

Keynote Speech

Greener Agriculture and Environment through Genomic Selection of Livestock

C.M.B. Dematawewa

Professor, Department of Animal Science, Faculty of Agriculture, University of Peradeniya

Abstract

Indisputable volumes of evidence are mounting to confirm the fact that climate change is occurring slowly but irreversibly. Agriculture has been recognized as a significant contributor to global greenhouse gas (GHG) emissions of which livestock is a shareholder. Many counter measures and technologies have been proposed at policy level and farm level to alleviate GHG emissions, accommodating further expansion of agriculture and livestock farming. DNA (genomic) technology is a useful tool to accurately identify and genetically select livestock having lesser tendency for GHG emissions (greener livestock), a trait that is difficult to measure at large scale. Converging such technology with many other potential greener technologies, such as waste management (biogas production, integration and recycling, etc.) and digital technology for identification of animal, their pedigree, performance and health, would add to improve production efficiency of animals and other production units, requiring fewer such units and thereby reducing emission of GHG leading to greener agriculture and environment.

Keywords: Genomic Selection, Greener agriculture, Greenhouse gases, Livestock, Methagene

Introduction

As the 21st century unfolds, agriculture remains fundamental to global food security, poverty alleviation, and environmental sustainability. Seventy five percent of the world's poor dwell in rural areas where agriculture is the most effective source of food and income. United Nations forecast that the global human population will reach over 9 billion by 2050 requiring a 70 percent increase in world food production, a challenge that farmers and fishers must conquer eventually (World Bank, 2012). Global milk production has exceeded 727 million MT, India being the largest milk producer in the world. New Zealand, USA, Germany, France, Australia, and Ireland have been reported as the producers with the largest milk surplus.

There is now overwhelming scientific consensus that climate change is one of the greatest threats facing the planet. Agriculture which uses 80 percent of the world's freshwater, is found to be the most vulnerable to the increasing effects of climate change compared with the other economic sectors (World Bank, 2012). The farmers and fishers need more knowledge and innovations to adapt to less predictable and more variable environment and to contribute to sustainable 'green' growth (OECD, 2009). New innovations and technology such as satellite imagery and aerial photography have enabled studying of farm conditions in remote areas and assess damage from climatic challenges like drought. Affordable technologies of wireless

devices such as radio frequency identification tags are improving livestock management, allowing identification of animals and animal products through supply chain and monitor migratory patterns and health of animals (World Bank, 2012).

Livestock Development in Sri Lanka in the 21st Century

Developing countries such as Sri Lanka have a unique role to play in greener agriculture, climate change and global warming. Similar to many developing countries, population of Sri Lanka has been growing steadily at a rate of 0.9% per year exceeding 20.97 million by the year 2015. In parallel, gross domestic product (GDP) has recorded an annual increase of about 7 percent (CBSL, 2015). Due to relatively faster growth of industry and service sectors, contribution of Agriculture to the national GDP has reduced in the year 2015 down to 7.7 % from over 11% in 2014 (CBSL, 2015). Contribution of livestock sector to the GDP also decreased to 0.7% due to its marginal (0.3%) growth during the year 2014. About 400,000 farmers are presently involved in dairy industry (DAPH, 2014). There were 21,833 cattle farms registered under the Department of Animal Production and Health in the year 2014. Alarmingly, new farm registration recorded a 24.6% decrease compared to the year 2013. Total cattle population in Sri Lanka in 2014 was 1,118,089 heads (61% local, 29% crossbred and 10% pure genotypes), which comprised of 223,400 milking cows, 237,579 dry cows,

141,294 infertile or aged cows, 172,219 heifers, 241,207 calves and 102,389 bulls. The total of 375,562 heads of buffalo population in the year 2014 was comprised of 256,988 buffalo cows including heifers, 27,212 buffalo bulls and 91,362 calves. Both cattle and buffalo populations have decreased by 11.6% and 20.8%, respectively in the year 2014 compared with the previous year. In spite of that, both cow milk and buffalo milk productions have increased by 9.8% relative to the year 2013 indicating increased productivity per animal. This is a favorable trend in terms of greener agriculture as smaller populations with higher productivity means lesser emission of greenhouse gases (GHG) from livestock and production units. Formal milk collection in the year 2014 increased by only 6.8% compared to the previous year, and consequently per-capita availability of milk improved up to 45.16 liters in the year 2014. Yet about 2/3rd of the national requirement of milk is fulfilled by imported products spending Rs. 44.3 billion/year (DAPH, 2014). These statistics indicate the need for further expansion of livestock industry while reducing GHG emissions.

Beef production remained static during the year 2014, with per capita availability of 1.55 kg/year, due to restrictions on slaughter. Total swine population of 71,838 in the year 2014 was a decrease of 11.5% compared to the previous year. Majority of the population of 312,846 heads of goats are still reared as traditional farms in Northern, Eastern and North Western provinces with minimum new technology. However, poultry sector has seen improvements in the year 2014 compared to 2013 in all sub sectors with 4% increase in meat production, 7.6% in egg production, 10.9% in feed production, 5.3% in broiler chick production and 4.1% in layer chick production (DAPH, 2014).

Constraints to Dairy Development

As domestic milk production of 419 million litres/year is not sufficient, Sri Lanka imports 71,027 Mt. of milk powder annually (DAPH, 2014). However, there are several major constraints for further expansion of the dairy industry. According to the Department of Census and Statistics (2014), retail price of milk was Rs. 69.19 per litre while the cost of production was about Rs. 46.2 per litre leaving a small profit margin for the small scale dairy farmer. Many small scale farmers remain in the dairy industry either on part-time basis or due to lack of alternative employment opportunities. Gradual reduction of cattle population, lack of

good quality animals, low success rates in artificial insemination, poor quality feed and feeding practices, high cost of concentrate feeds, disease impediments, lack of knowledge on feeding and other management practices (e.g. utilization of agricultural by-products, hygienic milk production, etc.) and, low efficiency in milk collection and distribution are among the major constraints to further expansion of dairy industry.

Dairy husbandry can be made profitable by expanding it into a commercial scale enterprise. Many critical measures have been identified to promote dairy industry such as enhancing commercial milk production, upgrading the local cattle population through artificial insemination, improving dairy extension service (particularly on feeding, establishing good quality pasture, by-product utilization, low cost feed formulation, preparation of total mixed rations and, silage and hay making, etc.), expanding veterinary service, introducing an individual milk testing and payment system at collecting points, improving infrastructure facilities at collection points and chilling centers, establishing transparency at all levels of milk collection and marketing system, to name but a few.

Greener Agriculture and Climate Change

It has been estimated that agriculture is responsible for about 14 percent of the greenhouse gas (GHG) emissions of the world such as CO₂ and methane. Those gases have the ability to trap the heat radiated back from the earth causing global warming and climate change. A significant portion of the GHG emissions from agriculture is methane, which is 23 times more powerful than carbon dioxide in causing global warming (FAO, 2007).

Greenhouse Gas Emissions from Livestock Industry

About 44 percent of livestock emissions are in the form of methane (CH₄) while the remaining part is almost equally shared between nitrous dioxide and carbon dioxide (FAO, 2007). Cattle raised for beef, milk, manure and draft power are responsible for 65% of the livestock sector emissions. They are followed by pigs (9%), buffalo (8%), chicken (8%), and small ruminants (6%). The remaining emissions are from other poultry species and non-edible products (FAO, 2007). The world cattle population of 1.5 billion heads and billions of other grazing animals emit dozens of polluting gases, including large amounts of methane through belching with a lesser amount flatulence

(Tubiello *et al.*, 2013). An average dairy cow expels an estimated 100 to 500 liters of methane per day, equivalent to pollution caused by an automobile. In New Zealand, 34 percent of GHG come from livestock, dominated by cattle and sheep.

GHG emissions occur not only from livestock but at various stages of livestock supply chains, including the production and transport of animal feed, on-farm energy use, animal digestion and manure decay, as well as post-slaughter transport, refrigeration and packaging of animal products amounting to 14.5 percent of human-caused GHG releases. In pig industry, the bulk of emissions occur during the feed supply and manure storage while feed supply is responsible for the bulk of emissions in poultry production, followed by energy consumption (FAO, 2007).

Mitigation of Methane Production by Livestock

Enteric ruminant methane is the most important greenhouse gas emitted from the livestock industry (Tubiello *et al.*, 2013) where dairy cattle were the second highest enteric methane producer (19.44%) behind nondairy cattle at 56.04% (FAOSTAT, 2013). Methane production is an energy loss for ruminants (Blaxter, 1962; Johnson and Johnson, 1995) which depends on feed intake and composition, fermentation of feed including passage rate and rumen volume, the physiological state of the animal, and genetic variations among animals (Hristov *et al.*, 2013 a,b; Pinares-Patiño *et al.*, 2013). Various management strategies can be adopted to reduce methane emissions per animal and per unit of production including improved productivity and efficiency of the animal, reduced culling at herd or flock level with better health management, better feed and feeding practices (to reduce methane production during digestion and release of gases from manure), immunization against methanogenic archaea, and direct selection on methane trait for genetic improvement (Wall *et al.*, 2010). Among these practices, genetic improvement has a cumulative and permanent impact on animals transferring the benefits to subsequent generations. Better management of grazing lands could help improve productivity and act as carbon sinks to counter GHG emissions. In monogastric animals, precision feeding, breeding and better animal health care can reduce amount of feed and manure production. It has been estimated that emissions can be reduced by 38 percent in South Asian mixed dairy farms by improving feed and feeding practices, as well as animal health and

husbandry (FAO, 2007). Extension services and financial incentives (emission taxes and carbon credit markets, etc.) must be provided for farmers to promote adaptation of better management practices according to their individual scenarios.

Genetic Improvement for Reduced Methane Emissions

Enteric ruminant methane production and emission encompasses a chain of processes starting with feed intake where the underlying physiological mechanisms (except activities of microbes) are governed by a series of enzymes produced within the animal under the instructions of genes (methagenes). Therefore, genetic improvement of this trait is possible and any gain achieved will be transmitted to the generations of offspring afterwards. However, methane production is a complex trait which may be practically handled by breaking down to some component traits or using some easy to measure indicators as the trait (called indicator traits). Some component traits can be recognized as rumen microbial composition, feed intake and direct methane emission. Measuring those traits in large scale is a challenge as it is practically difficult and expensive. Thus, new measurement techniques probably using correlated indicator traits must be further developed and validated.

Pickering *et al.* (2013) reviewed the studies on quantifying methane emissions in certain environments. Measurement of enteric methane using current respiration chamber techniques is expensive, thus identifying a low-cost measurement technique or appropriate proxy having a strong correlation with methane emissions is essential before entering this trait into breeding programs. Pickering *et al.* (2015) used a trait called predicted methane emissions (PME) calculated based on body weight, feed intake, milk yield and body condition score. They compared it with repeated measurements of a laser methane detector (LMD), another handy equipment to estimate methane emissions in cattle. Heritability estimates, which range from 0 to 1.0 indicating the proportion of genetic control over the variability of a trait, for PME and LMD were 0.13 and 0.05. Thus, the trait PME had 87% non-genetic (environmental) influence while LMD was almost completely (95%) controlled by non-genetic factors. Thus, PME was found to be a better trait for genetic selection having exhibited some genetic control over the trait. There was a strong genetic correlation between PME and LMD, which is

encouraging for further studies. Pinares-Patiño *et al.* (2013) also found high heritability estimates for methane emissions in sheep and recent studies suggest that an easy to measure indicator trait could be found in near future to be used in field level breeding programs.

Genomic Selection of Livestock for Methane Emissions

Direct and indicator traits measured on animals on methane emissions are called phenotypic measurements which are being influenced jointly by genetics as well as environment in varying degrees. If we could know the exact genotypes (methagenes) of the breeding animals, we can reach 100 percent accuracy in our genetic selection programs. Recent advances in DNA technology have enabled sequence parts or whole genome of the animal. These part-sequences may not necessarily be the exact genes affecting the trait of interest, but at least located close enough to the gene in the chromosome (closely linked) so that they inherit together to the next generation. Once we detect that sequence in an animal, we can be fairly certain that the linked allele of the gene of interest is also there in the animal. Such sequences that are used to infer the genotype of an animal (or a plant) are called genetic markers. A physiological indicator (such as enzyme level) also can be used to find the genotype of the animals. Such indicators are called physiological markers. An example for a physiological marker widely used in swine industry in the Western world is Halothane test (sensitivity to anesthesia using Halothane gas) which is directly associated with occurrence of pale soft exudative (PSE) muscles in pigs under stress. Use of such physiological and genetic markers in selection is called Marker Assisted Selection (MAS). With the advances of polymerase chain reaction based DNA technology, many genetic markers came into the scene such as restricted fragment length polymorphisms (RFLP), amplified fragment length polymorphisms (AFLP), micro satellite markers and single nucleotide polymorphisms (SNP). Single nucleotide polymorphisms are single base pair changes (point mutations) such as substitution of Adenine to Thymine. DNA strands of two random animals can have thousands of such SNP differences scattered all over the genome. If an SNP is closely located (linked) with an important gene, we can use it as a marker of that gene. Recently SNP chip panels have been developed to identify a large no. of SNPs (e.g. 700,000 SNPs) in an animal for a cost of 100 US dollars. The price tag is coming down

every year becoming more affordable to general public.

SNP panels are widely used to identify genetic diversity and effect of domestication in animals (Kijas *et al.*, 2009). Meuwissen *et al.* (2001) speculated that when a high density SNP panel is used (e.g. 700,000 SNPs scattered all over the genome) there is a high chance that all potential genes (or quantitative trait loci, QTL) are closely linked to at least one such SNP. Thus they developed a multiple regression model using all the SNPs as independent variables and the trait of interest as the dependent variable. When we use SNPs and phenotypic information of a large population of animals (called a Training Population) and run the regression analysis we can get estimates (partial regression coefficients) for each SNP indicating its magnitude of influence on the trait. Subsequently if we can genotype and find the exact SNPs in an individual outside the Training population (called a Validation population), we can get an estimate of its genetic potential for that trait as we know the effects of each SNP that animal possess. Such estimate is called genomic breeding value and selection based on such estimate is called Genomic Selection. Advantage of this method is once the effects of SNPs are found in the training population, we do not have to measure the phenotypes of the individuals which are not in the training population. Therefore, this method is very useful for traits which are not exhibited in some animals such as milk yield in bulls or litter size in boars (called sex limited traits) or meat quality of a live breeding boar (carcass traits). It is also useful when measuring phenotypes in large scale is very difficult such as feed efficiency or methane emission in livestock. Here, initially phenotypic measurements on methane emissions can be obtained with SNP information on a certain training population in the lab and afterwards only SNP information is used to evaluate the rest of the animals in the validation population. However, we may have to use several training populations depending on time and diversity of the populations. Furthermore, genomic breeding values can be combined with phenotypic information to obtain more accurate predictions of breeding values. Dematawewa *et al.* (2015 a & b) have shown the effectiveness of this method in difficult-to-measure health traits in nucleus breeding schemes of pigs.

Final Remarks

DNA (genomic) technology enables accurate genetic selection of animals against greenhouse

gas emissions. Converging genomic technology with many other greener technologies such as waste disposal (biogas, crop-livestock integration, recycling, etc.) and digital technology (in animal identification and performance recording, etc.) can lead to accurate detection of health status and true genetic potential of animals. Finally, accurate identification of animals could lead to improvement of production efficiency per animal and lesser no. of culls, resulting in lesser GHG emissions ensuring greener agriculture and environment.

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