A Global Strategy of Using Molecular Genetic Information to Improve Genetics in Livestock

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Contents

Traditional breeding programmes have largely contributed to disseminate the benefits of several quantitative traits in livestock. In developing countries such as Indonesia where animal population scattered throughout the country, it is difficult to invest for molecular research. On the other side, yet, it is worthy asset for breeding purposes. Based on theory and evidence, it has been proved that those scattered population evolved different genetic adaptations in response to a given natural pressure and subsequently resulting to the genotype diversity asset.

Introduction

Recent advances in biotechnology research have led to the promotion of some techniques to be applied towards genetic improvement. The application of molecular biology and biotechnology towards animal breeding in expecting to accelerate progress and to solve problems in animal production is now possible by implementation of molecular information. Selection of animal based on the molecular approaches is recently termed as molecular breeding (Thompson 2004). There are two primary strategies for molecular breeding, namely applying DNA marker technology for genetic diversity analysis, gene discovery, gene and quantitative trait loci (QTL) mapping and marker-assisted selection (MAS); and applying transgenic technology for transferring genes creating disease resistance, drought stress tolerance, low fat or milk compositions (i.e. casein and fat contents) through genetic engineering. Both strategies depend heavily on basic research in molecular biology and functional genomics.

Genome is defined as entire genetic makeup (material genetics or DNA) of an organism that stored in one or more chromosomes located inside each cell of an organism (Van Eenennaam 2004). The study of genome has been furnished by advanced techniques such as DNA sequencing. At present, whole-genome DNA sequences of some model organisms are now known, while functional genomics is a way or a ‘tool’ to identify the function of each gene of an organism. Concomitant with the trend of functional genomic study, bioinformatics or computational biology has therefore become essential component for biotechnology research.

Scattered Place – Genetic Diversity Asset

Indonesia consists of five big islands (Java, Sumatera, Kalimantan, Sulawesi and Irian Jaya) and thousands of islands (more located in eastern parts of Indonesia) with different climates from each other (Fig. 1). The climates of western parts of Indonesia are more humid and warmer compared with those of eastern parts of Indonesia. In South-east parts of Indonesia, the climate is under influence by the Australian continent having a wide range of climatic zones from semi-arid to arid. Based on 30-year (1971–2000) time series, the rainfall data in Indonesia vary from less than 1000 mm to more than 5000 mm (http://balitklimat.litbang.deptan.go.id). Forage grows better in western parts of Indonesia than in eastern parts of Indonesia, though, also influenced by the seasons of wet and dry, which usually occur starting in April through September and from October through March, respectively.

These scattered places with differences in climates have influenced the way of animal adaptation to the given natural pressure and subsequently resulting to the genetic diversity in livestock. This genetic diversity is worthy asset for breeding purposes in the aspect of improving animal productivity. Based on theory and evidence, it has been proved that those scattered population evolved different genetic adaptations in response to a given natural pressure selection (http://www.fao.org/biotech/docs/Gibson.pdf). The adaptation of different species and breed to a broad range of environments provides the necessary variability that offers opportunities to meet the increased future demands for food and provide flexibility to respond the changed markets and needs (Philipsson and Okeyo 2006).

Indigenous and adapted or domesticated cattle in Indonesia are located in several places throughout Indonesia. There are at least four indigenous cattle in Indonesia, that is Bali cattle, Aceh cattle, Coastal cattle...
and Madura cattle (Abdullah 2008). The Bali cattle were originally restricted only in Bali Island during Dutch era, while at the present, it can be recognized almost throughout Indonesia. The Aceh cattle are located in Aceh of Sumatera. The Coastal cattle are in Padang of West Sumatera and categorized as dwarf cattle. The Banteng cattle was considered as original of Banteng cattle are distributed in Madura Island, Kangean Island and now can be obtained in several Zoos in Indonesia. Those four cattle are as beef cattle. While Sumba-Ongole and Java-Ongole are also considered as original cattle breed of Indonesia (Dahlanuddin et al. 2003; Martoyo 2003), these cattle are also grouped as beef cattle. There are several very long adapted or domesticated cattle in Indonesia such as Grati cattle distributed in East Java and descendant Fries Holstein, both are as dairy cattle.

**Molecular Genetic Information**

Animal population that lives in given environment pressure (e.g. high-stress climate and low-nutrient for-age) in very long time should adapt to such stress to survive; otherwise, they will be extinct. In population genetics theory, the animal could survive till this present because they passed naturally in selection pressure. The effect of such different pressure results the animals performing differently among population. At least, a distinct genetic polymorphism will lead in such pressure. Plasticity owing to mutation may occur on such adapted animals. Mutation could express as negative or positive effects. The existing of mutation in animals is now possible to be detected by the ease of availability of molecular genetic information.

Advances in biotechnology research, such as molecular markers, can be used to detect the loci closely to genes associating with desired traits or can be used to map QTL (Margawati et al., 2006), then applied towards genetic merit improvement in livestock. Application of molecular genetics for genetic improvement relies on the ability to genotype individuals for specific genetic loci (Dekkers 2004). Therefore, for these purposes, genetic markers can be distinguished by three: (i) direct markers: loci that code for the functional mutation, (ii) LD markers: loci that are in population-wide linkage disequilibrium with the functional mutation and (iii) LE markers: loci that are in population-wide equilibrium with the functional mutation.

As described by Anderson (2001), those types of markers differ not only in methods of loci detection but also in its application in selection programmes. Direct markers and LD markers allow for selection genotype across the population because of the consistent association between genotype and phenotype. The use of LE markers has to allow for different linkage phases between markers and QTL from family to family.

It was introduced by Van der Werf (2000) that idea behind MAS is there may be genes with significant effects that may be targeted specifically in selection. Practically, MAS is also defined as a process of using results of DNA marker tests to assist in the selection of individual become the parents in the next generation of a genetic improvement programme (http://www.nbcec.org). Marker-assisted selection is predicted to be most beneficial for traits that have low heritability or are difficult, expensive or impossible to record in a normal breeding programme (http://www.fao.org/biotech/docs/Gibson.pdf, Van Eenennaam 2004).

Nowadays, the molecular marker information is used as a key component in genetic improvement programme. For instances, farmers or breeders can use molecular genetic markers based on the desired traits. It is to minimize the cost of undertaking an independent QTL mapping experiment. There have been identified for some traits either influenced by single (e.g. hair or coat colour, double muscling, certain diseases; Van der Werf 2000 and http://www.nbcec.org) or multi genes. Most of economically importance traits or quantitative traits are controlled by many number of genes or multigenes (Van der Werf 2000). As described by Margawati (2005) and Margawati, et al. (2006), QTL mapping of growth traits in Indonesian Thin Tail (ITT)
sheep was identified on ovine chromosome 18 and flanked by markers of CSSM018 and TMR1 or AKT1).

Conflicts of interest
The author has no conflict of interest to declare.

References


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