



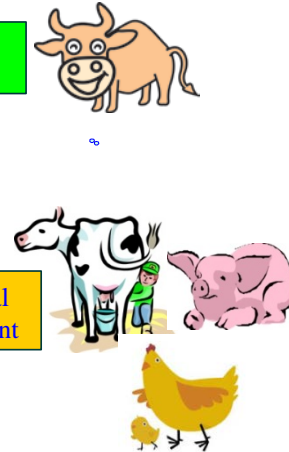
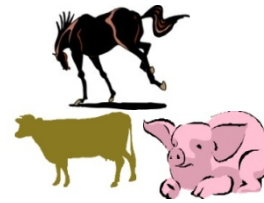
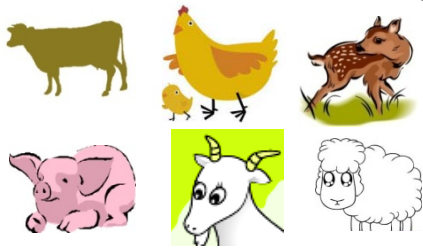
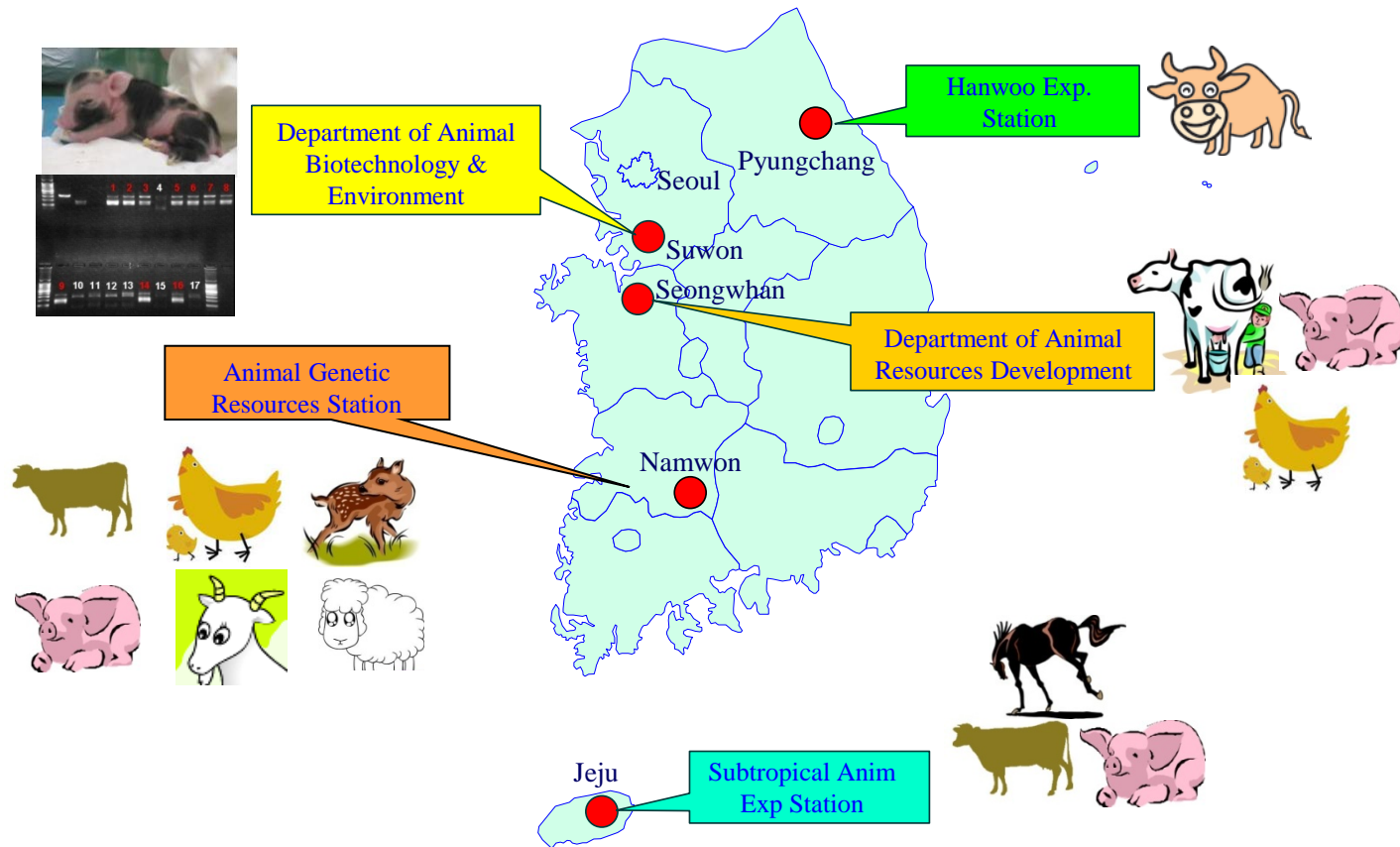
Genome wide association and genomic selection to speed up genetic improvement for meat quality in Hanwoo

Seung Hwan Lee, PhD
Hanwoo Experiment Station, National Institute
of Animal Science, RDA





National Institute of Animal Science, RDA





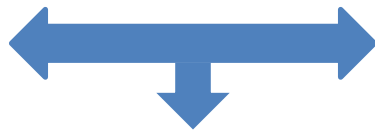
Genomic Networking in NIAS , RDA

Genetic Improvement

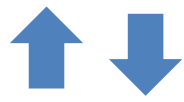
- National Breeding Program
- Planning, strategy of breeding program
- Development of Breeding tools
- Optimization of Breeding program

Animal Genome & Bioinformatics

- Genome project for Livestock
- Bioinformatics
- Development of Genomic tools
- QTL, GWAS, GS model

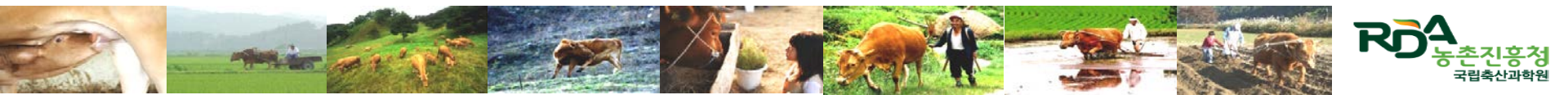


**Delivery
Genomics into
Breeding**



Hanwoo Experiment Station

- Evaluation of GS model
- Validation of QTL, GWAS etc
- Line breeding





Statistics for Hanwoo Industry

Location	farm	%	Head	%
Whole country	165,420		3,034,812	
Seoul	5	0	108	0
Busan	111	0.07	2,203	0.1
Daegu	1,106	0.67	19,728	0.7
Incheon	423	0.26	15,771	0.5
GwangJu	313	0.19	7,167	0.2
Daejeon	240	0.15	5,902	0.2
Ulsan	1,901	1.15	28,927	1
Gyeonggi	6,940	4.2	212,000	7.3
Gangwon	12,996	7.86	225,899	7.8
Chungbuk	10,114	6.11	184,387	6.3
Chungnam	21,376	12.92	391,808	13.5
Jeonbuk	15,099	9.13	357,163	12.3
Jeonnam	33,607	20.32	521,716	18
Gyeongbuk	35,405	21.4	580,394	20
Gyeongnam	25,180	15.22	322,142	11.1
Jeju	604	0.37	29,497	1

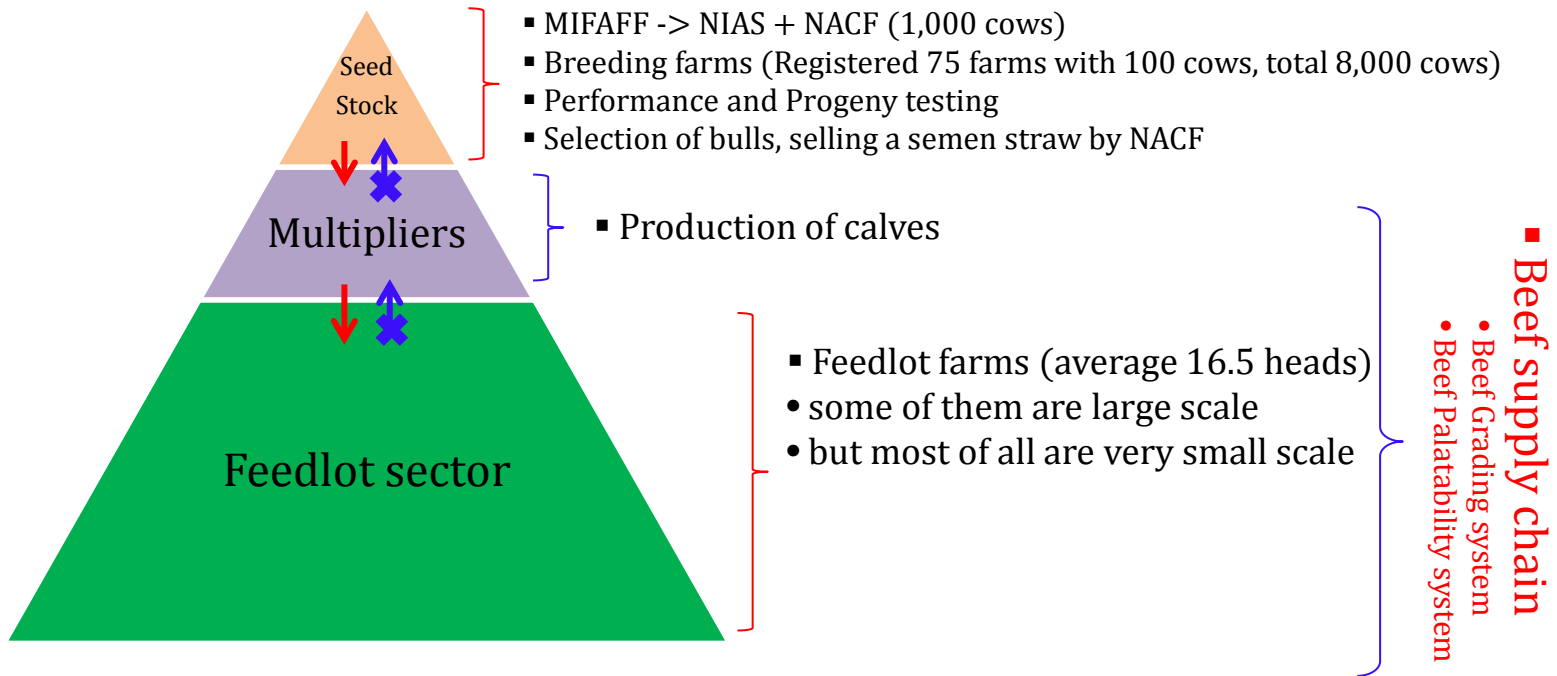
- 3 million head (total)
- 1.3 million head (Cow)
- 165,420 farm





Hanwoo Supply Chain

Government Funding

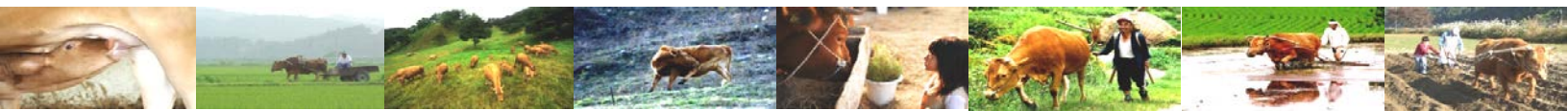
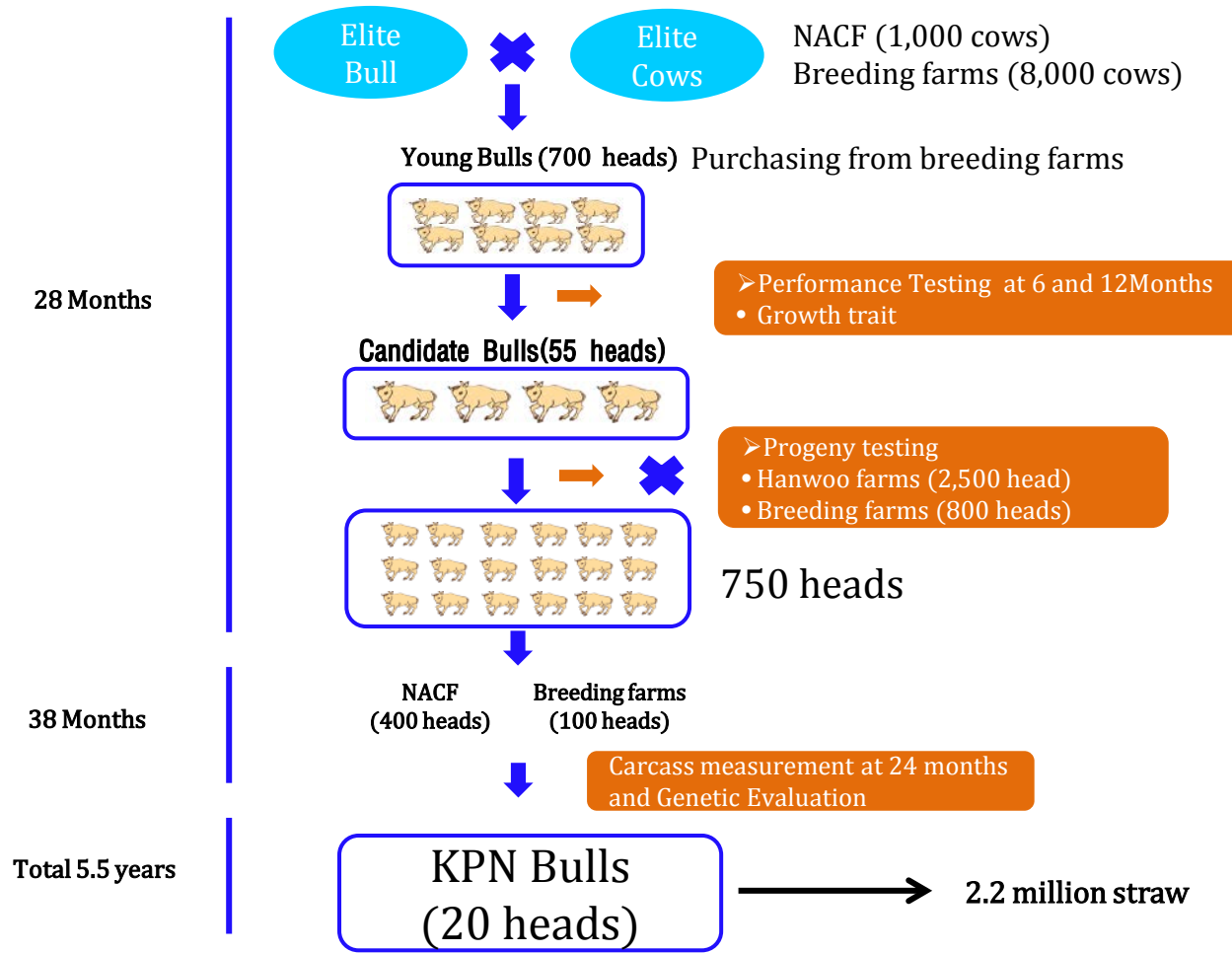


MIFAFF: Ministry for food, agriculture, Forestry and Fishery
 NACF: National Agricultural Cooperative Federation
 NIAS: National Institute of Animal Science
 KAPE : Korea Institute for Animal Products Quality Evaluation
 AIAK : Korea Animal Improvement Association





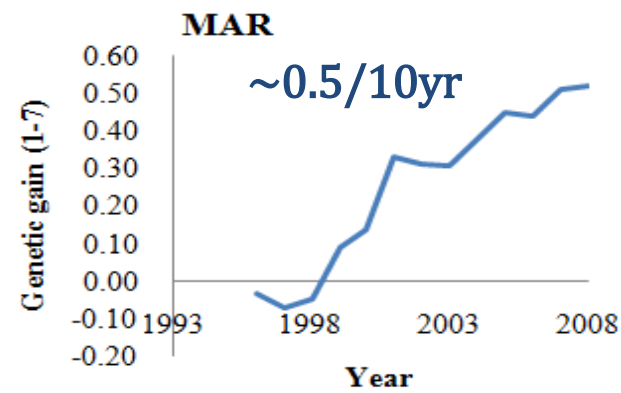
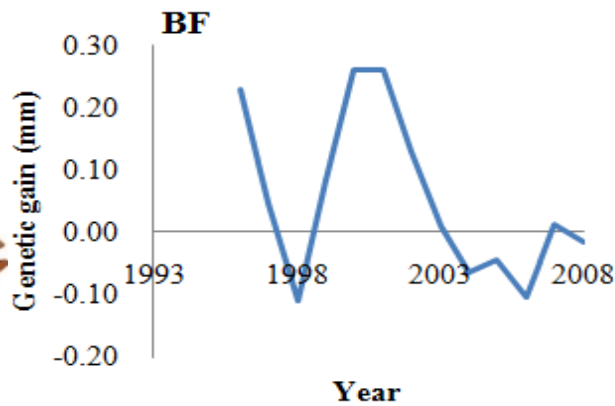
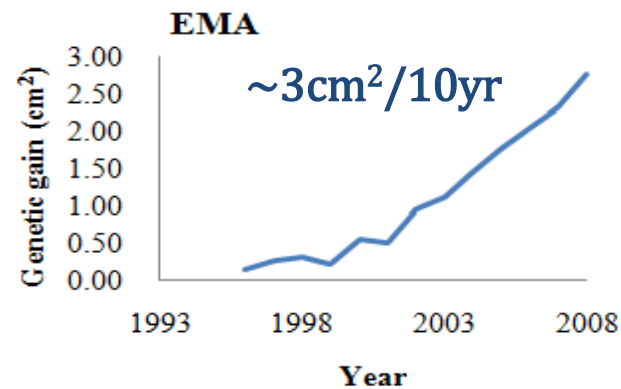
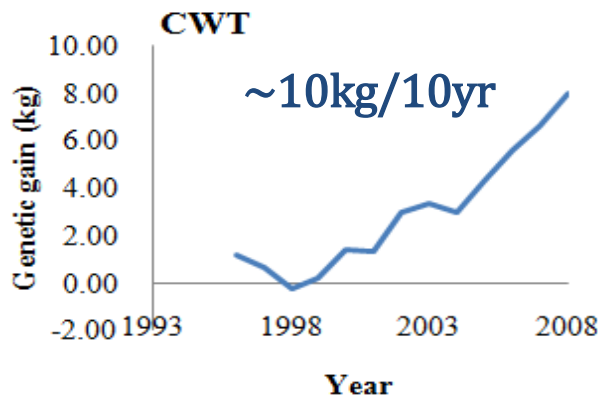
Bull selection in Seed Stock Sector





Trends in Korean Hanwoo Carcass traits

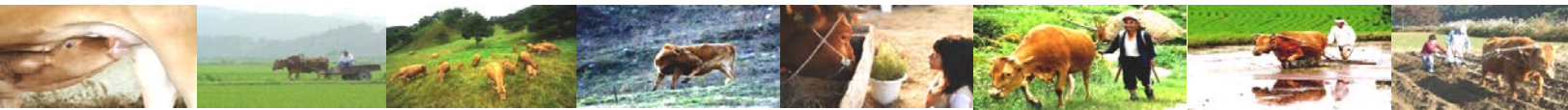
It is very successful !!!





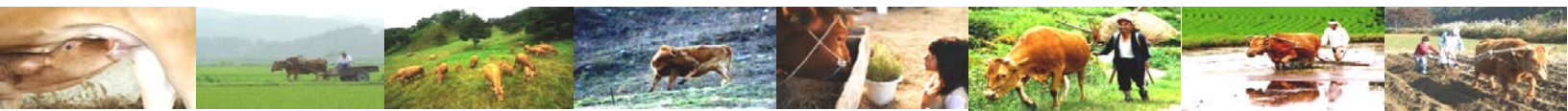
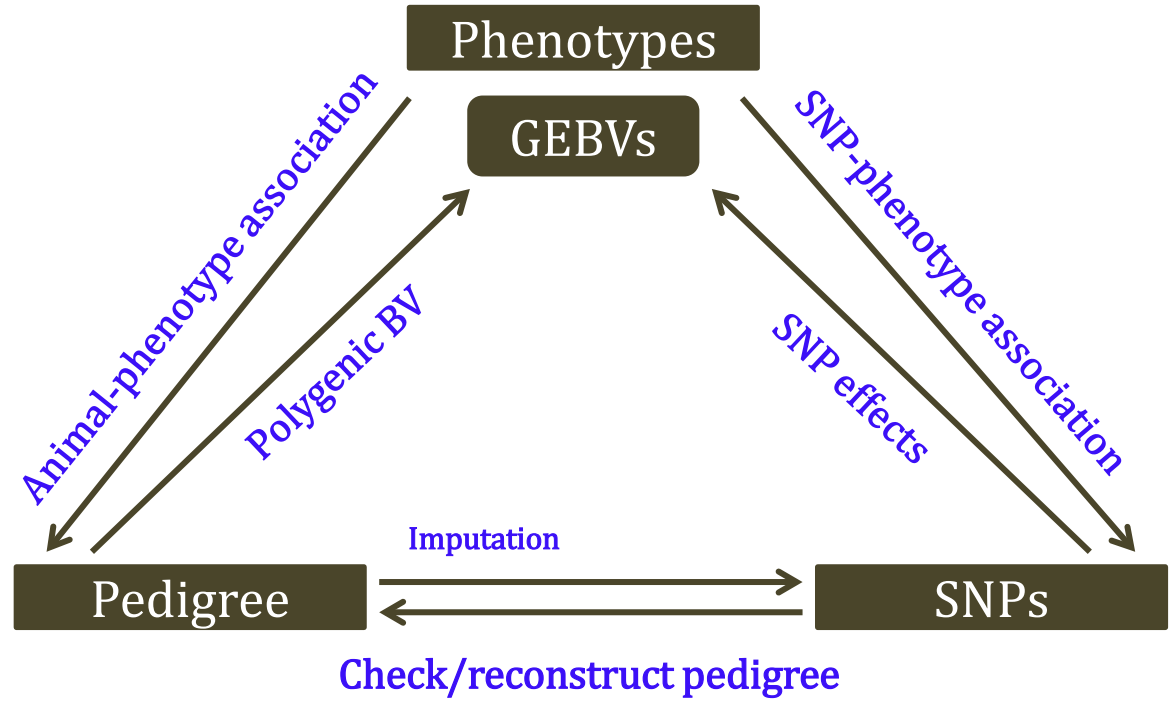
What is advantages of genomics in Hanwoo breeding ?

- More genetic gain in a short time
 - Reduce generation interval, Increased EBV
- Effective breeding program
 - Open nucleus system
- Benefit for New traits to breeding program
 - Low heritability traits
 - Traits that are hard to measure(eg, feed efficient etc)
- Benefit for reducing inbreeding
 - Own information rather than family information





Benefits of SNPs in Animal Breeding





This talk

Genetic architecture of carcass traits in Hanwoo

Accuracy of Genomic breeding value

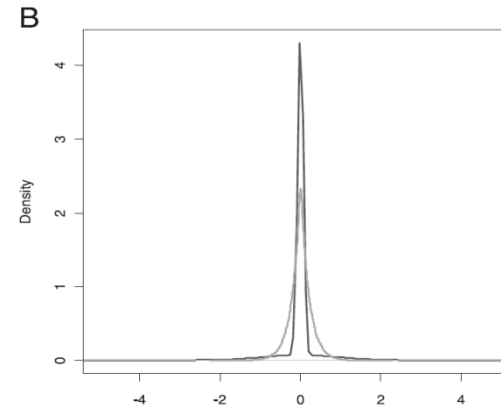
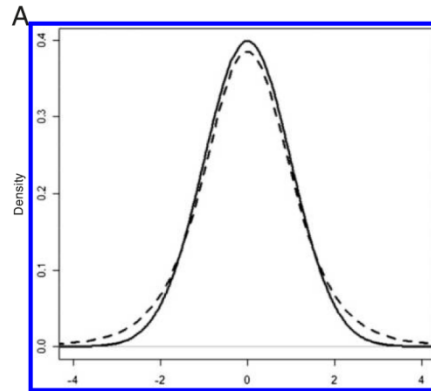
Requirement of accurate GEBV

- Effective pop size
- Num of SNPs
- Num of ref. pop size

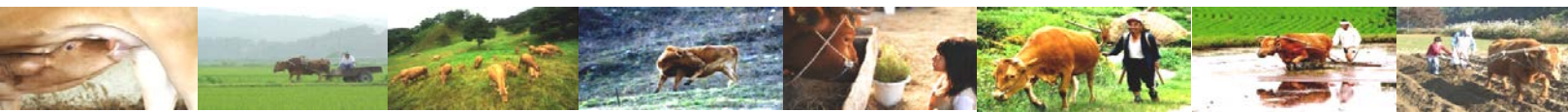




Distribution of gene effects vs Models



Name	Reference	Assumed distribution of SNP effects	Implication
BLUP	Meuwissen et al. (2001)	Normal	A very large number of QTL of small effect
BayesA	Meuwissen et al. (2001)	t distribution	A large number of QTL of small effect and a small proportion with moderate to large effect
BayesB	Meuwissen et al. (2001)	Mixture distribution of zero effects and t distribution of effects	A large number of genome regions with zero effect, a small proportion of QTL with moderate effects
Bayesian LASSO	Yi and Xu (2008)	Double exponential distribution of effects	Very large proportion of SNP with effect of close to zero, small proportion of moderate to large effect
BayesSSVS	Verbyla et al. (2009)	Mixture distribution of zero effects and t distribution of effects	A large number of genome regions with almost zero effect, a small proportion of QTL with moderate effects





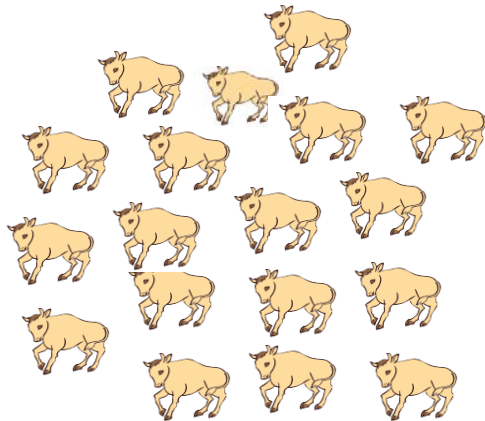
Genome wide association study to understand the **Genetic Architecture of carcass traits**

- Reference population (n=1,012) consisting of steers from progeny testing:

Reference pop for GWAS
(n=1,012)

Sire = 118, dam = 995

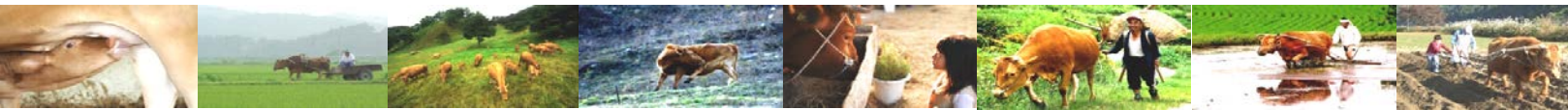
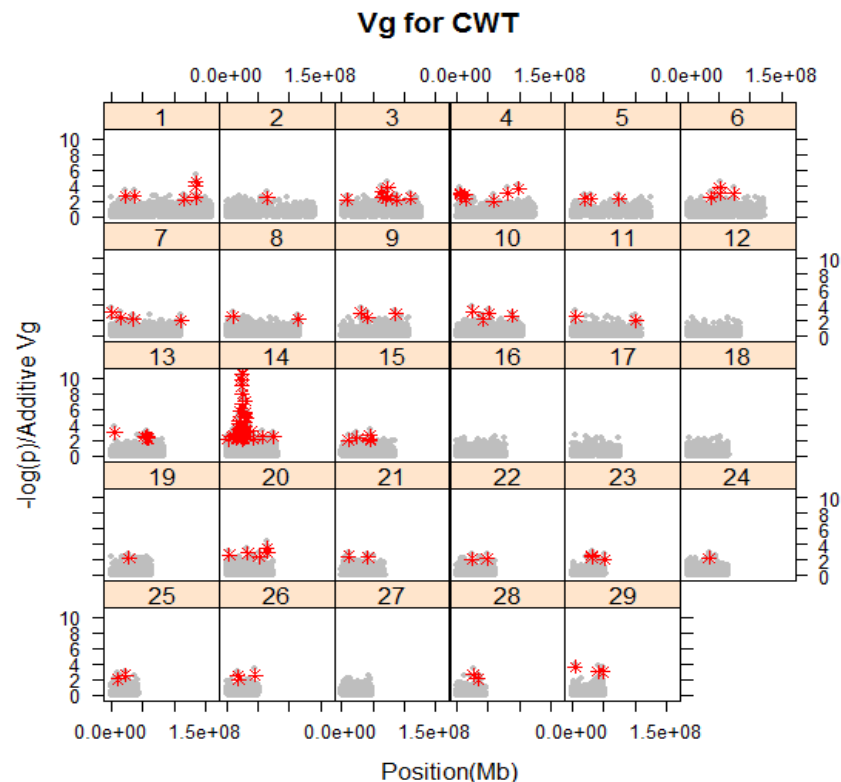
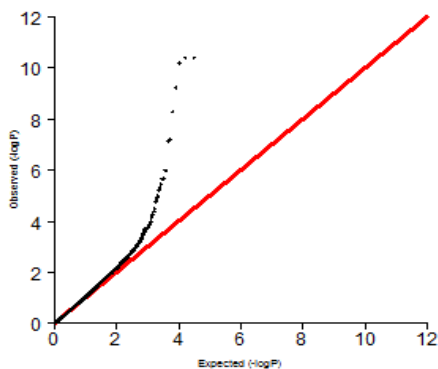
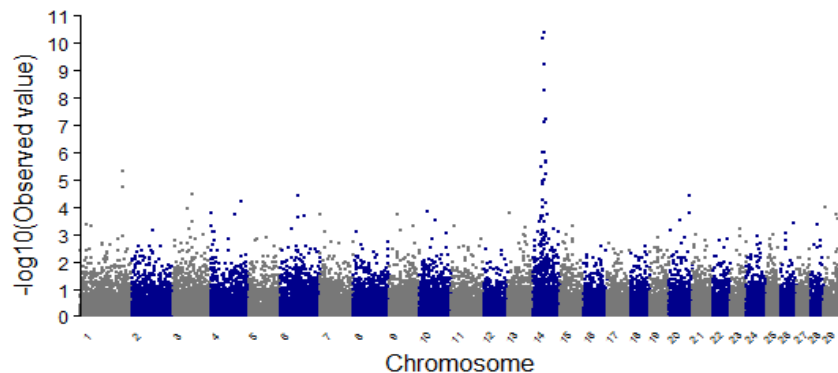
- Steers genotyped with 50K
 - MS, CWT, EMA and BF





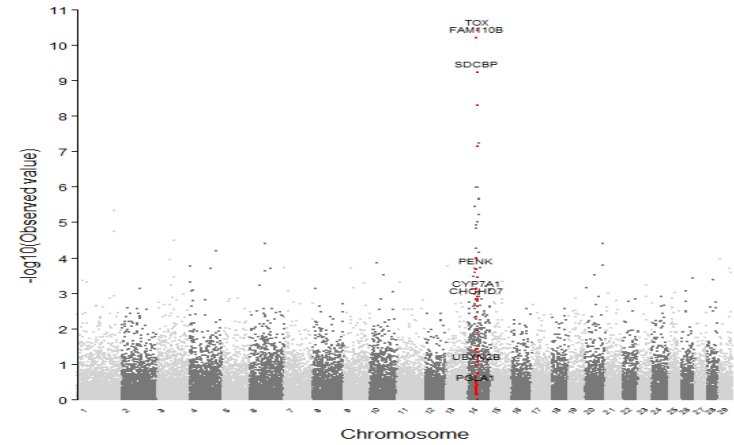
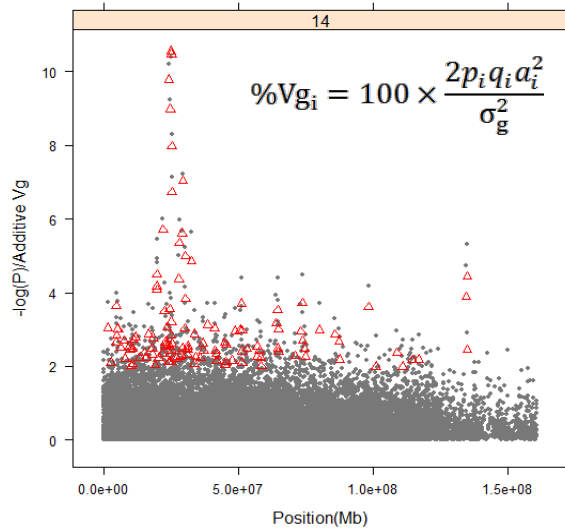
Genome wide association for Carcass weight

$$\%Vg_i = 100 \times \frac{2p_i q_i a_i^2}{\sigma_g^2}$$

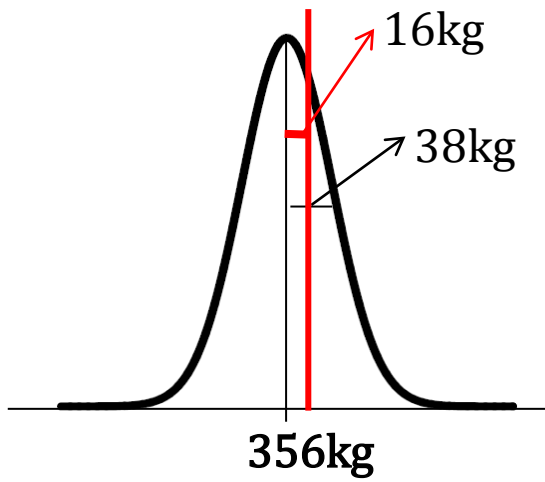




SNP effect (Vg)

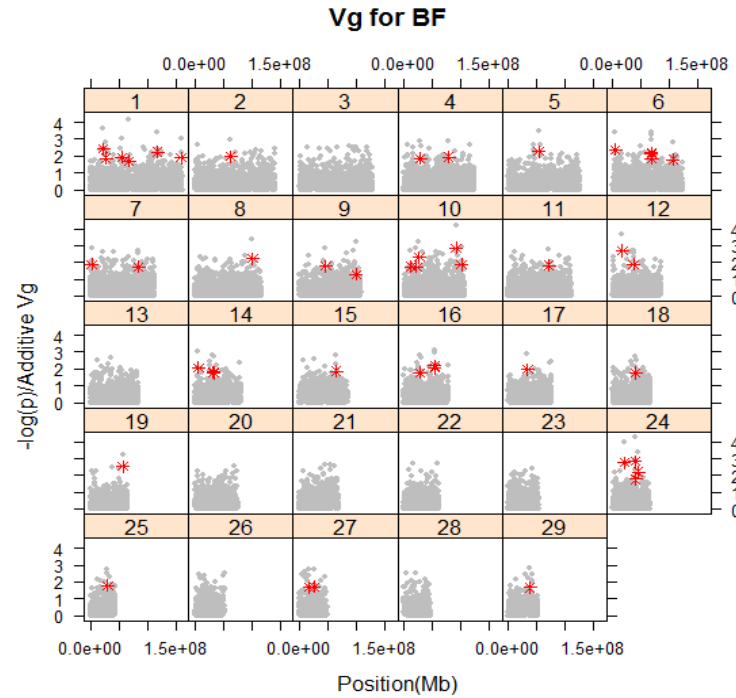
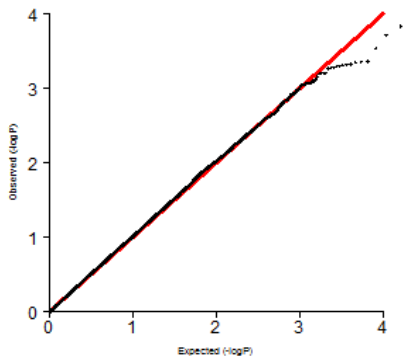
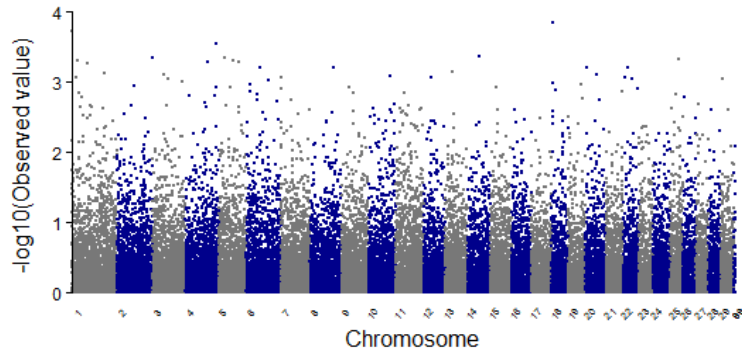


SNP effect (Vp)



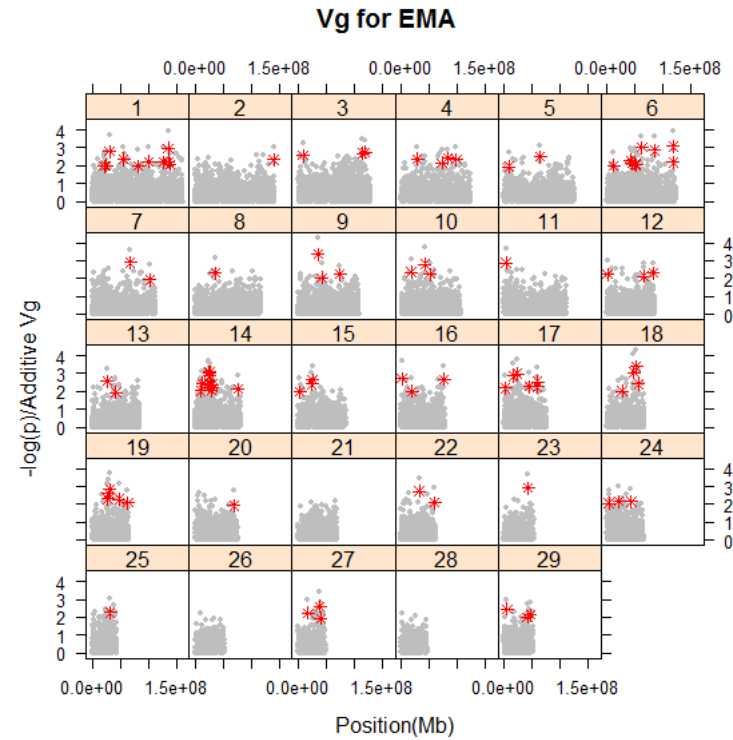
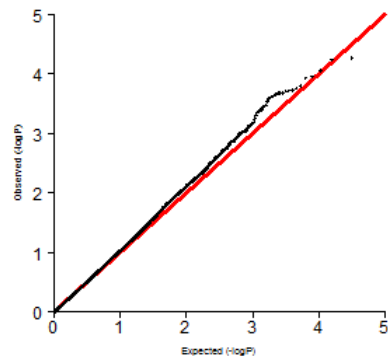
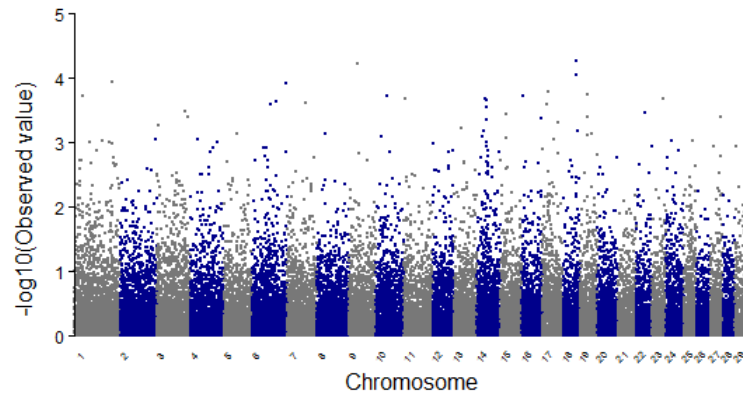


Back Fat Thickness



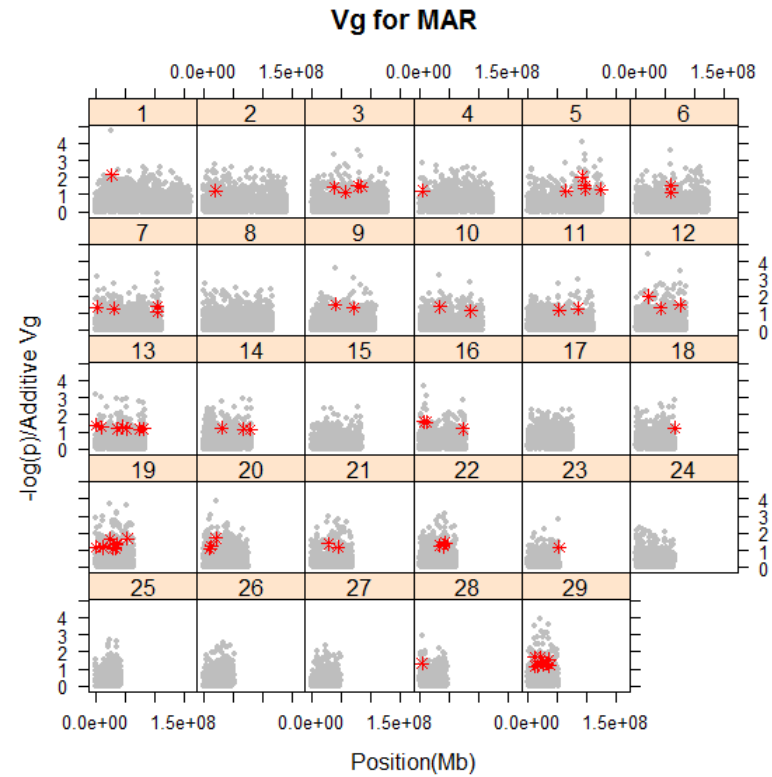
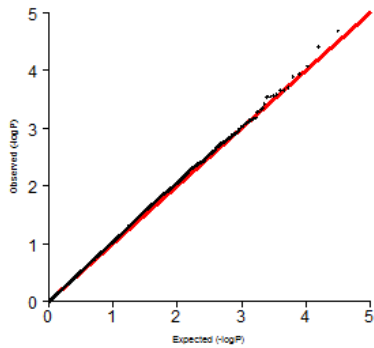
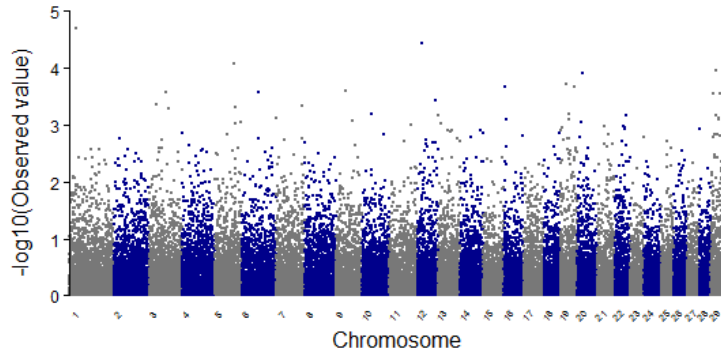


Eye muscle area





Marbling score





This talk

Genetic architecture of carcass traits in Hanwoo

Accuracy of Genomic breeding value

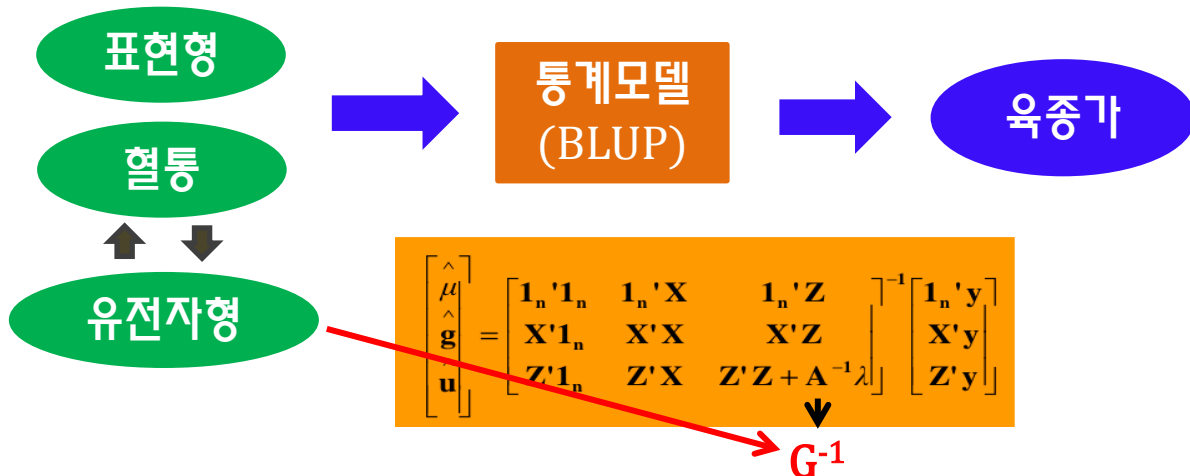
Requirement of accurate GEBV

- Effective pop size
- Num of SNPs
- Num of ref. pop size





GBLUP

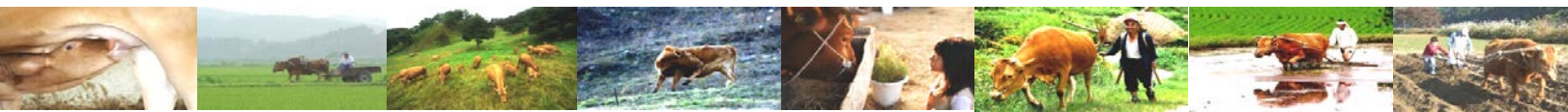


$$Var(g) = \mathbf{z}\mathbf{z}'\sigma_a^2$$

$$Var(g) = \mathbf{G}\sigma_u^2$$

$$\sigma_u^2 = 2 \sum p_i(1 - p_i)\sigma_a^2$$

$$\mathbf{G} = \frac{\mathbf{z}\mathbf{z}'}{2 \sum p_i(1 - p_i)}$$





Genomic Selection_Prediction of GEBVs

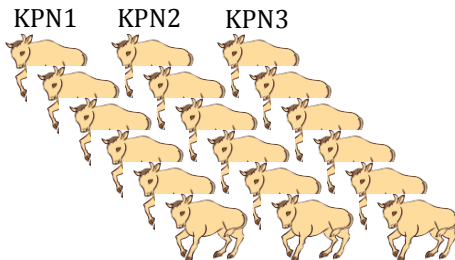
Reference pop vs Validation set

- **Reference population** (n=1,011) consisting of steers from progeny testing
 - **Val set 1** (n=106) consisting of KPN bulls of steers in ref pop
 - **Val set 2** (n=178) consisting of progeny without obs
 - **Val set 3** (n=236) consisting of Line breeding in Hanwoo station

Sire = 118, dam = 995

Reference pop
(n=1,011)

- Steers genotyped by 50K
- IMF, MS, CWT, EMA and BF



Progeny tested pop



Genomic Prediction
GBLUP

Val set 1 (n=106)
Candidate bull for progeny

Val set 2 (n=178)
Progeny without obs

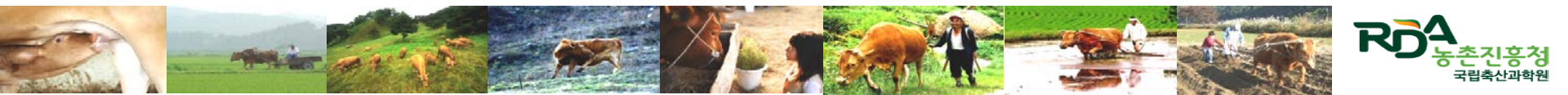
Val set 3 (n=236)
Bull and female for line
breeding in Hanwoo station





Accuracy of GEBV

Traits	BLUP	GBLUP	Diff.
Sire without obs. (n = 106)			
EMA	0.71(0.12)	0.72(0.11)	0.01
BF	0.75(0.13)	0.76(0.12)	0.01
MS	0.75(0.13)	0.76(0.12)	0.01
Progeny without obs.(n=178)			
EMA	0.30(0.03)	0.35(0.04)	0.04
BF	0.32(0.03)	0.37(0.04)	0.06
MS	0.32(0.03)	0.38(0.04)	0.06
Hanwoo station females without obs. (n=236)			
EMA	0.11(0.08)	0.29(0.07)	0.18
BF	0.11(0.08)	0.30(0.11)	0.19
MS	0.11(0.08)	0.27(0.12)	0.16





This talk

Genetic architecture of carcass traits in Hanwoo
Accuracy of Genomic breeding value

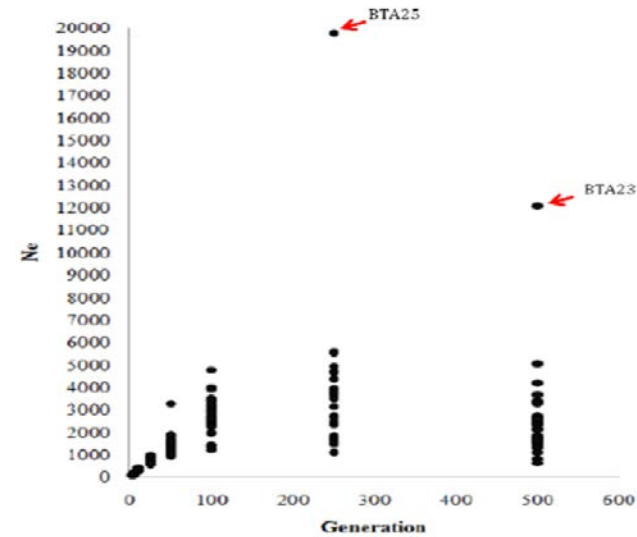
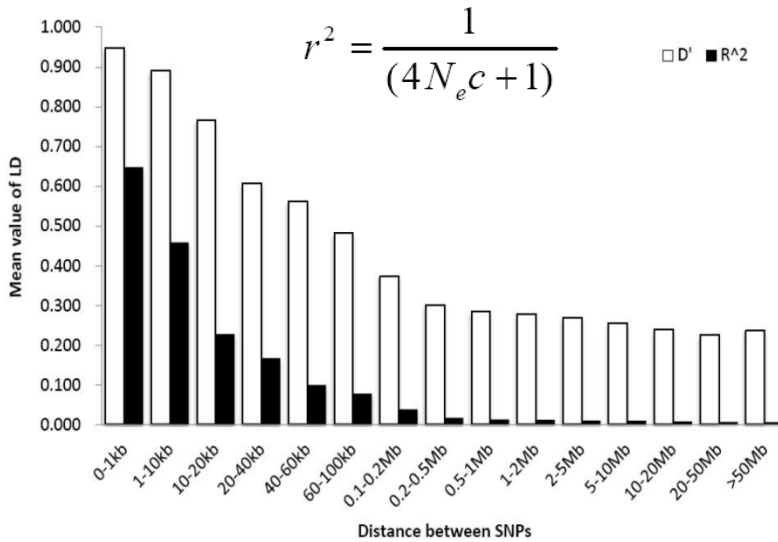
Requirement of accurate GEBV

- Effective pop size
- Num of SNPs
- Num of ref. pop size





Linkage disequilibrium vs Effective pop size



Fragment size (kb)	100	200	500	1,000	2,000	5,000	10,000	15,000
Effective population size (Ne)								
Mean	2,743.7	3,905.6	2,748.3	1,487.6	729.4	352	162.5	98.1
Median	2,362.3	3,533.2	2,712.3	1,476.5	718.2	352.2	163.1	96.3
Standard deviation	2,197.1	3,570	836.8	453.8	111.1	22.7	13.7	7.7
Minimum	625.6	1,132.9	1,259.5	925.6	555.7	306.8	137	87.3
Maximum	12,072.6	19,792.8	4,778.4	3,279.6	1,005.7	392.5	188.9	119.3
Linkage distance (cM)	0.1	0.2	0.5	1	2	5	10	15
Generations	500	250	100	50	25	10	5	3





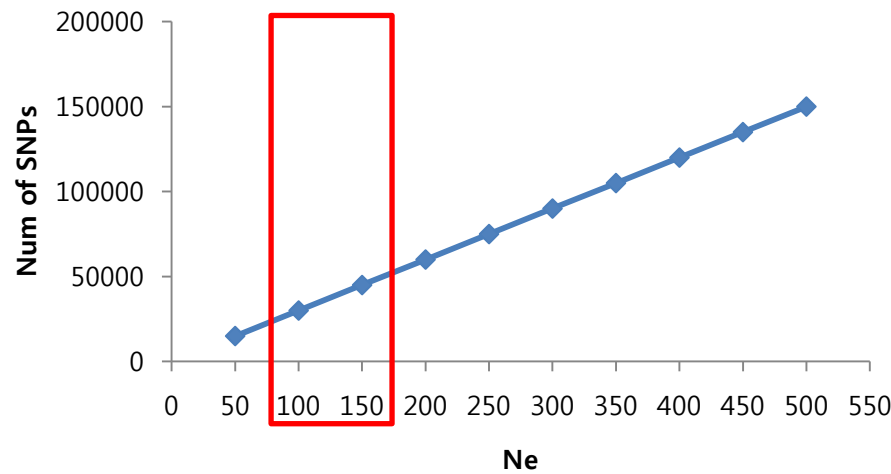
Num of SNPs

- Num of SNPs that is required to get accurate GEBV

10NeL

*Ne : Num of Effective pop. Size,

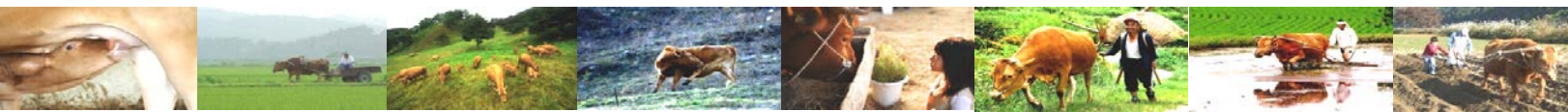
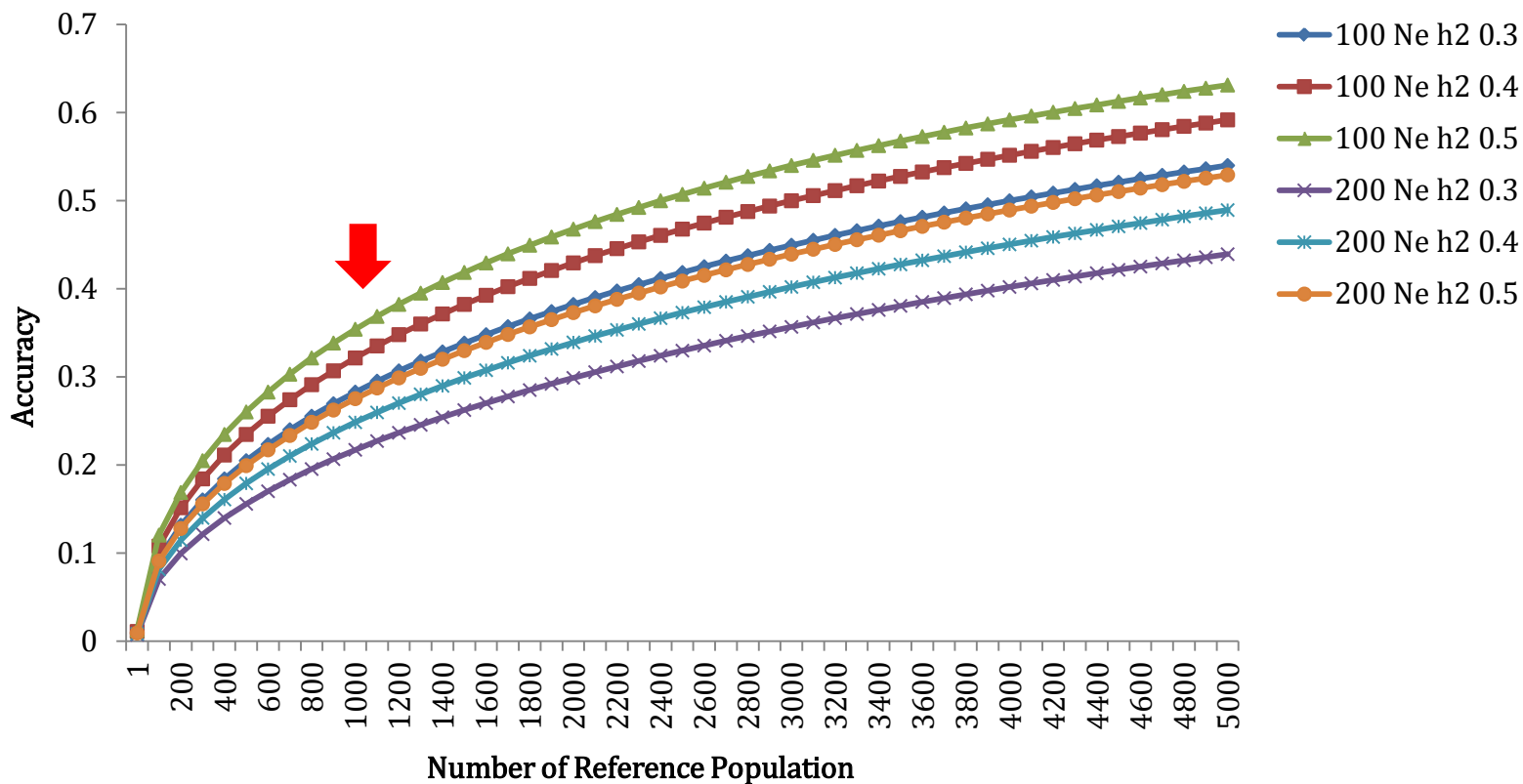
*L : Length of the genome in Morgan





Ref. Pop vs Accuracy of GEBV

Mike Goddard Equation
$$r = \sqrt{1 - \lambda / (2N\sqrt{a}) * \ln\left(\frac{1+a+2\sqrt{a}}{1+a-2\sqrt{a}}\right)}$$





Summary

- Technically Genomic selection for complex traits work well in Dairy cattle and can be used in Hanwoo
 - Very similar breeding scheme
- Reference population
 - Large reference population (Bulls or Steers)
 - Phenotypes involved in Breeding goal
 - Genotypes (50K or 700K)





Research Collaboration with EMBRAPA

- Imputation of whole genome sequence for individual using Key sire group with WGS
 - ✓ Development of Bioinformatics system
- Development of statistical model for GS
 - ✓ Pipeline for GS model
- Optimization of GS model to Breeding program
 - ✓ Controlling Inbreeding
 - ✓ More genetic Gains
 - ✓ Maintain genetic diversity etc.

