GENETIC ENGINEERING AND FARMING IN ANIMALS: A REVIEW

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ABSTRACT

Availability of animal protein for human consumption is very low in the developing countries mainly because of low productivity of existing livestock; ways and means to improve productivity through breeding are discussed and some basic issues requiring further research pointed out. Human beings have been altering the characteristics of farm animals through selective breeding since the beginning of domestication thousands of years ago. In recent decades, selective breeding has been aided by a number of assisted reproductive technologies such as artificial insemination and embryo transfer. Within the globalised animal breeding industry, a small number of large multinational companies control the vast majority of livestock and poultry breeding. Increasingly, specialized breeds have been developed that produce very high yields of a single commodity (such as meat, milk or eggs). The drive to increase productivity has, in many cases, had serious consequences for the health and welfare of the animals.

Keywords: Animal proteins, Organic farming, Breeding, Reproductive technology.

INTRODUCTION

This paper discusses the use of genetic engineering applications in animal breeding, including a description of the methods, their potential and current uses and ethical issues. Genetic engineering is the name of a group of techniques used to identify, replicate, modify and transfer the genetic material of cells, tissues or complete organisms [1]. Important applications of genetic engineering in animal breeding are:

1. Marker-assisted selection (MAS). The objective of this technology is to increase disease resistance, productivity and product quality in economically important animals by adding information of DNA markers to phenotypes and genealogies for selection decisions.

2. Transgenesis, the direct transfer of specific genes/alleles between individuals, species, or even Kingdoms, in order to change their phenotypic expression in the recipients. Compared to the 'traditional' improvement techniques based on

phenotypic information only, these *gene-by gene* techniques allow theoretically a more complete management of animal genomes for animal breeding. In spite of high expectations and new technical developments, its actual efficiency is not always high, as they require a thorough knowledge of functional genomics, and pose additional technical, economical and ethical problems. The possible role for cloning adult animals in breeding is also discussed [2].

These procedures are of use to identify, replicate, modify and transfer the genetic material of cells, tissues or complete organisms [3]. Most techniques are related to the direct manipulation of DNA oriented to the expression of particular genes. In a broader sense, genetic engineering involves the incorporation of DNA markers for selection (marker-assisted selection, MAS), to increase the efficiency of the so called 'traditional' methods of breeding based on phenotypic information. The most accepted purpose of genetic engineering is focused on the direct manipulation of DNA sequences these techniques involve the capacity to isolate, cut and transfer specific DNA pieces, corresponding to specific genes [4]. the mammalian genome has a larger size and has a more complex organization than in viruses, bacteria and plants. Consequently, genetic modification of animals, using molecular genetics and recombinant DNA technology is more difficult and costly than in simpler organisms. In mammals, techniques for reproductive manipulation of gametes and embryos such as obtaining of a complete new organism from adult differentiated cells (cloning), and procedures for artificial reproduction such as in vitro fertilization, embryo transfer and artificial insemination, are frequently an important part of this processes [5].

CATTLE AND BUFFALO BREEDING FOR MILK PRODUCTION

Milk production under traditional conditions in Africa and Asia has since long been a part of extensive production systems where the production of milk is combined with or exists as a sideline to beef production (e.g., the Sahelian zone of Africa), the production old draught animals (e.g., India) or a combination of all three (e.g., buffaloes in India and Pakistan). Milk production per animal in these traditional systems is very low. AMBLE and estimated that the average annual milk production of the 45.5 million cows of India was only 174 kg, while

the corresponding average for the buffaloes was 491 kg. The traditional systems are likely to continue for quite some time but simultaneously more intensive systems are being developed. As will be shown below, breeding measures have a very important role in the development of these improved production systems [6].

BREED COMPARISONS

Excessive heat has a detrimental effect on milk production. The most common lasts to measure the animals' reaction and ability to tolerate high ambient temperatures are based on the changes in rectal temperatures, respiration rate and feed intake Europeanism-type dairy cattle show a marked decrease in feed intake when kept for prolonged periods at 27" and above. Zebu type cattle do not start losing appetite until temperatures of about 35" are reached [7]. However even at temperatures, the feed intake and milk production generally remain considerably higher in absolute terms for European-type dairy cattle than for zebus. There are individual variations between cows within breeds in their ability to maintain iced intake and production under heat stress. Although heat tolerance tests and the various indirect ways of measuring adaptability to hot climates may become important in selection for high milk yield in hot climates in the future, the main criterion for selection at the present time is performance, i.e., milk yield under the existing type of climate [8].

USE OF GENOMIC INFORMATION IN ANIMAL IMPROVEMENT

The use of genomic information (sequences or DNA marker polymorphisms) for the genetic improvement and selection of animals requires the knowledge of the effect of physically mapped genes with effects on economically important traits or quantitative trait loci (QTL). This information is also required in order to effectively use Transgenesis and MAS for genetic improvement [9]. In MAS, the genomic information is combined with the classical performance records and genealogical information to increase selection accuracy, performing selection earlier in life and reducing costs. The traits, on which the application of marker-assisted selection can be more effective, are those that are expressed late in the life of the animal, have low heritability, are sex-limited, are expensive to measure or are controlled by a few genes. Examples are longevity, carcass traits in meat producing animals, and diseases or defects of simple inheritance [10].

Expected increments in selection response from MAS for a Single complex trait, using known QTL genotypes plus linear model predictions (BLUP), compared to selection on BLUP alone, ranges from -0.7 to 64 percent. In practice, results will depend on many parameters which are likely to be very different for each trait combination and population. The statistical properties of genetic evaluations (predictions) of animals for quantitative traits obtained through mixed model methodology using phenotypic records and genealogical information as inputs are known as BLUP. Best -means minimum variance of prediction, Linear -because predictions are linear functions of observations, Unbiased -means that the expected value of predictors obtained with linear model have an expected value equal to the expected value of the mean of the breeding values, conditional to data, and Prediction - because involves prediction of random breeding values). Most experiments on QTL detection in animals allow only the estimation of wide chromosomal regions (practical maximum resolution is of about 1 cm, but usual resolution is about 30 cm) that harbor a QTL in a 'statistical sense', estimated from the effects of some marker heliotypes on quantitative traits. Thus, further confirmation is required in order to assure the use of the causative gene. Identification of the causative gene has proven to be difficult. The process to identify the gene responsible for the effect is known either as 'fine mapping' studies (targeting mapping smaller genomic regions) or 'candidate gene' studies (targeting individual genes based on their probable function). In practice, MAS is useful to select genes with effects well identified and precisely located in the genome such as those controlling monogenic recessive diseases such as the pig stress syndrome gene. However, for most recessive alleles with lethal or semi-lethal effects, natural selection will maintain their frequencies very low making MAS unnecessary. Unless the additive and no additive effects for most genes involved in the phenotypic expression of complex, economically important traits are determined, MAS should be regarded just as a tool to increase the rates of genetic gains and not a method to fully open the 'black box' of the genetic control of complex traits, that would render phenotypic selection 'obsolete'. Therefore, the perspectives on the optimum use of DNA marker information in the framework of a genetic program is still a matter of debate. Quantitative trait loci experiments using crosses between breeds or lines with extreme genotypes for a trait, increases the power of detecting QTLs for that trait, compared to within-family designs. These across population's polymorphisms are not necessarily useful to perform MAS for within-population selection. The favorable allele could be fixed in parental

populations and crosses may be commercially irrelevant. Wide genome scans for positioning a QTL using crosses or within-family experiments are only the initial phase of the search for a true mayor gene involved in a complex trait.[10] another source of complexity for detection and use of QTL for selection is genetic heterogeneity, where DNA mutations in several sites produce the same phenotype. Major single gene effects can be sometimes compensated in the organism using alternative metabolic pathways [11].

CLONING METHODS

In the case of Dolly, mammary gland cells in culture from a 6-year old donor ewe, where subjected to a reduction in the concentration of serum and thus obliged to enter in a quiescent state of the cell cycle (G0). Nuclear transfers to enucleated oocytes, was followed by electrical pulses for fusion of the donor cell nucleus and oocyte membranes and activate division.

USE OF CLONING IN ANIMAL BREEDING

Use of cloning in animal genetic improvement may increase the rates of selection progress in certain cases, particularly in situations where artificial insemination is not possible, such as in pastoral systems with ruminants. Currently, high costs of cloning are one of the main factors limiting their use as a technique in practical animal breeding. Clonally groups, however more uniform than full sibs, will have all differences caused by the environmental fraction of variation for measured traits, which is usually more than 50% of total variation [12].

DISCUSSION

Detecting genes related to disease and their expression in humans from studies on the genome, could lead to the development of therapies and the development of drugs for specific individuals, and enhanced early diagnosis of individuals with high-risk genotypes, allowing for preventive or remedial actions, even gene therapy. In animals, this knowledge could lead, in addition, to select against defective genes. In livestock, knowledge of effects of specific genes and gene combinations on important traits could lead to their enhanced control to create new, more useful populations. The use of specific gene information is not a

panacea, but could help to increase rates of genetic improvement, and open opportunities for using additive and non-additive genetic effects of domestic species, provided wise improvement goals are used and this new technology is optimally used together with the so called 'traditional' or 'conventional' methods based on phenotypic and genealogical information.

REFERENCES

1. ADAMS, N.R.; BRIEGEL, J.R. and WARD, K.A. The impact of a transgenic for bovine growth hormone on the performance of two breeds of sheep. Journal of Animal Science, September 2002, vol. 80, no. 9, p. 2325-2333.

2. ANDERSSON, Leif. Genetic dissection of phenotypic diversity in farm animals. Nature Reviews Genetics, February 2001, vol. 2, no. 2, p. 130-138.

3. ARCHIBALD, A.L. and HALEY, C.S. What can the genetics revolution offer the meat industry? Outlook on Agriculture, December 2003, vol. 32, no. 4, p. 219-226.

4. BARBIERI, M.E.; MANFREDI, E.; ELSEN, J.M.; RICORDEAU, G.; BOUILLON, J.; GROSCLAUDE, F.; MAHE, M.F. and BIBE, B. Effects of the alpha(s1)-casein locus on dairy performances and genetic-parameters of alpine goats. Genetics Selection Evolution, September- October 1995, vol. 27, no. 5, p. 437-450.

5. BOICHARD, D.; LE ROY, P.; LEVÉZIEL, H. And ELSEN, J.M. Utilisation des marqueurs moléculaires en génétique animal. Productions Animales, January 1998, vol. 11, no. 1, p. 67-80.

6. BONNEAU, M. and LAARVELD, B. Biotechnology in animal nutrition, physiology and health. Livestock Production Science, June 1999, vol. 59, no. 2-3, p. 223- 241.

7. AMBLEV, . N. and J. P. JAIN, 1965 Comparative performance of different grades of cross bred

8. BRANTONC,. , R. E. MCDOWELML,. A. BROWN1,9 66 Zebu-European crossbreeding as a basis of COCKRILWL, . R., 1974 The husbandry and health of the domestic buffalo. FAO, Rome. (In CREEKM, . J., D. DESTROD,. G. MILES,D . M. REDFERN,J . ROBB, E. W. SCHLEICHaEnRd H. A.

9. A case study in the transfer of technology: the UNDP/FAO feedlot project Sheep production potential in eastern Mediterranean. World Anb. Cows on military farms in India. J. Dairy Sci. 50: 1695-1709.

10. FOURNET, F.; ELSEN, J.M.; BARBIERI, M.E. and MANFREDI, E. Effect of including major gene information in mass selection: A stochastic simulation in a small population. Genetics Selection Evolution, January- February 1997, vol. 29, no. 1, p. 35-56.

11. FRIES, R. and RUVINSKY, A. The genetics of Cattle. Wallingford, UK, CABI Publishing, 1999. 72 p. ISBN 0851992587.

12. FUKUYAMA, F. and STOCK, G. Engineering Humans: A Reason Online debate featuring Francis Fukuyama vs. Gregory Stock. Reason Online [online]. March 21, 2002. Available from Internet: http://reason.com/debate/ehde bate1.s.html.