

#### ABSTRACT

### **Genomic Information and Its Application in Hanwoo (Korean Native Cattle) Breeding Program - A Mini Review**

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Economic traits are quantitative traits and are mostly controlled by a large number of genes. Some these genes tend to have a large effect on quantitative traits in cattle and are known as major genes primarily located at quantitative traits loci (QTL). However, in practice, QTL is linked to allele associates of the gene controlling traits of interest. It is hypothesized that if QTL explaining a part of genetic differences between animals are detected, the effect of the genes located at QTL could assist in estimating an animal's true genetic value. Therefore, QTL information could probably provide accuracy of breeding value estimation as well as more genetic gain through selection of animals at relatively younger age. Marker assisted selection (MAS) is the indirect selection process where a quantitative trait of economic importance is selected not just based on the trait itself but also on the basis of marker linked to QTL. MAS could be useful for traits that are difficult to measure, exhibit low heritability, and are expressed late in development. Major genes which are responsible for QTL could possibly be identified first by using different techniques such as gene expression analysis and QTL mapping. Thereafter, the information generated could be implemented for MAS in estimating breeding value. In this review we focused on delivering genome information into Hanwoo breeding program. MAS could be useful for traits that are difficult to measure, exhibit low heritability, and are expressed late in development. Major genes which are responsible for QTL could possibly be identified first by using different techniques such as gene expression analysis and QTL mapping. Thereafter, the information generated could be implemented for MAS in estimating breeding value. In this review we focused on delivering genome information into Hanwoo breeding program. MAS could be useful for traits that are difficult to measure, exhibit low heritability, and are expressed late in development. Major genes which are responsible for QTL could possibly be identified first by using different techniques such as gene expression analysis and QTL mapping. Thereafter, the information generated could be implemented for MAS in estimating breeding value. In this review we focused on delivering genome information into Hanwoo breeding program. Major genes which are responsible for QTL could possibly be identified first by using different techniques such as gene expression analysis and QTL mapping. Thereafter, the information generated could be implemented for MAS in estimating breeding value. In this review we focused on delivering genome information into Hanwoo breeding program. Major genes which are responsible for QTL could possibly be identified first by using different techniques such as gene expression analysis and QTL mapping. Thereafter, the information generated could be implemented for MAS in estimating breeding value. In this review we focused on delivering genome information into Hanwoo breeding program.

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