BREEDING DESIGN FOR DISEASE RESISTANCE IN DAIRY CATTLE AND BUFFALO

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Abstract: Selection for single trait of milk yield for many years have led to genetic erosion of genes responsible for disease resistance, adaptability etc. Therefore, selection strategies to include these neglected traits in the selection objectives of dairy animals are need of the hour for sustainable dairy in the unpredictable climatic condition.
Keywords: disease resistance, selection for mastitis, genetic improvement.

Introduction

The unique aspects of Indian dairy husbandry lies in its low to medium milk producing breeds, its scattered distribution, inadequate feeds and fodders, varying climate condition, suboptimal management and maze marketing. In this scenario, genetic improvement of dairy cattle and buffalo at farmers herd is feasible only through usual three 'tier' system. So far, selection objectives have been revolved around milk yield, and in some cases associated production traits such as fat per cent etc. Selection for disease resistance had not been in the selection objectives due to difficulty in trait measurements. As a result genetic erosion of genes responsible for disease resistance and adaptability is evident through increasing susceptibility to various diseases of high producing animals. Therefore to check the genetic death further, it is essential to induct disease resistance as one of the selection objectives in dairy animals not only to enhance the productivity but also to safeguard the welfare of the dairy animals.

Genetic basis of disease resistance

Susceptibility or resistance to disease is a threshold trait. Phenotypically it behaves like a qualitative trait but genetically it follows quantitative traits. Measurement of trait perse is very difficult as there is no clear cut stage between the healthy animal and diseased animal. The term 'disease' refers to disorders caused by bacteria, viruses, parasites and feed-borne toxins, as well as to genetic disorders caused by inborn errors. These two types of diseases

are described as 'disease from without' and 'disease from within', respectively (Nicholas, 2005).

In farm animal species, extensive genetic variability of disease incidence has been reported (Morris *et al*. 1998). This genetic variation prevailed in term of breed differences in disease resistance or susceptibility, and also within-breed inherited differences in disease resistance or susceptibility.

Disease from without

It can be approached via therapeutic, prophylactic and genetic resistance. The advantage of genetic resistance over other two approaches is it is permanent and cumulative. It should also be noted that resistance to disease from without is often multifactorial (polygenic) and therefore resistance is unlikely to be absolute. Thus selection for genetic resistance is likely to be used in conjunction with other disease control measures to reduce the size of challenge or to assist in treating existing infections or infestations.

Disease from within

Here, reducing the frequency of affected animals is the main commercial objective. In cases where the gene(s) controlling expression of an affected phenotype has been identified, then a gene test may be available, and selection can be applied to increase the frequency of the desirable phenotype in the population. If the genetic cause has not been identified, then removing or culling affected animals and their relatives may be effective, but the success depends on the disease incidence, and progress will become slower as the incidence falls.

The bovine genome webpage http://omia.angis.org.au/ reveals that there are 367 'disorders / traits' in cattle. Of these, 65 are 'single-locus disorders or traits', with 34 being 'disorders and traits' for which the causative mutation has been identified at the DNA level.

Measurement of disease resistance:

Mastitis among other diseases has been a single, foremost condition in reducing dairy economy. Hence, augmentation of genetic resistance to mastitis in dairy animals would bring back the dairy economy in order. Recording of concerned trait is the first step in any successful breeding programme. Resistance traits (RT) are the traits by which the capacity of a cow to resist infection by udder pathogen can be measured. An ideal RT must be objectively, easily, cheaply and accurately measured, preferably early in life.

Selection for Mastitis resistance

Identification of mastitis resistance animals can be done directly based on occurrence of clinical mastitis or indirectly based on correlated traits such as somatic cell count (SCC),

etc. or combination of both. Molecular markers and QTL are latest options available which could effectively be utilized in selection for disease resistance at younger age.

Direct Selection

The h^2 of clinical mastitis is 0.06-0.12. Response to selection (R) = h. i. σA. Progeny group size must be large to get more accuracy of selection (γ). For example, assume, h^2 of clinical mastitis is 0.03; Then the accuracy $\{\gamma=\sqrt{nh^2/4+(n-1)h^2}\}$ of selection for different progeny groups will be 0.66, o.78 and 0.83 for 100, 200 and 300 progeny group size respectively. In addition σ_A of mastitis resistance is reasonably large. Thus, effective direct selection for mastitis resistance can be expected as long as proper recording and sufficiently large daughter groups are used for progeny test. There is 5% reduction in mastitis frequency among daughters of bulls with the best estimated BV for mastitis compared to daughters of bulls with the best estimated BV for milk yield.

Indirect Selection

It is based on SCC on monthly basis. The h^2 of SCC is 0.08-0.19. Efficiency of SCC as a proxy/an indicator of mastitis depend on the correlation between SCC and mastitis, progeny group size. The SCC covers sub-clinical mastitis mostly. Thus, selection on SCC alone appears to be less effective than selection directly on clinical mastitis.

Selection for other disease resistance

Apart from mastitis, there are enough evidences of heritability of different diseases which can effectively be included while formulating the selection strategies for disease resistance along with milk yield to improve the genetic architecture in totality for a given environment.

Table 1: Heritability of different traits of disease resistance

Diseases	Resistance traits	Heritability	References
Susceptibility to Nematode Parasites	Fecal egg count	0.04 (preweaning)	(Barlow and Piper, 1985)
		0.32 (post weaning)	(Morris et al., 2003)
	Antiparasite antibody concentration	0.3 (4-9 months) 0.22 (11-20 months) 0.3 (peripartum cow)	(Morris et al., 2003)
External parasitic infestation	Tick count	0.41 (Bos Taurus)	(Henshall, 2004)

Conclusion

• Dairy population that have been genetically selected for high milk production seem to be more at risk for susceptibility to mastitis as these two traits are positively correlated

• Data recording on health aspects of animals is an essential primary step to identify the resistant animals to diseases

• SCC is an excellent screening test for the presence of mastitis

• Detection of more and more QTLs for mastitis/disease resistance may make MAS a complementary or an efficient alternative selection strategy to improve the genetic disease resistance of dairy animals

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