



## Molecular-Genetic Processes and Analysis in Domestic Animals

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**Abstract:** Genetic variations that lead to easily identifiable phenotypic changes have always been of interest to animal breeders since domestication. Molecular genetics has opened up possibilities for identifying these variations and understanding their biological and population effects. The following is about it.

**Key words:** domestic animals, genetic variability, molecular markers.

### Introduction

In domestic animals, the first signs of mutations were obtained during phenotypic observation, i.e. direct contact led to the observation of animals with a different phenotype that could be passed on to their offspring. Some of the earliest examples are the five-toed gudan birds, polled Hereford cows, and the short-legged Ancon sheep. Based on the first discoveries of genetic mechanisms, researchers tried to infer the inheritance of these traits in domestic animals, often based on other living things.

Human actions through domestication and phenotypic selection have altered the genetic constitution of livestock populations. An example is the fixation of alleles of genes associated with the behavior of rabbits that were selected for obedience during domestication. Nowadays, with the development of molecular genetic methods, it has become possible to "visualize" changes in hereditary molecules and understand spontaneous variations, their phenotypic effects and their transmission to offspring. In addition, molecular genetics plays an important role in animal husbandry, allowing paternity testing and the detection of fraud and genetic diseases, among other possibilities that will be explored in this review.

Therefore, the purpose of this article was to report on the various perspectives on the application of molecular genetics not only in animal husbandry and genetics, but also in animal husbandry, by providing examples of successful and repetitive use, in addition to better contextualizing it. information, showing you how to use it.

Selection based on genetic variants. When we talk about molecular genetics applied to animal husbandry, we immediately think of the identification of genes, their polymorphisms, their phenotypic effects, and hence their possible use in breeding. There are two main uses for genetic

variants: selection based on a functional mutation, and inclusion of that genetic variant in a model used for genetic evaluation.[1]

### Literature review

The literature used to write the article was used on the basis of sources related to the topic of molecular genetic processes in animals and their analysis. The necessary sources were obtained and included in the list of references.

### Research Methodology and Empirical Analysis

**Paternity tests.** Paternity tests in pets have two main uses: registering animals with breed associations and providing accurate pedigree information for genetic evaluations. Some breed associations require paternity testing for registration, while others randomly select animals to be submitted for paternity testing for registration.

In genetic evaluations, pedigree among the animals being evaluated is fundamental to predicting breeding value. Wrong ratios can lead to prediction errors. Nowadays, with the advent of genomic selection, paternity errors are easy to identify because SNP array genotyping used for selection can also be used for paternity testing. [2]

**Genetic diseases.** There are a number of genetic diseases that affect domestic animals and therefore affect the performance of animals. The identification of genetic variants of these diseases allows mating to be controlled and directed to prevent the spread of damage caused by the disease.

An example of a livestock disease that has a direct impact on livestock production is hyperkalemic periodic paralysis in horses. It is a dominant autosomal genetic disorder that is important in Quarter Horses and related/derived breeds. Symptoms of the disease include attacks of weakness, tremors, and intermittent paralysis. Animals also exhibit a hypertrophied muscle phenotype. This phenotype was highly sought after by Quarter Horse conformation line breeders, leading to the spread of the disease along with its detrimental effects.

**Fraud detection.** Molecular genetic markers are very useful in detecting possible forgeries in animal products such as meat, milk and their derivatives. This type of fraud is common to reduce production costs; for example, cow's milk is mixed with milk of other species (goat, buffalo or sheep) and meat and meat products of domestic mammals (cattle, sheep, goats, pigs and horses) and poultry (chicken, turkey). Fraud can be detected by protein analysis, but DNA tests have proven to be cheaper and equally or even more effective.[3]

**Parasite identification.** Parasitology is an important area of animal husbandry. High costs are associated with preventive practices. Moreover, poor sanitation management can lead to reduced productivity, disease and death of animals. High rates of invasion require the use of specific antiparasitic agents. The intensity of application and drug of choice must be appropriate to avoid selection of resistant parasite populations. Available methods such as faecal egg count, larval culture or microscopic examination are insensitive and time consuming. Thus, the effective identification of parasite species is very important, since it allows tracking drug resistance and the spread of parasites depending on climate change. In this regard, molecular biology techniques can be used to identify parasites as well as to control infestation.[4]

### Results

**Genetic diversity.** Molecular genetics also contributes to population studies designed to assess genetic diversity. Genetic diversity is important in maintaining the variability of a population

influenced by domestication or selection, and in initiating and maintaining breed conservation programs. Molecular markers make it possible to assess the degree of heterozygosity in a population and thus to observe the possible effects of inbreeding. Then, population studies of inbreeding are completed or, if there is no pedigree data for the population, in loco inferences can be made about its genetic variability (Kristensen et al. 2015). The markers most commonly used to test for this variability are microsatellites, which are multi-allelic markers distributed throughout the genome. Santos et al. (2016) report examples of loss of genetic variation in tambaki (*Colossoma macropomum*), a fish species of commercial interest, due to captive rearing and lack of relationship control. Other genotyping methods such as SNP arrays can be used to assess genetic diversity. Makina et al. (2014) studied the population structure of six South African cattle breeds using the SNP chip. The authors found low to moderate genetic variation in the breeds, as well as a divergence between local breeds and breeds locally bred from European breeds, suggesting the importance of conservation to cope with environmental changes. Mastrangelo et al. (2017), studying the endangered Barbaresca sheep, showed the importance of using SNP chips in small populations and future strategies to be used for better genetic conservation. Barbaresca sheep have a small effective population, a high level of inbreeding, and many homozygous loci. Genomic information plays a critical role in breed management.[5]

**Editing the genome.** Genome editing is the latest frontier of molecular biology achieved in animal husbandry. This procedure consists of identifying a specific target and then inducing a mutation or knockout of a gene in an organism in order to achieve improvements in livestock production that reflect positively on the people who depend on it. According to Petersen (2017), there are three main methods for editing the genome. Their application to pets is still in research but is already showing results of potential applicability.

Examples of successful genome editing in animal husbandry are the production of comologo Holstein cattle (Carlson et al. 2016) by introgression of a causal mutation in Celtic breeds by editing the genome and interrupting the *MSTN* and *FGF5* genes in goats (Wang et al. 2015) to improve animal performance, as well as *MSTN* in cattle and sheep with spectacular phenotypic changes (Proudfoot et al. 2015).

There are also applications of genome editing in domestic animals for biomedical purposes, such as breeding pigs that have genes encoding cell surface proteins removed to reduce organ rejection in xenotransplantation (Butler et al. 2016).

It should be remembered that genome editing does not apply to transgenics, since in most cases it only causes modifications to the DNA of one species, not combining it with DNA from another species, and therefore, has the potential to be more regulated in terms of legislation.[6]

### **Conclusion**

Molecular genetics has many applications in animal husbandry. Knowledge of methods and their application is essential for the management of intensive livestock production. The inclusion of disciplines or subjects in undergraduate and graduate courses on the topics mentioned above is fundamental to preparing specialists for providing services to the market and developing future technologies related to this area. This review was intended to collect information on the application of these molecular techniques in animal production.

**References:**

1. Abell CE, Dekkers JCM, Rothschild MF, Mabry JW, Stlader KJ (2014) Estimating the total cost of implementing genomic breeding in a multi-level pig production system. *Genetics, breeding, evolution* 46, 32. doi: 10.1186/1297-9686-46-32
2. Alyethodi RR, Singh U, Kumar S, Alex R, Deb R, Sengar GS, Raja TV, Prakash B (2018) T-ARMS PCR genotyping of SNP rs445709131 using thermostable chain displacement polymerase. *BMC Research Notes* 11, 132. doi: 10.1186/s13104-018-3236-6
3. Tavares KCS, Carneiro IS, Rios DB, Feltrin C, Ribeiro AKC, Gaudêncio Neto S, Martind LT, Aguiar LH, Lazzarotto CR, Calderón CEM, Lopes FEM, Teixeira LPR, Bertolini M, Bertolini LR (2015) Quick and easy method for sex determination of livestock embryos based on polymerase chain reaction. *Genetics and Molecular Research* 15. doi:10.4238/gmr.15017476
4. Kristensen TN, Hoffmann AA, Pertoldi C, Stronen AV (2015) What can livestock breeders learn from conservation genetics and vice versa? *Frontiers in Genetics* 6, 38. doi:10.3389/fgene.2015.00038
5. Hashimoto DT, Senhorini JA, Foresti F, Porto-Foresti F (2012) Interspecific fish hybrids in Brazil: management of genetic resources for sustainable use. *Reviews in Aquaculture* 4, 108–118. doi:10.1111/j.1753-5131.2012. 01067.x
6. Rudolph JA, Spier SJ, Byrns G, Rojas CV, Bernoco D, Hoffman EP (1992) *Tabiat genetikasi* 2, 144-147. doi:10.1038/ng1092-144