Strategies to Multiply Elite Cow in Hanwoo Small Farm

**Seung Hwan Lee[1], Ui Hyung Kim[1], Chang Gwan Dang[1], Sharma Aditi[1], Hyeong Cheul Kim[1], Seung Heum Yeon[1],
Gi Jun Jeon[1], Sun Sik Chang[1], Sung Jong Oh[2,*], Hak Kyo Lee[3], Bo Suk Yang[1] and Hee Seol Kang[1]**

[1]Hanwoo Experiment Station, National Institute of Animal Science, RDA, Pyeongchang 232-952, Korea
[2]Department of Animal Biotechnology, Jeju National University, Jeju 690-756, Korea
[3]Department of Animal Biotechnology, Hankyung National University, Ansung 456-749, Korea

ABSTRACT

The recent development in genetic assisted selection (combining traditional- and genome assisted selection method) and reproduction technologies will allow multiplying elite cow in Hanwoo small farm. This review describes the new context and corresponding needs for genome assisted selection schemes and how reproductive technologies can be incorporated to get more genetic gain for cow genetic improvement in Hanwoo. New improved massive phenotypes and pedigree information are being generated from commercial farm sector and these are allowing to do genetic evaluation using BLUP to get elite cows in Korea. Moreover cattle genome information can now be incorporated into breeding program. In this context, this review will discuss about combining the reproductive techniques (Multiple Ovulation Embryo Transfer; MOET) and genome assisted selection method to get more genetic gain in Hanwoo breeding program. Finally, how these technologies can be used for multiplication of elite cow in small farm was discussed.

(Key words : genome assisted selection, multiple ovulation embryo transfer (MOET), Hanwoo)

INTRODUCTION

National Genetic Evaluation System of Hanwoo called progeny test selects 20 superior KPN (Korea Proven Bulls) bulls per annum and semen straws of the selected KPN bulls are distributed to 14 million Hanwoo farms in the country. Along with the National Genetic Evaluation program for bull genetic improvement, Hanwoo farmers emphasize the importance of genetic improvement for cow (female) to get more real incomes from better carcass score when they slaughter in abattoir. In addition, we expect more genetic gain for Bull in National Genetic Evaluation System because of cow genetic improvement in Hanwoo breeding farms participating to the National Genetic Evaluation System in Korea.

In order to assess genetic evaluation for cow genetic performance, phenotypic data such as carcass weight (CWT), marbling score (MAR), back fat thickness (BF) and eye muscle area (EMA) including management information (for example, birth day, feeding, feedlot age and slaughter age etc), growth traits (body weight at 12, 18 and 24 month of age) and body stature of the cow progeny as well as pedigree data are required. In particular, as for the cow breeding in Hanwoo smallholder, genetic performance should be predicted based on either a traditional genetic evaluation system which uses well recorded phenotypic and pedigree data or genomic information of large reference population.

In terms of predicting cow genetic performance, recent animal traceability program allow to trace back their management history for all registered animals in the country. Carcass data for all registered animals are loaded into a database managed by the Korea Institute for Animal Products Quality Evaluation (KAPE), and massive pedigree information for registered animals are recorded by Animal Genetic Improvement Association (AIAK). Given that information such as abattoir data for carcass traits, pedigree and traceability information (management and environmental effect) can be used for genetic evaluation, cow genetic performance would be predicted very accurately in the country.

Recent advances in molecular genetic technology facilitate not only detection of genes that contribute to genetic variation of quantitative traits but also incorporation of genomic information into a conventional animal breeding program. The incorporation of DNA information into estimation of genomic breeding value (GEBV) may achieve an improvement of estimated breeding value (EBV) and selection accuracy in cattle populations. The main application of DNA information in

* Correspondence : E-mail : ohsj@jejunu.ac.kr

breeding program was a marker assisted selection (MAS), which is a method of selection that makes use of phenotype, genotype and pedigree data as Fernando and Grossman (1989) presented. However, genomic selection (GS) that is an extended model of marker assisted selection (MAS) has the potential to improve accuracy of estimated breeding value and to overcome some of the drawbacks which exist in the traditional BLUP such as a relatively long generation interval. Once large reference population representing Hanwoo population in genetic build up, GEBV for cow will be confidently predicted at young animal and it will be very helpful to reduce generation interval for cow. Young elite cow selected by GEBV or EBV can be multiplied by advance reproduction technology such as Multiple Ovulation Embryo Transfer (MOET) in Hanwoo smallholder sector.

This review will describe each of the technology and how it will impact combining each of the technologies in genetic improvement of Hanwoo cow population.

HANWOO BREEDING PROGRAM AND PRODUCTION SYSTEMS

As Kim *et al.,* (2011) described a process of Hanwoo breeding programs, the first genetic breeding program, named 'Hanwoo-Gaeryang-Danji (HGD)' was initiated by MAF in 1979. The HGD program specified eight provinces across Korea with 3,967 cows. One HGD site was assigned in each province, with the exception of Jeju Island. Farms which were designated HGD sites in each province were enrolled in the program, which identified cows and managed the pedigree data from the farms. Since then the number of HGD sites steadily increased to 250 with 175,540 cows by 1998 (NLRI, 2009). The cows enrolled in the HGD program have been used as major breeding sites for the 'Hanwoo Performance and Progeny Test (HPPT)' program from 1983 to 1998.

However, the information from HGD was limited only to sire pedigree and identification of cows. This constraint was imposed because of the scarcity of supervisors hired by local livestock cooperatives and of the farmers' lack of awareness for the necessity of record keeping.

Artificial insemination and phenotypic record management were usually done by a small number of supervisors who were in charge of managing records of thousands of cows and it downgraded the data quality. To overcome the problems of the HGD program, a new program called 'Hanwoo-Gaeryang-

Nongga (HGN, Individual breeding farm with cow)' was introduced in 1999. The HGN program focused more on the individual farms rather than region (HGD), but still used the data recording system used in the HGD program.

Since 1999 the cows from the HGN program also have been used as major breeding stock for HPPT program (MAF, 1999). Before the advent of the HPPT program, semen for artificial insemination was produced from bulls selected through a nationwide livestock contest from 1969 to 1986. Bulls were selected solely on their phenotypes. The HPPT program was implemented in 1983 and produced the first proven bulls in 1987. As shown in Fig. 1, the program used two stage selection comprising a performance test for young bulls, followed by a progeny test of selected young bulls (n=40). Young bull calves (n=400) of current proven bulls were harvested at the age of 6 months from HGN belonging to HGD based on their phenotypic values and underwent a performance test up to age of 12 months. At this stage young bulls were selected based on a combination of their breeding values of
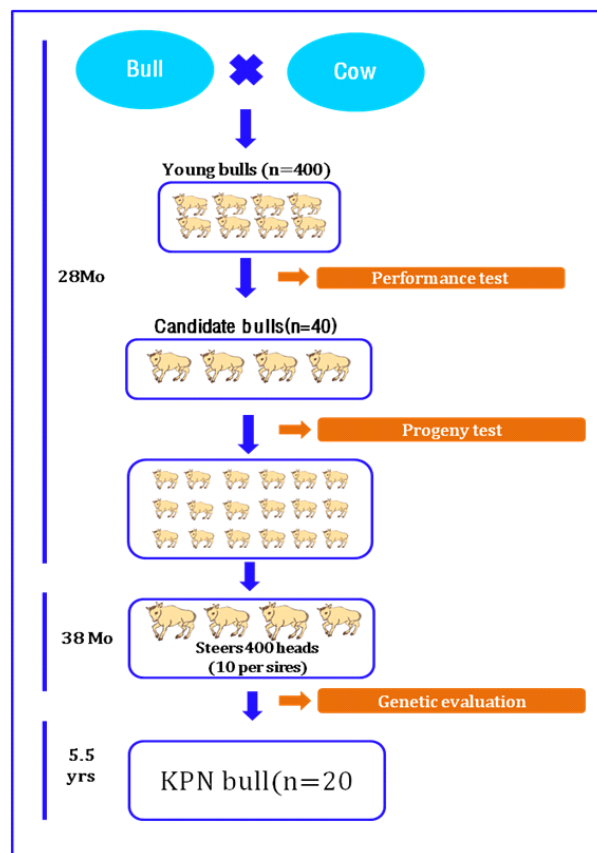

Fig. 1. Scheme of progeny test to selection KPN bull in the National Genetic Evaluation system.

weight at 12 months and average daily gain estimated from its performance test records.

In the progeny test, cows from the HGN program were inseminated with semen of young bulls and the male calves were harvested from farms and raised for the station progeny test. These steers were raised in a group until slaughter at 24 months. Carcass data comprised eye muscle area (EMA), back-fat thickness (BF), marbling score (MAR), and carcass weight (CWT). Based on the progeny test results 20 bulls are selected into the AI program. Selection is based on a selection index which used weighted breeding values for CWT, MAR and EMA. The 40 bulls that entered the progeny test stage were mated via artificial insemination to around 1,800 cow (two cow nucleus population, HGN (n=10,000) and Livestock Improvement Main Center of National Agricultural Cooperatives Federation (LI-MC, NACF (n=8,000)). The performance of cows from the HGN program was not recorded and therefore there was little contribution from the female selection (Kim *et al.,* 2011).

As shown in Fig. 2, Hanwoo production system consists of three tiers which are seed stock sector, multiplier and feedlot sector. Seed stock sector is being run by Government leading National Genetic Evaluation system to select KPN bulls and is disseminated to Hanwoo smallholder (Hanwoo farm). Using artificial insemination (AI), multiplier (ie. Hanwoo reproduction smallholder) produce calves selling to feedlot sector. Feedlot sector rears animals until 30 to 32 month age which is the slaughter age (Lee *et al.,* 2012). It is a very structured beef production system to control Hanwoo industry because superior genes from KPN bulls selected in seed stock sector spread down through multiplier to feedlot sector quite quickly. Moreover, this structured beef supply chain allows to build a national pedigree data for all registered animals even in Hanwoo

Fig. 2. Hanwoo production systems.

smallholder across country. Also this kind of structured beef production system accompany with a national traceability system will help to use abattoir carcass data for all registered animals as a phenotypes for genetic evaluation of cow in Hanwoo smallholder.

SELECTION OF ELITE COW FROM FARM

50% of the animal's genetic performance is inherited from each of the parent. Current genetic evaluation system of Hanwoo just contributed 50% of genetic portion in total genetic improvement. Therefore, cow genetic evaluation for carcass traits need to be done to select better cow for replacement in Hanwoo smallholder. As mentioned previously, Hanwoo production system is very structured system being able to use all the information such as pedigree, abattoir carcass data even management and environment information from national traceability system. This system is very similar to BREEDPLAN in Australia. BREEDPLAN uses an advanced, modern genetic evaluation system (based on Best Linear Unbiased Prediction (BLUP) technology incorporating multi-trait analysis procedures) to produce estimates of breeding values (EBVs or EPDs) for recorded cattle across a range of important production traits. BREEDPLAN technology can be used at a number of levels, such as within-herd analyses for individual breeders, across herd analyses for members of a breed association (or breeding group) or international genetic evaluation where breed associations from a number of countries pool their data for analysis. The rationale for this is simple - the larger the population of cattle being evaluated the higher the chance of finding elite genetic material which can then be rapidly disseminated using modern artificial breeding techniques (Allen 2001).

As shown in Fig. 3, since we started national traceability system (2007. Dec), entire abattoir carcass data for all registered animals and their management history (birth, birth season, birth place, herd information etc) and pedigree information can be collected from the Korea Institute for Animal Products Quality Evaluation (KAPE), and massive pedigree information for registered animals are recorded by Animal Genetic Improvement Association (AIAK). It will allow doing genetic evaluation using all the information. Therefore, like BREEDPLAN, it will possibly be herd (Hanwoo smallholder) comparison and contemporary group comparison to select elite cow in Hanwoo smallholder.
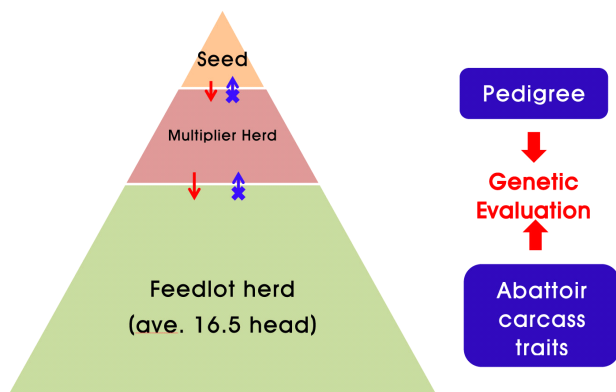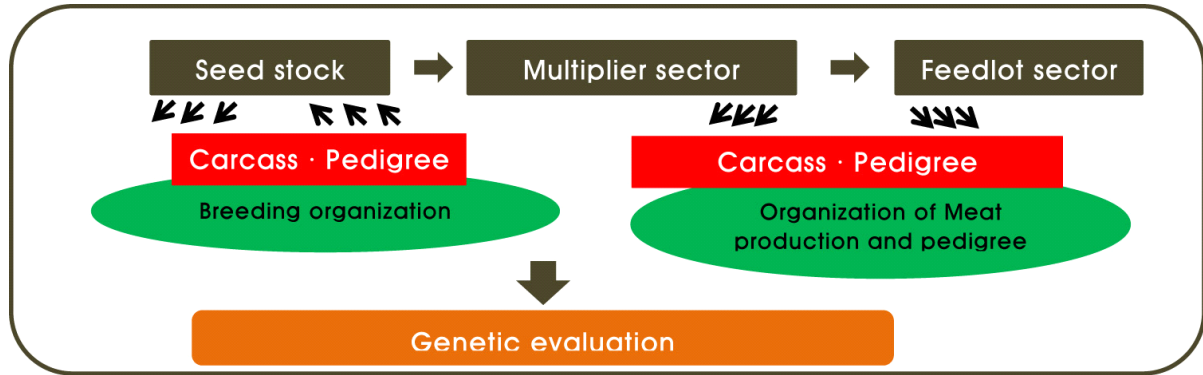
Fig. 3. Management of carcass traits and pedigree in National database.

In this regard, Won *et al.,* (2010) reported genetic evaluation for cow using data collected from the Gangwon producer groups. In addition, Koo *et al.,* (2011) collected an abattoir carcass data (n=231,382) from 2006 to 2009 and pedigree information across the country to set up a statistical model controlling all the management and environment effects. In the United State of America, Cundiff *et al.,* (1969) reported that carcass traits are known to be differently evaluated with different indirect genetic responses according to slaughter endpoints, and Koch *et al.,* (1995) reported that slaughter endpoints can affect the expression of genetic and environmental differences. Wickham and Durr (2012) built an infrastructure collecting data for multi-breed genetic evaluation system in Iceland. Therefore, current genetic evaluation system uses abattoir carcass data and pedigree information to do herd and contemporary comparison.

Hanwoo Experiment Station, National Institute of Animal Science, RDA has performed a trial analysis using Hanwoo abattoir carcass data and pedigree to estimate cow breeding value for carcass traits. Data (n=18,000) and pedigree were collected from volunteer Hanwoo smallholder between 2007 to 2012 yrs in Pyeong-Chang, Gangwon province. We tried to estimate cow breeding value and accuracy of EBV. As shown in Fig. 4, pedigree information was 9 generation and well connected between sire group and dam group. Average accuracy of EBV for cow was 0.4 to 0.7 which is very higher than we expected. Based on the EPD for 4 traits (carcass weight, eye muscle area, back fat thickness and marbling score), around 200 cow was in 5% higher group ant the other 200 cow was very inferior for carcass traits. This kind of information (EPD value) will be helpful to make a decision for replacement animal and culling animals in Hanwoo smallholder.
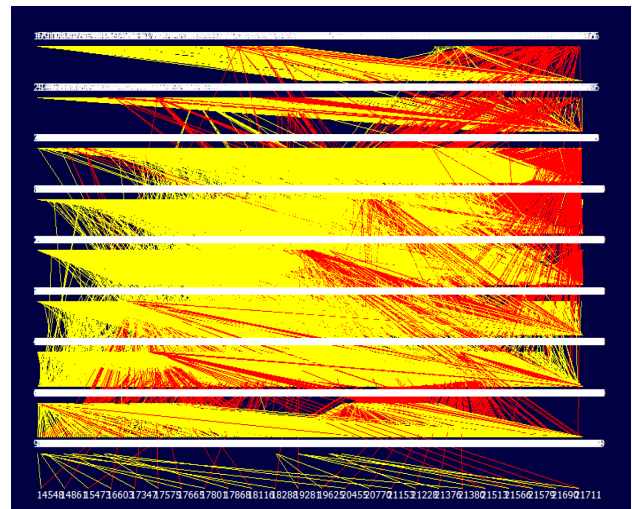

Fig. 4. Diagram of pedigree information for Hanwoo steers in Pyeong-chang. Red indicate sire and yellow is dam pedigree.

GENOMIC PREDICTION OF BREEDING VALUE

Production traits of cattle can be considered to be controlled by many genes which individually have only a small effect. This hypothesis has underpinned the best linear unbiased prediction (BLUP) method for estimation of animal breeding value (Henderson, 1984). However, after the human genome sequencing was completed, Ewing and Green (2000) proposed that the number of genes which actively impact on traits may be as low as $20,000 \sim 25,000$ across the whole genome. This is a relatively small number and makes it more likely that there are some loci with relatively large effects on particular quantitative traits (Hayes, 2008). The search for these loci with large effect and the use of this information might improve the
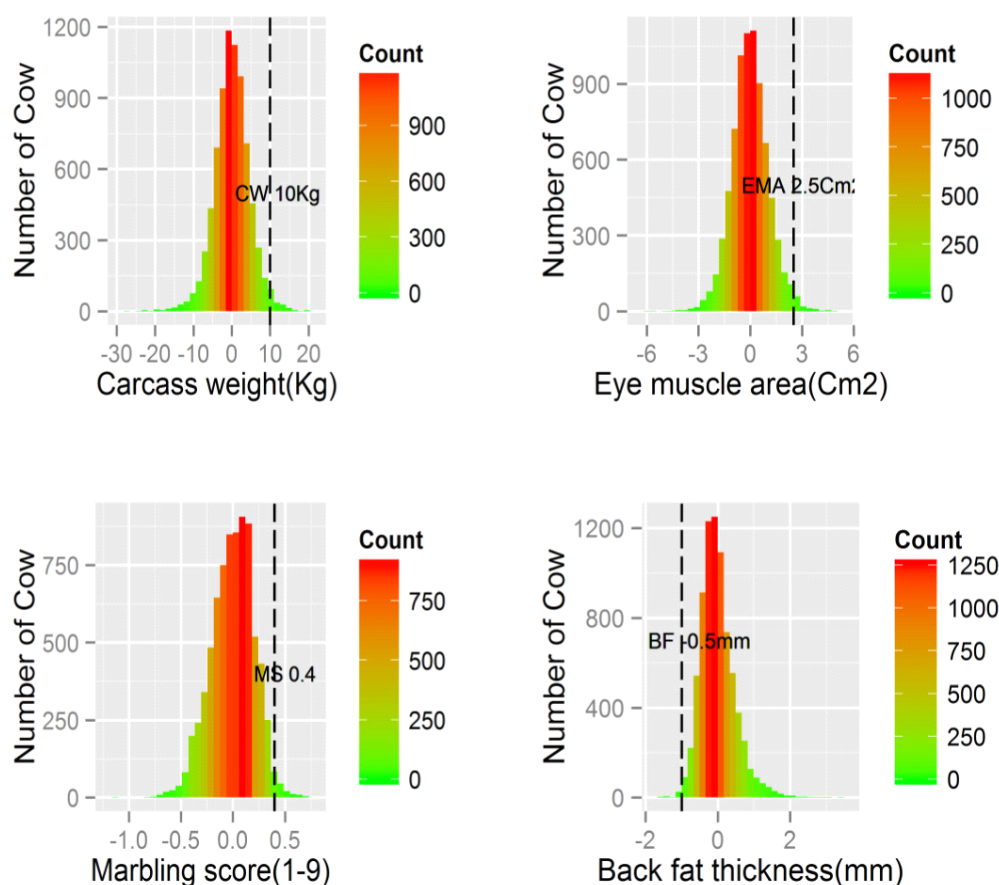
Fig. 5. The distribution of expected progeny differences (EPD) for cow in Pyeong-chang.

selection accuracy in animal breeding. This motivation has driven intensive research efforts to detect Quantitative Trait Loci (QTL) in the different livestock species over last two decades.

Recent advances in molecular genetic technology facilitate not only detection of genes that contribute to genetic variation of quantitative traits but also incorporation of genomic information into a conventional animal breeding program. The incorporated DNA information will help to reconstruct pedigree errors in Hanwoo smallholder as well as to estimate accurate genomic breeding value (GEBV) in Hanwoo.

Several studies have suggested that marker based selection methods such as MAS and GS allow more accurate breeding value estimation than traditional selection of young animal, especially for low heritability traits (Meuwissen *et al.*, 2001). Genomic selection (GS) is indirect selection process where a quantitative trait of economic important is selected not based on the trait itself but on a marker linked to QTL of the trait. GS can be useful for traits that are difficult to measure, exhibit

low heritability, and are expressed late in development. Major genes which are responsible for quantitative traits and QTL that are linked to major genes are identified by using genome wide association test. Various methods are developed to predict a reliable genomic breeding value (GEBV) in cattle. Goddard and Hayes (2009) presented that genomic selection require building reference population which consists of large number of samples genotyped by dense SNPs and recorded for the traits. This sample is analysed to derive a prediction equation that predicts breeding value from marker genotypes (Fig. 6).

In real dataset of Hanwoo reference population (n=1,011), we compare a conventional BLUP and Genomic selection method for cow selection population. As shown in Table 1, genomic prediction method was shown higher accuracy in cow breeding value.

Therefore, genomic selection is particularly advantageous for traits that are difficult to record at a young age. Beef cattle selection program will take 5.5 years to produce their progeny. Genomic selection of bulls at 1 years of age could greatly re-
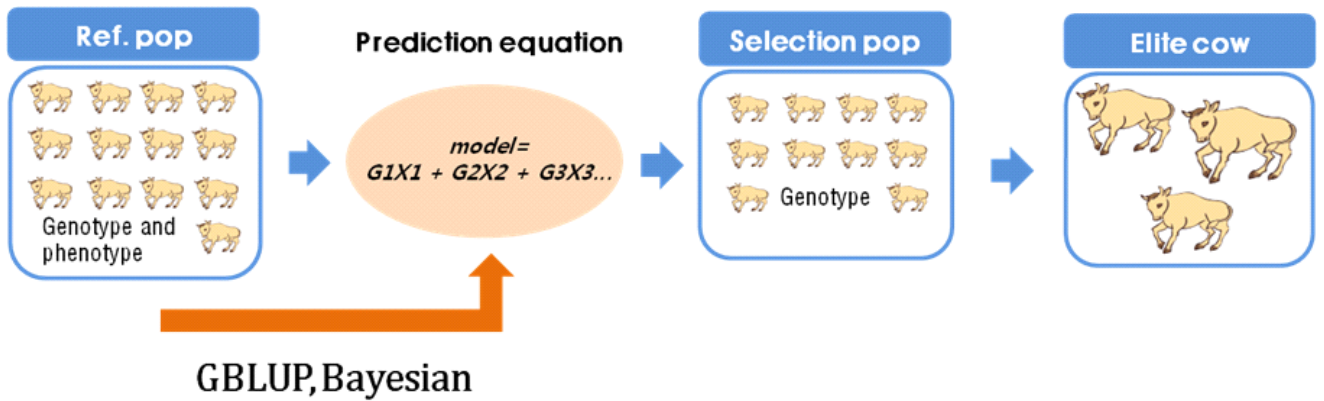
Fig. 6. Diagram of genomic selection process. For example, a large sample of animals is measured for the trait and genotyped for markers as shown in Fig. 6. The genotypes can be recorded by a variable (X), which takes the value 0 or 1 or 2 for AA, AB and BB. The statistical analysis of the ref. pop estimates SNP effects for each marker (G) and hence a prediction equation can be generated that combines all the marker genotypes with their effects to predict the genomic breeding value (GEBV) for each animals in selection population.

Table 1. Accuracy of genomic EBV for cow estimated by 50 K SNP chip using 1,011 ref. pop in Hanwoo

Traits	BLUP	GBLUP	Difference
Eye muscle area (cm^2)	0.11(0.08)	0.29(0.07)	0.18
Back fat thickness (mm)	0.11(0.08)	0.30(0.11)	0.19
Marbling score (1~9)	0.11(0.08)	0.27(0.12)	0.16

duce the generation interval to speed up the rate of genetic improvement in beef cattle. In particular, so far there is no consideration of cow breeding for carcass traits in Hanwoo smallholder. There are many constraints for cow breeding because of not enough phenotypes for any traits. However, if genomic prediction tools with reproduction technologies such as Multiple Ovulation Embryo Transfer (MOET) in are used in cow breeding, it will allow to select elite cow for special breeding objective for smallholder and to multiply elite cow faster in Hanwoo smallholder.

GENOMIC SELECTION AND REPRODUCTION TECHNOLOGY SPEED UP COW GENETIC IMPROVEMENT

As discussed in this review, as for cow breeding and multiplication in Hanwoo smallholder, selection of elite cow will be very critical point at the moment. There are two ways to estimate cow estimated breeding value (EBV) for certain

traits (currently, carcass weight, eye muscle area, backfat thickness and marbling score). One way is the conventional BLUP method using abattoir carcass traits and pedigree information as addressed in part 3 of the review. The other way is to use genomic information for estimation of cow breeding value at young age. However, there is still one drawback to do genotyping because cost is still very high (120 US $ per animal) in Korea. If the cost of genotyping get down to 10 to 20 $ per animal it would be very powerful to get Hanwoo smallholder to participate into cow breeding program.

In particular, if we can combine genomic selection and Juvenile beef MOET technology, it will allow cow to reduce generation interval to multiply elite cow in smallholder. As shown in Fig. 7, once we get genomic breeding value at cal-
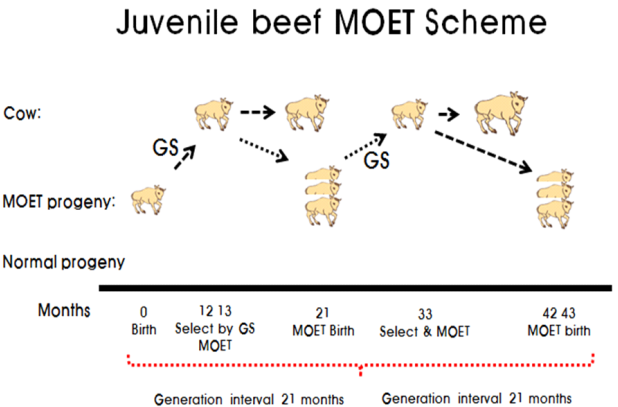
Juvenile beef MOET Scheme

Fig. 7. Juvenile beef MOET scheme with genomic selection to reduce generation interval.

ves based on their genotype, first MOET can be started at 12 to 13 months of age, after birth of first MOET, GEBV for calves from first MOET will be estimated on genotypes then second MOET will be tried. Consequently, overall 44 month of duration, we can multiply elite cow selected by GEBV two times.

CONCLUSION

In conclusion, after National traceability system is running from 2007, Hanwoo smallholder will be able to collect abattoir carcass traits from the Korea Institute for Animal Products Quality Evaluation (KAPE), and massive pedigree information for registered animals are recorded by Animal Genetic Improvement Association (AIAK). These data lead to do a genetic evaluation of cow in smallholder to selection elite cow for breeding. Moreover, combining genomic tools and reproduction technology will allow reducing generation interval and easily multiplying elite cow for breeding in Hanwoo smallholder. Many of advanced technologies have been developed during recent 10 years in Hanwoo industry, so that integration and harmonization of each technology will make a sustainable Hanwoo industry.

REFERENCES

Allen J. 2001. An Overview of BREEDPLAN. ACIAR PROCEEDINGS NO. 108: 105-113.

Cundiff LV, Gregory KE, Koch RM and Dickerson GE. 1969. Genetic variation in total and differential growth of carcass components in beef cattle. J. Anim. Sci. 29: 233-244.

Ewing B and Green P. 2000. Analysis of expressed sequence tags indicates 35,000 human genes. Nat. Genet. 25:232-234.

Fernando RL and Grossman M. 1989. Marker assisted selection using best linear unbiased prediction. Genet. Sel. Evol. 21:467-477.

Goddard ME and Hayes BJ. 2009. Mapping genes for complex traits in domestic animals and their use in breeding programs. Nat. Rev. Genet. 10:381-391.

Henderson CR. 1984. Applications of Linear Models in Animal Breeding. Can. Catal. Publ. Data, Univ. Guelph, Canada. pp. 1-130.

Hayes BJ. 2008. QTL Mapping, MAS and Genomic Selection. Text Book for Armidale Summer Animal Breeding Course. pp. 30-38.

Kim HS, Hwang JM, Choi TJ, Park BH, Cho KH, Park CJ and Kim S. 2010. Research on the peformation of the selection index for Hanwoo proven bull. Journal of Animal Science and Technology 52(2):83-90.

Kim HC, Lee SH, Cho YM, Kim S, Lim D, Park EW, Oh SJ and Hong SK. 2011. Genomic information and its application in Hanwoo (Korean Native Cattle) breeding program-A mini review. Annals of Animal Resource Sciences 22(2):125-133.

Koch RM, Gregory KE and Cundiff LV. 1995. Genetic aspects of beef carcass growth and development. Proc. 5th Genetic Prediction Worship, Kansas City, MO. PP. 9.

Koo YM, Kim S, Kim JI, Song CE, Lee KH, Jeoung YH, Lee JY, Jang HG, Park BH, Choi TJ, Cho KH, Lee SS, Lee JG and Kim HS. 2011. Research of statistical model for genetic evaluation of Hanwoo carcass traits. J. Anim. Sci. & Technol. (Kor.). 53(4): 283-288.

Lee SH. 2012. Genome information and Hanwoo breeding. ISSN 11-1390906-000145-01. pp. 92.

Meuwissen THE, Hayes BJ and Goddard ME. 2001. Prediction of total genetic value using genome-wide dense marker maps. Genetics 157:1819-1829.

Ministry of Agriculture and Fishery (MAF) 1999. Code of practice for development programs in agriculture and forestry. pp. 40.

National Institute of Animal Science. (NIAS) 2009. Annual Report for Hanwoo Genetic Evaluation. pp. 17.

Wickham BW and Durr JW. 2011. A new international infrastructure for beef cattle breeding. Animal Frientier. 1(2): 53-59.

Won JI, Kim JB and Lee JK. 2010. Evaluation of genetic ability for meat quality in Hanwoo cow. J. Anim. Sci. & Technol. (Kor.). 52(4):259-264.