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Quantitative genetics: principles of farming in livestock production Genética cuantitativa: principios de la crianza en la producción pecuaria

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Abstract

The objective of the research was to describe quantitative genetics and breeding principles in animals destined for livestock production. Economically important characteristics, such as body weight gain, egg, milk, and meat production rate are quantitative or metric typologies, traits with continuous variability. The action of additive genes tends to originate a normal phenotypic distribution between the means of two progenitor populations, while multiplicative genes create geometric series governed by genes with multiplicative action. In addition, it should be considered that the most important factor in the creation of effective breeding techniques to optimize the genetic quality of animals is heritability, as they contain all types of gene action. In addition, parametric and non-parametric methods offer us a solution that becomes helpful or appealing to the questions that arise from the research and testing of hypotheses that are presented, we should also mention the models that explain the action of genes, such as breeding value and selection and production ability. Animal producers apply selection following several criteria in parallel as mating methods (panmixia, inbreeding, and heterosis). Finally, the application of breeding processes leads to a sensible selection by mating with special intentions without restrictions

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Resumen

El objetivo de la investigación fue describir sobre la genética cuantitativa y principios de la crianza en animales destinados a la producción pecuaria. Las características importantes, económicamente hablando, como: la ganancia de peso corporal, la tasa de producción de huevos, leche y carne son tipologías cuantitativas o métricas, rasgos con variabilidad continua. La acción de genes aditivos, tienden a originar una distribución fenotípica normal, entre las medias de dos poblaciones progenitoras, con respecto a los genes multiplicativos crean series geométricas regidas por genes con acción multiplicativa. Además, se debe considerar que el factor más importante en la creación de técnicas de crianza efectiva para optimizar la calidad genética de los animales es la heredabilidad, ya que contienen todos los tipos de acción génica. Además, los métodos paramétricos y no paramétricos nos ofrecen una solución que llega a ser de ayuda o atrayente para las interrogaciones que surgen de la investigación y pruebas de hipótesis que se presenten, también se debe mencionar los modelos que explican la acción de los genes, como es el valor de cría y selección y habilidad de producción. Los productores de animales aplican la selección siguiendo varios criterios paralelamente como métodos de apareamiento (panmixia, endogamia y heterosis). Finalmente aplicar procesos de crianza conllevan a una selección sensata realizando apareamientos con intenciones especiales sin restricciones.

Introduction

Quantitative genetics (QG) is a tool that allows us to determine the relative importance of the genotype and environment in certain cases of experimental organisms, it is possible to separate genotype and environment with respect to their effects on the measured phenotype that the most notable examples in genetics of the characteristics quantitative measures for improvement are milk production, birth weight, fleece weight in cattle, weaning weight, marble, among others¹. Quantitative traits exhibit a continuous distribution of phenotypes, they cannot be analyzed in the same way as traits controlled by larger genes. These characters are then described in terms of statistical parameters, the two mainly used are the mean variance² the factors mentioned are of a genetic nature but there are also environmental factors that affect the quantitative characters. The primary effect of the environment is to change the value for a particular genotype, it is necessary to compare the performance of the same genotype in different environments and evaluate the effect of the environment^{3,4}.

Research in animal breeding in recent years has focused on the study of production traits. Animal breeding programs in the last 50 years have focused on increasing production traits, while more recently they have focused on other traits, for example, in sheep for carcass typology, in pigs for daily back fat gain, lean meat percentage and ram size, in beef cattle for fertility, productive life, body condition and feed intake, and in cattle for fertility, productive life, body condition and feed intake⁵. The characteristics mainly studied in the world have been related to yield, but today the great challenges lie in selection tools for secondary characteristics, such as fertility, longevity and resistance to disease^{6,7}. For developing countries, the rapid changes in production systems are accompanied by the loss of local or natural gene-

tic material, actions should be considered to facilitate the characterization of these resources and use them in such a way as to take advantage of the benefits of transboundary breeds⁸. Local or native resources are fundamental to conserve options for future genetic improvement, given their advantages in certain characteristics of interest, a complete description of the production environments in which they are deployed in a direct way for their valuation and balance of the behavior of different breeds⁹. The subsistence of genetic variability in livestock is important, especially if we consider possible future changes in production parameters¹⁰. In recent decades there has been a significant increase in publications related to the maintenance of genetic resources, often using molecular genetic equipment, to determine, classify populations¹¹. The congruence's for increasing meat production in developing countries indicate that the most significant aspect of study is to have production environments, and to identify genotypes that are best adapted to particular sites, in order to improve the performance of animal genetic resources⁷. Similarly, two types of methods could be distinguished when dealing with quantitative traits and genetic effects to identify appropriate heritability. mentions that two types of methods could be distinguished: quantitative characters and genetic effects to find adequate heritability¹².

With respect to models that explain gene action such as: breeding value and selection, progeny difference, production ability, if we were to define "best" we would simply choose those individuals with the best breeding values. However, in real life the true breeding values are unknown¹³. In models seen above, the repeating traits are described as good or bad deviations from a population mean. Thus the average of components - ability to produce - whole population

will be equal to zero. $BV = GCV = G = E_p = E_t = P_A = 0$. The values BV - GCV , E_p and E_t will be independent of each other. In the case of the environment, the genetics of the horse will remain in the race performance, making it show no relationship in its genetic merit¹⁴.

At present, studies on QG and principles of breeding directly influence animal genetic improvement, becoming a significant element for the knowledge of professionals related to livestock production. In addition, research carried out by professors would make possible the continuous improvement of education and its linkage between theory and practice¹⁵. The study and monitoring of the consequences of scientific activity, through its dissemination, is useful to optimize research planning and decision making in scientific policy¹⁶. The main objective of this literature review study was to describe research on quantitative genetics and principles of breeding in livestock production animals.

Development

Quantitative and qualitative traits. QG is one of the main branches of genetics, it studies traits that are controlled by several genes, these traits are known as polygenic, it can also describe genetic properties in populations¹⁷.

Polygenetic traits are characteristics that are continuously dispersed, referring to the existence of many genes that help in the expression of various characteristics, and elements of the environment also participate in influencing this expression. Within QG, the additive genetic variance (expression of particular characteristics as a result of all genotypic expressions) is known as the intensity of similarity or resemblance that the offspring possesses from its parents².

Quantitative inheritance, a branch of genetics concerned with the study of the inheritance of measurable phenotypic/genotypic traits. In animal production, it is important to estimate this variability of countable qualities in a population and to interpret it¹⁸. This group of techniques is used to study variations in characters, whether morphological, behavioral or physiological. A clear example, the body size, also a certain locomotion performance, feeding behaviors and certain stimuli that exist towards some prey, etc¹⁹.

The objectives of QG are: to develop valid models for phenotypic expression when genotypes and environments are not identified, to develop models to describe population dynamics under natural, artificial selection, and to use this model to choose among a wide number of available artificial selection methods²⁰.

When the individual has a genotype contributed by several genes, it is called polygyny, and is within the additive model, a gene can have an additive allele (A), which contributes to the expression of a characteristic, and non-additive alleles (a) that do not contribute to the expression of a characteristic²¹. For example, carcass size, live weight of an animal or post-weaning weight, meat quality, etc. $P(\text{phenotype}) = G(\text{genotype}) + E(\text{environment})$. It depends on gene traits and is independent of the environment for its expression, the phenotype reflects genotype and is distributed in the class, which are coat color, presence or absence of antlers, some diseases. In the meat quality is taken into account by an appearance, composition and organoleptic characteristics²².

It is also responsible for the counting of traits, which are in whole numbers, such as the number of eggs a hen lays in a given time, the number of hens in a lit-

ter, etc²³. Other characteristics examined are threshold traits, those with few phenotypes and their inheritance is established by multiple genes affected by the environment, such as those traits that could determine the survival of a disease. They have a discontinuous distribution. Examples are twins of a cow or the parthenogenesis of turkeys, hip dysplasia, patent ductus arteriosus²⁴. In addition, the time that is given in the optimum value that some attributes have and they are the organoleptic ones in which it has a high geographical and cultural component²⁵.

Parametric tests in the calculation of additive characteristics. Ontogenetic variation, which consists of not having repetitions in different stages of growth of the individual, is considered as if it did not have genetic bases and is therefore within the environmental variation. The variance that exists between individuals can be considered as the differences that families present, therefore, it is within the genetic variance. Hence, parametric and non-parametric methods provide us with a solution that becomes helpful or interesting for the questions that arise in research. The parametric methods help with hypothesis tests that are presented, at the same time they require fulfillment of several assumptions²⁶.

The action and effect of an animal's development, known as ontogeny, explains how an organism develops from the ovule to the adult stage. When we talk about animal development, there are certain functions: to generate diversity at the cellular level by organizing cell types and reproduction to avoid the extinction of the species. When we speak of its variation, it refers to not carrying out certain maturation processes, in addition to the direction in which it will be forced to follow by some genetic change that has arisen in its ontogeny, which may alter its onto-

genetic process²⁷. If the ontogenesis process is altered, suppressed or deformed, a phenotypic variation will appear and a process of natural selection will begin. In order to generate some modification in the organism, when it reaches its adult stage, evolution must be present and atrophy the ontogenetic process. Regardless of what the alteration may be, it must be accessible to development, in addition to being produced by the individual's own ontogenesis. If evolutionary change is to occur, it must be ontogenetically possible. This would explain why there are traits that are more viable than others, if we have B and it changes to B+ or B-, the viability of B+ will depend on the occurrence of another series of trait changes, thus B- does not depend on this and will therefore be more accessible²⁸.

We can understand the concept of phenotype, which can extend to variations, below the gene level, that affect the fitness of an organism. Comparison of tadpoles consumed according to the 4 developmental categories, silent mutations that do not change the amino acid sequence of a gene, can transform the frequency of guanine-cytosine base pairs²⁹. These base pairs have a higher thermal stability (melting point) than adenine-thymine pairs, this property can be transmitted between organisms living in high temperature environments²⁹. These base pairs have a higher thermal stability (melting point) than adenine-thymine pairs, this property can be transmitted between organisms that live in high temperature environments.

Models explaining gene action

Value of breeding and selection. In the selection of traits, the breeder has the objective of identifying and selecting the most favorable genotypes in each individual. In the case of selection of more than one trait, the same principle is used, in this case differentiating

genotypes ends up being an impossible task, in this situation the breeder identifies the genetic value of the individual³⁰.

Phenotypic value is a record of the performance of each individual on a specific trait. On the other hand, the genetic value is related to the effects generated by the individual's genes on his performance. Phenotypic value, unlike the previous ones, is not measured directly. Environmental effects, which include non-genetic factors that act on the individual's performance for a trait⁴. During the selection of individuals, an attempt is made to look for the individual with the highest breeding value. This value is referred to as the sire value. But it is not only the phenotypic value of the individual that is taken into account, but also the genotypic value, since it frames general effects. The breeding value refers to the heritable part of the individual for the next generation³¹.

Production ability. For commercial production it is important to know the production ability, that is, if the feeding will be based on her production ability. For each cow, it is calculated based on the performance antecedents. The MMPPA (Most Probable Production Ability) when added to the population mean for a trait, will be a prognosis for the next record³².

Genetic model and threshold characteristics. These are polygenic characteristics that will not be continuous at the time of their expression, but expose categorical phenotypes. For example, fertility is believed to be influenced by many genes, but it will not be common to polygenic traits, but to a threshold trait³³. The threshold traits, like the polygenic quantitative traits, will not be very different, but the difference is in the phenotypes, they will not be expressed on a continuous scale in the threshold traits and that creates a number of problems. We should think as if we

have the underlying constant scale, the threshold will be considered the site on an underlying assignment scale above, demanding phenotypes and below it others³³.

Importance of heritability of traits. The calculation of h^2 is of great importance in the genetic value of breeders and in the prediction of the selection response³⁴, heritability is a genetic parameter specific to a population, given at a given time, which means that it varies from population to population, and is fundamental for the definition of selection methods, and estimates the relationship between genotype and phenotype³⁵. Heritability can be understood as the relationship between phenotypic values and breeding values to determine the character found in a population. The variations that exist between individuals are due to the influence of genetic and environmental factors. The heritability value is responsible for revealing the degree to which a trait is affected by genetic or environmental causes³⁶.

The importance of heritability lies in the fact that it is used for genetic research. There is much curiosity to know the different phenotypic characteristics, their causes, consequences and how transmission from generation to generation is possible. It should also be added that it determines the rate at which these changes arise within the population, their evolution, and response to natural selection³⁷. One of the most important elements in the formulation of effective breeding plans to improve genetic quality is heritability. If the heritability, in the strict sense h^2 , of a trait has been determined, and we know certain population values, then we can estimate the phenotypic value of that heritability. We can speak of heritability as a phenotypic variation that has an origin in additive genetics, and to place it in a range we can take values between 0 and 1, then we can estimate that, if

this variation is of genetic origin, then its offspring will have greater phenotypic characteristics of its parents and the heritability will have values close to 1.³⁸ On the other hand, Manjarrez Silva²¹ mentions that if it is of environmental origin, its values are estimated at 0.

Usefulness of heritability. It helps to predict the response given to selection, the magnitude with a directly proportional relationship with its genetic progress, plan another type of adaptation. So if the level of heterosis increases the intensity of heritability in that characteristic will also increase³⁹.

Heritability in the broad sense. It represents the proportion of the phenotypic variance reacted with the genotypic variance determined by the following letters VG/VP. That is, as the differences in the phenotype that we are observing are related to differences in the genotypes⁴⁰. On the contrary, if we have a high heritability in a broad sense, it means that the effect of the environment on the variation is relatively small, and there are genetic differences in the population⁴¹. According to Lineros Fuentealba⁴², he mentions that these proportions are measured by the variance (total phenotypic variance), which is determined by an additive genetic variance. This determines the genetic properties from the population point of view, it is worth mentioning that this also fulfills the function of a determinant in the rate at which a change occurs in the character of a population, this as a response to such selection⁴³.

Crossbreeding selection methods

Mating methods (panmixia, inbreeding and heterosis). In practice, selection is rarely made on the basis of a single characteristic. Animal breeders often practice selection on several criteria simultaneously. However, the more traits that are selected, the less

selection pressure can be exerted on each trait. Therefore, selection should be limited to the two or three traits that the breeder considers to be the most economically important⁴⁴. The methods used to determine an index can be very diverse, but generally they all consider the heritability and relative economic importance of each character, in addition to the genetic and phenotypic correlations between characters⁴⁴. Where X is the record of the efficiency or performance carried out by an individual, \bar{X} is the average efficiency or performance of the population and ΩX is the standard deviation of the trait. In the comparison of different traits, one is confronted with the fact that the mean and variability of each trait is different and often not expressed in the same units⁴⁵. However, the standardized variable is an abstract number (i.e., independent of the units used) based on the mean and standard deviation. Therefore, any recorded or graded production of a quantitative nature can be aggregated to any other characteristic if it is expressed in a standardized form⁴⁶.

Also known as kin selection, it emphasizes the changes in genetic frequencies through the generations and this is due to the fact that there has been some type of interaction between individuals of the same family. For example, if in a gene there is an increase in the aptitudes of the relatives, but at the same time the level of individual aptitude of the gene decreases, its frequency can also increase, and this is due to the fact that the relatives are usually carriers of the same genes. If there is an improvement in the fitness of the relatives, it is because sometimes it is necessary to compensate for the loss of fitness of the subjects with this trait⁴⁷.

If it is planned to improve the quality of the carcass or to reduce the fat present in the viscera, the animal, in this case the fish, must be slaughtered in order to

be able to control precise measurements. When the animal is already dead, it will obviously not be able to mate, but in order to improve these characteristics, family selection should be used¹³.

Bravo Gil⁴⁸, mentions that, if we want to verify that a male animal produced good offspring, we must observe his progeny, to which those genes were transmitted, as an example we have, that we mate a certain number of bulls with approximately twenty-five cows and we will compare the offspring of a bull with respect to the offspring of the other bulls⁴⁶. The bull that has managed to produce the best offspring in a given group of cows for a reproductive trait will be the bull with the best genotype.

Panmixia. In genetics it is a particular pattern of reproductive exchange in which each individual of one sex mates with the opposite sex at random with a phenotypic and genotypic preference^{49,50}. In itself, panmixia is an improvised mating where in a population that is panmictic there will be no limitations at the moment of mating, neither of its genetics nor even worse of its behavior, this means in a few words that any recombination will be feasible and possible, the mating is free of physical, social and genetic preferences, so that the environment does not intervene, the mating is given by means of a principle that is the Hardy-Weinber principle where the possibility that a subject mates with another that is X will be equivalent to the frequency of X in a certain population⁵¹.

Inbreeding. This is reproduction between individuals that are genetically related, i.e. animals mate with members of the same family. As an example, in a herd, a male mate with his daughters or sisters. Inbreeding is determined as the homozygous condition of genes that are found in the same chromosomal site, it presents a benefit in the genetic improvement of animals and plants, where the controlled conduct of

matings between individuals assigns homogeneous inbred lines that are different from each other increasing the chances of the offspring being affected by recessive traits⁵². As a consequence of this reproduction is the inbreeding depression, which appears by the mating of related individuals causing a loss of biological fitness, the genetic basis of this phenomenon is linked to the inbreeding that occurs in the descent of their parents, taking into account that they may be one or more ancestors, livestock species have effects on their production and reproduction⁵³. Among the advantages of inbreeding, being a production system, the result of the characteristics of the progeny will be very similar to that of their ancestors, although inbreeding can generate vulnerability to diseases, it can also increase the protection of deleterious alleles, the latter are alleles that have genes that cause death, because when they mutate they cause a lethal gene called essence gene⁵⁴. The main disadvantage of inbreeding in production animals is reflected in their reproductive properties, as the physiological characteristics of the reproductive organs are degraded, making it more difficult for these individuals to reproduce⁵⁵.

Types of Heterosis. Individual: has superiority of the F1 individual because it is hybrid. It is the perceived difference in the crossbred progeny corresponding to the average of its purebred parents. In addition, it is the deviation of the sum of the means of the reciprocal crosses to the sum of the two parental means and in the case of the F1 is regularly maximum. *Maternal*: it has superiority of the F1 individual because its mother is a hybrid. It is perceived by the use of heterozygous mothers. It is also the result of good care as a consequence of the superior performance of F1 females, but will be much higher in degree if the off-

spring is the offspring of an exogamous cross. *Paternals*: has superiority of the F1 individual due to the pure sire not related to the female. It significantly affects libido and semen production traits. They are used in areas where pure males would not be able to perform⁵⁶.

Genetic basis of heterosis. Over-dominance will exist when $Aa \geq AA$ or aa , with Aa being the heterozygote and AA and aa the homozygotes for the genes involved in the trait. Theoretically, it may be possible to fix the superiority of a line by making all individuals of that line homozygous dominant for all pairs of genes⁵⁷.

The measure of heterosis is very simple, it is generally expressed as the percentage increase or decrease in the performance of a hybrid compared to a reference genotype or a parameter⁵⁸.

Discussion

QA develops valid forms for phenotypic expression when genotypes and environments are not identified, develop models to describe population dynamics under natural, artificial selection, and use this model to choose among the large number of artificial selection methods available²⁰. Economically important characteristics such as qualitative traits and quantitative traits such as weight gain, egg or milk production, are metric traits, the number of genes that contribute to phenotypic variability and the degree to which the phenotype can be modified by environmental factors are attributed, and the metric traits are mentioned in whole numbers such as the number of eggs a hen lays in a given time, the number of hens in a given flock, the number of offspring in a flock, the number of hens in a flock, the number of hens in a flock, the number of hens in a flock, the number of hens in a flock, the number of hens in a flock.

flock, the number of hens in a flock, the number of hens in a flock, the number of hens in a flock, and the number of hens in a flock²³. On the other hand, Noguera¹⁸ states that quantitative inheritance is a branch of genetics that deals with the study of the inheritance of measurable phenotypic/genotypic characteristics. When studying continuous traits, referring to phenotypic characteristics influenced by the environment. The similarity between parents and progeny is referred to in a margin of geneticist terminology as such, as additive genetic variance, Hartl & Jones⁴ mention that environmental effects encompass non-genetic factors that act on the performance of the individual for a trait. Notivol²⁰ describes how population dynamics under natural and artificial selection and use this model to choose among the wide number of artificial selection methods available. Salas et al.²⁶ state that parametric methods help with the hypothesis testing that is presented, while requiring the fulfillment of several assumptions. In the case of selection of more than one trait using the same principle, differentiation of genotypes ends up being an impossible task, in this situation the breeder identifies the genetic value of the individual⁵⁹.

One of the most important factors in the formulation of breeding plans to improve genetic quality is heritability, which Saliba et al.³⁸ define as a phenotypic variation that has an origin in additive genetics, and to place us in a range we can take values between 0 and 1, then we can estimate that if such variation comes from genetic origin then their offspring will have greater phenotypic characteristics of their parents and the heritability will have values close to 1. On the other hand, it is mentioned that if it is of environmental origin, its values are estimated at 0²¹. Likewise, indices can be very diverse, but generally they all tend to consider the heritability and relative

economic importance of each character, in addition to the genetic and phenotypic correlations between characters, an index for three characters can have the general form⁴⁵. The magnitude with a directly proportional relationship to its genetic progress, plan another type of matching. So if the level of heterosis increases the intensity of heritability in that characteristic will also increase⁴⁰.

Conclusion

The assessment of traits investigated, such as discrete traits are under genetic control of one or one or several genes with little or no environmental disturbance that masks their effects. In contrast to this, variability exhibited by many important traits does not conform to separate phenotypic classes (dis-continuous variability), but forms a phenotype appearance that changes imperceptibly from one type to another (continuous variability). Quantitative traits may be governed by many genes each contributing a small amount to the phenotype such that their individual effects cannot be detected by Mendelian methods. Heritability is considered as an important factor in the formulation of effective breeding procedures to optimize the genetic quality of animals the knowledge of the relative contribution they make to the variability of the genes of a trait under consideration. The variability of phenotypic values for a quantitative trait can be disaggregated into its genetic and environmental components.

Thus determining that breeding techniques lead to reflexive selection by performing special-purpose matings without limitations. It is clear that in QG there are several methods for the value of genetic parame-

ters as it takes into account the traits that are controlled with the genes for existing populations. Besides being of great importance in the study of traits, QG is also used to perform statistical analysis and to calculate variations in the classification of phenotypes.

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Conflicts of interest

The manuscript was prepared and reviewed with the participation of the author, who declares that there is no conflict of interest that jeopardizes the validity of the results presented.

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Ethical considerations

The research complied with the ethical standards of the information process.

Authors' contribution to the article

The authors carried out the information gathering and bibliographic compilation, as well as the revision and writing of the final article.

Literature cited

1. Tirados SP. La mejora genética animal en la segunda mitad del siglo XX. *Arch Zootec* 2001; 50(192):517-46.
2. Falconer DS. *Introducción a la Genética Cuantitativa*. 3ra Edición. Nueva York: Longman Scientific and Technical; 1989.
3. Forsman A. Effects of genotypic and phenotypic variation on establishment are important for conservation, invasion, and infection biology. *Proc Natl Acad Sci USA* 2014;111(1):302-7. DOI: <https://doi.org/10.1073/pnas.1317745111>
4. Hartl D, Jones E. *Genética Cuantitativa* [Internet]. Burlington: Jones & Bartlett Learning; 1997 [citado 22 de octubre de 2021]. Recuperado a partir de: <http://uvigen.fcien.edu.uy/utem/gencuan/Gen%E9tica%20cuantitativa.pdf>
5. Toro MA. Achievements of research in the field of animal breeding and selection. In: Rosati A, Te-wolde A, Mosconi C, editors. *Animal production and animal science worldwide* [Internet]. The Netherlands: Wageningen Academic Publishers; 2005. p. 37-48. Recuperado a partir de: https://books.google.com.bo/books/about/Animal_production_and_animal_science_worldwide.html?id=0_3CegomgG4C&redir_esc=y
6. Misztal I. Shortage of quantitative geneticists in animal breeding. *J Anim Breed Genet* 2007; 124(5):255-6. DOI: <https://doi.org/10.1111/j.1439-0388.2007.00679.x>
7. Scholtz MM, McManus C, Okeyo AM, Theunissen A. Opportunities for beef production in developing countries of the southern hemisphere. *Livest Sci* 2011;142(1-3):195-202. DOI: <https://doi.org/10.1016/j.livsci.2011.07.014>
8. Rege JEO, Marshall K, Notenbaert A, Ojango JMK, Okeyo AM. Pro-poor animal improvement and breeding-What can science do?. *Livest Sci* 2011;136(1):15-28. DOI: <https://doi.org/10.1016/j.livsci.2010.09.003>
9. Groeneveld LF, Lenstra JA, Eding H, Toro MA, Scherf B, Pilling D, et al. Genetic diversity in farm animals-a review. *Anim Genet* 2010;41(Suppl 1): 6-31. DOI: <http://doi.org/10.1111/j.1365-2052.2010.02038.x>
10. Boettcher PJ, Tixier-Boichard M, Toro MA, Simianer H, Eding H, Gandini G, et al. Objectives, criteria and methods for using molecular genetic data in priority setting for conservation of animal genetic resources. *Anim Genet* 2010;41(Suppl 1):64-77. DOI: <https://doi.org/10.1111/j.1365-2052.2010.02050.x>
11. Hohenboken WD. ASAS Centennial Paper: Animal breeding research and the Journal of Animal Science: A century of co-evolution. *J Anim Sci* 2009;87(1):390-9. DOI: <https://doi.org/10.2527/jas.2008-1306>
12. Blasco A. *Apuntes de Genética Cuantitativa* [Internet]. Valencia: Universitat Politècnica de Valencia; 2010 [citado 22 de octubre de 2021]. 112 p. Recuperado a partir de: <https://www.mastergr.upv.es/Asignaturas/Apuntes/06.%20Cuantitativa%201/Libro%20cuantitativa.pdf>
13. Tave D. Programas de cría selectiva sencillos para aumentar la tasa de crecimiento y mejorar otros caracteres cuantitativos. En: Tave D, editor. *Programas de cría selectiva para piscifactorías de tamaño medio* [Internet]. Oregon: Organización de las Naciones Unidas para la Agricultura y la Alimentación; 1996. Recuperado a partir de: <https://www.fao.org/3/v8720s/V8720S00.htm#TQC>

14. Ordás López B, Malvar Pintos RA. Métodos clásicos de análisis de caracteres cuantitativos [Internet]. Pontevedra: Misión Biológica de Galicia; 2012 [citado 22 de octubre de 2021]. 53 p. Recuperado a partir de: https://digital.csic.es/bitstream/10261/167020/1/Ordas_Metodos_clasicos..pdf
15. Romera-lruela MJ. La investigación-acción en la formación del profesorado. Rev Esp Doc Cient 2011;34(4):597-614. DOI: <https://doi.org/10.3989/redc.2011.4.836>
16. Indicadores Bibliométricos de la Actividad Científica Española 2010 [Internet]. Fundación Española para la Ciencia y la Tecnología. 2013 [citado 5 de marzo de 2021]. Recuperado a partir de: <https://www.fecyt.es/es/publicacion/indicadores-bibliometricos-de-la-actividad-cientifica-espanola-2010-publicacion-2013>
17. Sosa Reyes B. Evolución de las estrategias de mejoramiento genético aplicado al ganado bovino [Internet]. Ergomix. 2011 [citado 3 de mayo de 2021]. Recuperado a partir de: <https://www.ergomix.com/ganaderia-carne/articulos/mejoramiento-genetico-bovino-t28872.htm>
18. Noguera JL. Mejora genética de los caracteres reproductivos en el porcino. SUIIS [Internet]. 2001 [citado 5 de octubre de 2021];(78):22-32. Recuperado a partir de: <http://www.ciap.org.ar/Sitio/Archivos/mejorageneticadeloscaracteresreproductivos.pdf>
19. Brodie ED. Genetic correlations between morphology and antipredator behaviour in natural populations of the garter snake *Thamnophis ordinoides*. Nature 1989;342:542-3. DOI: <https://doi.org/10.1038/342542a0>
20. Notivol E. Genética cuantitativa [Internet]. Centro de Investigación y Tecnología Agroalimentaria de Aragón. 2016 [citado 3 de mayo de 2021]. Recuperado a partir de: http://www.aecidcf.org.co/Ponencias/2016/septiembre/MI120916-1/6.Genetica_cuantitativa.pdf
21. Manjarrez Silva J. Selección natural, genética cuantitativa y evolución en culebras. Ciencia Ergo Sum 2001;8(1):56-61.
22. Calidad de la carne de cerdo [Internet]. Universo porcino. 2012 [citado 5 de septiembre de 2021]. Recuperado a partir de: http://www.universoporcino.com/articulos/carne_porcina_calidad_de_la_carne_de_cerdo.html
23. Ramírez-Valverde R, Núñez-Domínguez R, Fabián-Barrios E. Caracterización de las publicaciones sobre mejoramiento genético animal en revistas científicas mexicanas. Ecosistemas y Recursos Agropecuarios 2014;1(1):59-71.
24. Conte A, Marrube G, Pinto G, Robledo G, Rozen F. Bases para el diagnóstico de las enfermedades hereditarias en los animales domésticos [Internet]. Buenos Aires: Universidad de Buenos Aires; 2004 [citado 22 de octubre de 2021]. 56 p. Recuperado a partir de: <https://www.yumpu.com/es/document/read/16403423/bases-para-el-diagnostico-de-las-enfermedades-hereditarias-en-los->
25. Costea M, Brenner DM, Tardif FJ, Tan YF, Sun M. Delimitation of *Amaranthus cruentus* L. and *Amaranthus caudatus* L. using micromorphology and AFLP analysis: an application in germplasm identification. Genet Resour Crop Evol 2006;53:1625-33. DOI: <https://doi.org/10.1007/s10722-005-2288-3>
26. Salas C, Ene L, Ojeda N, Soto H. Métodos estadísticos paramétricos y no paramétricos para predecir variables de rodal basados en Landsat ETM+: una comparación en un bosque de Araucaria araucana en Chile. Bosque (Valdivia) 2010;31

- (3):179-94. DOI: <http://doi.org/10.4067/S0717-92002010000300002>
27. Caponi G. Selección interna: el control de la filogenia por la ontogenia en una perspectiva variacional. *Theoria* 2008;23(2):195-218. DOI: <https://doi.org/10.1387/theoria.395>
 28. Caponi G. El retorno de la ontogenia: un conflicto de ideales de orden natural en la biología evolucionaria actual. *Sci Stud* 2007;5(1):9-34. DOI: <https://doi.org/10.1590/S1678-31662007000100002>
 29. Briceño K. Qué son las variaciones fenotípicas [Internet]. Lifeder.2021 [citado 3 de octubre de 2021]. Recuperado a partir de: <https://www.lifeder.com/variaciones-fenotipicas/>
 30. Barbadilla A. Herencia Cuantitativa [Internet]. Genética. 2021 [citado 3 de octubre de 2021]. Recuperado a partir de: http://bioinformatica.uab.es/base/documents/genetica_gen/Tema%209%20Herencia%20cuantitativa2015_4_30D11_49.pdf
 31. Genghini R, Bonvillani A, Wittouck P, Echevarría A. Introducción al mejoramiento animal [Internet]. Sitio Argentino de Producción Animal. 2002 [citado 3 de mayo de 2021]. Recuperado a partir de: <https://www.produccion-animal.com.ar/genetica-seleccion-cruzamientos/genetica-en-general/05-introduccion-al-mejoramiento-animal.pdf>
 32. Pinto-Escalante D, Ceballos-Quintal JM, Castillo-Zapata I, López-Avila MTJ. Fundamentos y actualidades del asesoramiento genético. *Rev Biomed* 2001;12(3):186-95.
 33. López Santillán IC, Figueroa Gutiérrez AH. Estudio de la herencia poligénica [Internet]. Reportes de investigación o prácticas. 2017 [citado 3 de mayo de 2021]. Recuperado a partir de: <https://www.uaeh.edu.mx/scige/boletin/icsa/n4/p1.html>
 34. Montes D, Vergara O, Barragán W. Diferencia esperada de progenie como herramienta de selección para peso al destete en ganado Brahman. *Rev MVZ Córdoba* 2011;16(1):2381-90. DOI: <https://doi.org/10.21897/RMVZ.297>
 35. Ossa G, Suárez Tronco M, Pérez J. Efectos del medio y la herencia sobre el peso al destete de terneros de la raza Romosinuano. *Rev MVZ Córdoba* 2005;10(2):673-83. DOI: <https://doi.org/10.21897/rmvz.471>
 36. Martínez-González JC, Castillo-Rodríguez SP, Lucero-Magana FA, Ortega-Rivas E. Influencias ambientales y heredabilidad para características de crecimiento en ganado Sardo Negro en México. *Zootecnia Trop* 2007;25(1):1-7.
 37. Téllez Barragán MC. Estudio de la heredabilidad en la Queiloscopia. *Revista de La Escuela de Medicina Legal* 2011;0(17):32-44. DOI: https://doi.org/10.5209/rev_reml.2011.v17.36233
 38. Saliba A, Figueiredo ACV, Baroneza JE, Afiune JY, Pic-Taylor A, Oliveira SF, et al. Genetic and genomics in congenital heart disease: a clinical review. *J Pediatr (Rio J)* 2020;96(3):279-88. DOI: <https://doi.org/10.1016/j.jped.2019.07.004>
 39. Ríos-Utrera Á, Hernández-Hernández VD, Villagómez Amezcua-Manjarréz E, Zárate-Martínez JP. Heredabilidad de características reproductivas de Vacas InduBrasil. *Agron Mesoam* 2013;24(2):293-300. DOI: <https://doi.org/10.15517/am.v24i2.12529>
 40. Pistorale SM, Abbott LA, Andrés A. Diversidad genética y heredabilidad en sentido amplio en agropiro alargado, *Thinopyrum ponticum* *Cienc Inv Agr* 2008;35(3):259-64. DOI: <https://doi.org/10.4067/S0718-16202008000300003>

41. Herrera Martínez M, Fernández Caraballo D, Estrada López K, Yera Vázquez M, Chaviano Machado S, Pérez Rodríguez LM, et al. Heredabilidad del fenotipo longevo en familias de excepcional larga vida, procedentes de Villa Clara. *Medicentro Electrónica* 2017;21(2):127-38.
42. Lineros Fuentealba YA. Heredabilidad del largo de internudo en un ensayo de progenie de polinización abierta de uninodales de *Pinus radiata*. Valdivia: Universidad Austral de Chile; 2006.
43. Vergara Garay OD, Martínez Humanes N, Flórez Murillo JM, Hernández Pérez M, Almanza Loaiza R, Rúgeles Pinto C, et al. Heredabilidades, correlaciones y tendencias genéticas para características reproductivas en una población bovina multi-racial en Colombia. *Ces Med Vet Zootec* 2015;10(1):8-17.
44. van Arendonk JAM, Bijma P. Factors affecting commercial application of embryo technologies in dairy cattle in Europea modelling approach. *Theorigenology* 2003;59(2):635-49. DOI: [https://doi.org/101016/s0093-691x\(02\)01245-1](https://doi.org/101016/s0093-691x(02)01245-1)
45. Willis MB. Dalton's introduction to practical animal breeding. Oxford: Blackwell Scientific Publications; 1991. p. 166.
46. Glenn T. Principles of genetics. Ámsterdam: Wageningen Academic Publishers; 2002.
47. Tave D. La selección de caracteres cuantitativos. En: Tave D, editor. Programas de cría selectiva para piscifactorías de tamaño medio [Internet]. Oregón: Organización de las Naciones Unidas para la Agricultura y la Alimentación; 1996. Recuperado a partir de: <https://www.fao.org/3/v8720s/V8720S00.htm#TOC>
48. Bravo Gil A. Selección de pie de cría [Internet]. Bogotá: División de Formación a Distancia; 1985 [citado 22 de octubre de 2021]. 42 p. Recuperado a partir de: https://repositorio.sena.edu.co/bitstream/11404/483/12/vol3_seleccion_pie_cria_op.pdf
49. Alors D, Dal Grande F, Cubas P, Crespo A, Schmitt I, Molina CM, et al. Panmixia and Dispersal from the Mediterranean Basin to Macaronesian Islands of a Macrolichen Species. Frankfurt: Universitätsbibliothek Johann Christian Senckenberg; 2017.
50. Curtis H, Barnes NS, Schnek A, Massarini A. Biología [Internet]. Buenos Aires: Editorial Medica Panamericana; 2008 [citado 22 de octubre de 2021]. 1160 p. Recuperado a partir de: <https://books.google.com.ec/books?id=mGadUVpd-TLsC&pg=PA355&dq=panmixia&hl=es-419&sa=X&ved=2ahUKEwiz7cag-penqAhXnc98KHcIYA9EQ6AEwA-HoECAAQAg#v=onepage&q=panmixia&f=false>
51. Kalmes R, Huret JL. Modelo de Hardy-Weinberg [Internet]. Atlas of Genetics and Cytogenetics in Oncology and Haematology. 2001 [citado 3 de mayo de 2021]. Recuperado a partir de: [http://atlasgeneticsoncology.org/Educ/HardySp.html#:~:text=El%20equilibrio%20de%20Hardy%2DWeinberg%20es%20un%20modelo%20te%C3%B3rico%20para,al%20azar%2C%20\(panmixia\)](http://atlasgeneticsoncology.org/Educ/HardySp.html#:~:text=El%20equilibrio%20de%20Hardy%2DWeinberg%20es%20un%20modelo%20te%C3%B3rico%20para,al%20azar%2C%20(panmixia))
52. Aguirre-Valverde J, Vargas-Leitón B, Romero-Zúñiga JJ. Efectos de la endogamia sobre parámetros Reproductivos en vacas holstein y jersey de Costa Rica. *Agron Mesoam* 2013;24(2):245-55. DOI: <https://doi.org/10.15517/am.v24i2.12523>
53. Escorcia-Gutiérrez N, Molina-Galán JD, Castillo-González F, Mejía-Contreras JA. Rendimiento, heterosis y depresión endogámica de cruza simples de maíz. *Rev Fitotec Mex* 2010;33(3):271-9. DOI: <https://doi.org/10.35196/rfm.2010.3.271>

54. Definición de deletéreo [Internet]. Definición de. 2008 [citado 5 de marzo de 2021]. Recuperado a partir de: <https://definicion.de/deletereo/#:~:text=Estos%20genes%20se%20presentan%20en,se%20conoce%20como%20gen%20esencial>
55. Ocampo GR, Cardona CH. La endogamia en la producción animal. Rev Colombiana Cienc Anim 2013;5(1):463-79. DOI: <https://doi.org/10.24188/recia.v5.n2.2013.458>
56. Walters R. Heterosis (vigor híbrido) y consanguinidad [Internet]. 3tres3.com. 2015 [citado 3 de mayo de 2021]. Recuperado a partir de: https://www.3tres3.com/articulos/heterosis-vigor-hibrido-y-consanguinidad_35039/
57. Bueno Pérez JA. Cruzamientos [Internet]. Ergomix. 2018 [citado 3 de mayo de 2021]. Recuperado a partir de: <https://www.engormix.com/ganaderia-carne/articulos/buenovet-cruzamientos-t42274.htm>
58. Lagos TC, Criollo H, Checa O. Divergencia genética y heterosis. Rev Cienc Agríc 2003;20(1-2):10-26.
59. Barbadilla A. Genética de poblaciones [Internet]. Genética. 2015 [citado 3 de mayo de 2021]. Recuperado a partir de: <http://bioinformatica.uab.es/base/base3.asp?sitio=geneticapoblaciones&anar=concep&item=Hardy-Weinberg>

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