates as well as the incomplete sensitivity and specificity of tests.

References

1. Alsan M (2015) The effect of the tsetse fly on African development. Am Econ Rev 105: 382–410.

2. Swallow, BM (2000) Impact of trypanosomiasis on African agriculture. PAAT Technical and Scientific Series.

3. Shaw APM, Wintd B GC, GRW, Mattiolie RC, Robinson TP, et al. (2014) Mapping the economic benefits to livestock keepers from intervening against bovine trypanosomosis in Eastern Africa. Prev Vet Med 113:197–210.

4. NTTICC (2004) National Tsetse and Trypanosomosis Investigation and Control Center.

5. Franco JR, Cecchi G, Priotto G, Paone M, Diarra A, Grout L, et al. (2018) Monitoring the elimination of human African trypanosomiasis: Update to 2016. PLoS Negl Trop Dis 12: 1–16.

6. Shaw A, Wint W, Cecchi G, Torr S, Waiswa C, et al. (2017) Intervening against bovine trypanosomosis in eastern Africa: mapping the costs and benefits. Food and Agriculture Organization of the United Nations PAAT Technical and Scientific Series.

7. Meyer A, Holt HR, Oumarou F, Chilongo K, Gilbert W, et al. (2018) Integrated cost-benefit analysis of tsetse control and herd productivity to inform control programs for animal African trypanosomiasis. Parasites and Vectors 11:1–14.

8. Tekle T, Terefe G, Cherenet T, Ashenafi H, Akoda KG, et al. (2018) Aberrant use and poor quality of trypanocides: a risk for drug resistance in south western Ethiopia. BMC Vet Res 14: 4.

9. Mulandane FC, Fafetine J, Abbeele J Van Den, Clausen P-H, Hoppenheit, A, et al. (2017) Resistance to trypanocidal drugs in cattle populations of Zambezia Province, Mozambique. Parasitol Res 117: 429–436.

10. Vreysen MJB, Seck MT, Sall B, Bouyer J (2013) Tsetse flies: Their biology and control using area-wide integrated pest management approaches. J Invertebr Pathol 112.

11. Scoones I (2014) The politics of trypanosomiasis control in Africa. STEPS Working Paper 57 Brighton STEPS Centre.