

## Breeding for Reduced Methane Emissions in Livestock Species

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### Editorial

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### Editorial

Livestock improvement has taken quite a rapid pace in past two or more decades. The era of rapid genetic progress started with the advent of biotechnological tools specially like artificial insemination, multiple ovulation embryo transfer, in vitro maturation and fertilization, coupled with breeding programs like progeny testing and open nucleus breeding schemes, these played an important role in increasing the selection intensity not only in males but in females and also in improvement in number of observation per individual. The next wave came with the advent in genomics and sequencing technology. With the improvement in marker genotyping techniques many quantitative trait loci were identified for various production and reproduction traits in almost all major livestock species and even in fishes. This leads to selection being carried out by use DNA markers, an indirect way of selecting animals based on marker genotypes and thus increasing the accuracy of selection and reducing the generation interval, as recording of individual trait for selection was not mandatory once a association has been established. Then came the genomic selection, in which instead of certain markers whole genome was genotypes by means of SNP chips and its inheritance was then studied and association was established between the traits of interest and particular genotypic score. These methods not only made early selection possible, but also allowed selection for late expressing traits, difficult to measure traits and traits with low heritability without compromising the accuracy. Selection has been carried for general production and reproduction traits, also for morphological traits, disease resistance traits and even for traits related with physiological or immunological responses. However, there are now some important new traits that have

emerged which currently are not part of any breeding programme but they will have to be included in near future [1].

One such trait is the methane emission from ruminant microflora. Methane is a potential greenhouse gas and is produced actively during ruminant fermentation. Methane is about 25 times more potent greenhouse gas as compared to carbon di-oxide [2]. Agriculture sector as a whole contributes 5 -10 % of total anthropogenic greenhouse gas (GHG) emissions worldwide, livestock contributes about 65% of agricultural GHG and enteric fermentation account 90 % of these emissions [3]. Due to its potential role in greenhouse effect and global warming methane emissions are now being considered as a selection objective. Due to improved management practices, improved feeding practices and feed type a significant amount of emissions had been reduced in developed countries however scope still remains in developing nations that carry a significant animal population which is contributing towards GHG emissions.

Hence, selection and breeding for methane resistance has now gained momentum. Researches have shown that there is genetic component of methane emissions which means it is heritable and hence it is possible to select individual animals with reduced methane production and use them for future breeding purposes [4]. In Angus breed of cattle heritability for methane production (L/day) was estimated to be  $0.40 \pm 0.11$  [5]. However, direct selection for reduced emissions may be difficult due to lower heritability estimates as well as difficulties in measurement of methane production. Thus, for this genomic breeding values can be used. Methane

production is not only variable between individuals but is also a function of the ruminant microflora. These microorganisms and their type significantly affect the ruminal fermentation and the type and amount of gas produced. Thus, with advent of next generation sequencing technologies this ruminal microflora can be sequenced in bulk and as the type of microorganism carried by any individual is also affected by the individual itself it can be considered as its own phenotype and subject to genetic variation and selection. In mice, QTLs have been identified that affects the gut microflora of the host [6]. Therefore, selection of candidates that will provide gut environment for such microbes that will produce less methane is possible. Secondly, there could also be an added advantage, breeders who choose for breeding and selection for methane emissions can also be incentivised. The steps to improve efficiency of an animal for reduced methane emissions should include better management, feeding (& feed resources) and breeding methods and only a single component may not work alone, especially in developing nations that carry a large number of cattle populations and where genomic breeding values have still not gained much popularity.

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