

Pig Genome Research

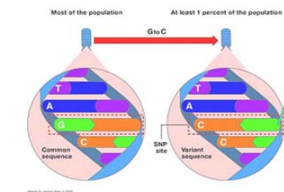
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Prof. Kang-Seok Seo



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Pig Genome Study

- The increasing importance of meat quality has implications for animal breeding programs
- Research has revealed much about the genetic background of pigs, and many studies have revealed the importance of various genetic factors
- Genomic-Wide Association Study
- Future Tech : Genomic Selection

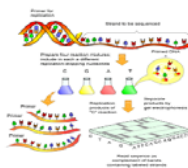


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Pig GWAS

Previous Our Study : GWAS

- We looked for a genomics region related to meat quality of pig



| | | | |
|----------|----------|-----|-----------|
| Karen | AGCTTGAC | TCC | ATGATGATT |
| Debo | AGCTTGAC | GCC | ATGATGATT |
| Jose | AGCTTGAC | TCC | TGATGATT |
| Thomas | AGCTTGAC | GCC | TGATGATT |
| Anupriya | AGCTTGAC | TCC | ATGATGATT |
| Robert | AGCTTGAC | GCC | ATGATGATT |
| Michelle | AGCTTGAC | TCC | TGATGATT |
| Zhijun | AGCTTGAC | GCC | TGATGATT |

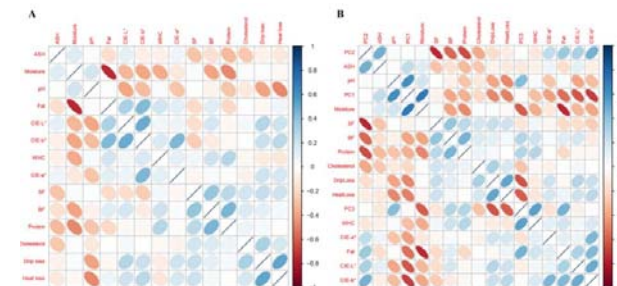
Single Nucleotide Polymorphism

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Pig GWAS

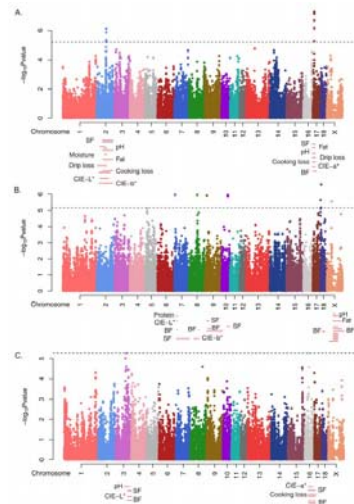
Previous Our Study : GWAS

- We identified significant SNPs as results of the GRAMMAR method against PC1, PC2 and PC3 of 14 meat quality traits of 181 Duroc pigs
- The Genome-wide association study (GWAS) found 26 potential SNPs affecting various meat quality traits
- The loci identified are located in or near 23 genes



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▪ Pig GWAS



Previous Our Study : GWAS

- Twenty-five of the significant SNPs also located in meat quality-related QTL regions, these result supported the QTL effect indirectly

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▪ Missing Heritability



- We can not explain complex traits using some genetic loci
- So we have to use total genome information to explain complex traits
- BLUP (Animal Model) is a very useful method to explain complex traits

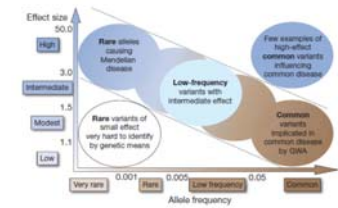
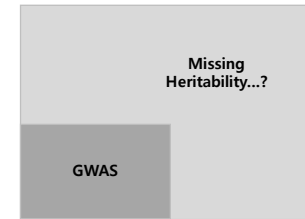


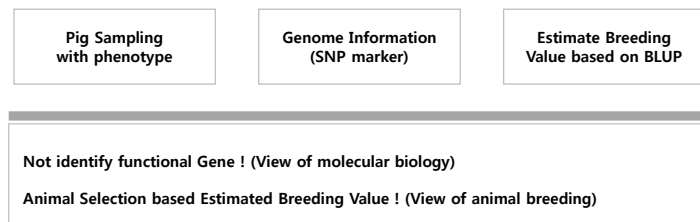
Figure 1 | Feasibility of identifying genetic variants by risk allele frequency and strength of genetic effect (odds ratio). Most emphasis and interest lies in identifying associations with characteristics shown within diagonal dotted lines. Adapted from ref. 42.

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▪ Pig Genomic Selection



- We can not explain complex traits using some genetic loci
- So we have to use total genome information to explain complex traits
- BLUP (Animal Model) is a very useful method to explain complex traits



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▪ Pig Genomic Selection



- “Fixed effect model” VS “Random effect model”

Fixed effect model

- We identified functional gene related to trait, and we used these genes in animal breeding
- GWAS, Gene expression, QTL mapping, MAS

Random effect model

- We regard genomic information as random effect
- GBLUP, Bayesian, SSblup, SSSblup

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▪ Pig Genomic Selection



▪ Historical Flow of Genomic Selection

▪ QTL Mapping : MAS

Fixed

▪ Simulation, Attempting : Bayes A,B

Random

▪ Official Use : Bayes Cπ, Dπ, GBLUP

▪ Practical Use : SSblup, SSSblup

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▪ Pig Genomic Selection



Simulation, Attempting : Bayes A,B

▪ Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps (2001)

TABLE 2
Comparing estimated vs. true breeding values
in generation 1003

| | $r_{TBREV} + SE$ | $b_{TBREV} + SE$ |
|--------|------------------|------------------|
| LS | 0.318 ± 0.018 | 0.285 ± 0.024 |
| BLUP | 0.732 ± 0.030 | 0.896 ± 0.045 |
| BayesA | 0.798 | 0.827 |
| BayesB | 0.848 ± 0.012 | 0.946 ± 0.018 |

TABLE 5
The correlation between estimated and true breeding values
in generations 1003–1008, where the estimated breeding
values are obtained from the BayesB marker estimates
in generations 1001 and 1002

| Generation | r_{TBREV} |
|------------|-------------|
| 1003 | 0.848 |
| 1004 | 0.804 |
| 1005 | 0.768 |
| 1006 | 0.758 |
| 1007 | 0.734 |
| 1008 | 0.718 |

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▪ Pig Genomic Selection



Official Use : GBLUP

▪ Using GRM (Genomic Relationship Matrix)

Invited Review : Reliability of genomic predictions for North American Holstein Bulls (2009)

Here!!

Averaged across traits, the GEBV had a reliability of 50%, compared with 27% from the parent average alone. Using BLUP rather than the Bayesian approach gave only a slightly (1%) reduced reliability, as was observed in the Australian and New Zealand results.

the United States

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▪ Pig Genomic Selection



- Best of Current Genomic Evaluation Models : “Single Step BLUP (SSblup)”
- Accurate integration of genotyped animals into conventional evaluation
- Single step GBLUP model works perfectly for closed populations with all genotypes and phenotypes in one hand

$$\mathbf{H} = \begin{bmatrix} \mathbf{A}_{11} & \mathbf{A}_{12} \\ \mathbf{A}_{21} & \mathbf{G}_{22} \end{bmatrix} = \mathbf{A} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_{22} - \mathbf{A}_{22} \end{bmatrix}$$

$$\mathbf{H}^{-1} = \begin{bmatrix} \mathbf{A}^{11} & \mathbf{A}^{12} \\ \mathbf{A}^{21} & \mathbf{G}_{22}^{-1} + \mathbf{A}^{22} - \mathbf{A}_{22}^{-1} \end{bmatrix} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_{22}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

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▪ Pig Genomic Selection



“Gblup” VS “Single Step BLUP (SSblup)”

▪ Case of Pig (Landrace) Production Traits

Table 7. Average accuracy estimates for breeding values of genotyped animals using pedigree and genomic relationship coefficients

| | ABF | | |
|------|----------------|------------------------|---------------------------|
| | Total n=448 | Genotyped Male n=31 | Genotyped Female n=417 |
| Ntot | 0.653 | 0.639 | 0.654 |
| N448 | 0.280 | 0.335 | 0.276 |
| G05 | 0.544 | 0.601 | 0.540 |
| GN | 0.534 | 0.592 | 0.530 |
| G0F | 0.546 | 0.607 | 0.541 |
| | D90KG | | |
| | Total n=448 | Genotyped sire n=31 | Genotyped Female n=417 |
| Ntot | 0.631 | 0.618 | 0.632 |
| N448 | 0.194 | 0.240 | 0.190 |
| G05 | 0.358 | 0.376 | 0.357 |
| GN | 0.343 | 0.362 | 0.342 |
| G0F | 0.353 | 0.376 | 0.352 |

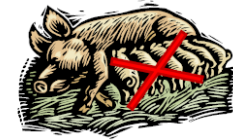
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▪ Pig Genomic Selection



“Gblup” VS “Single Step BLUP (SSblup)”

▪ Case of Pig (Landrace) Reproduction Traits



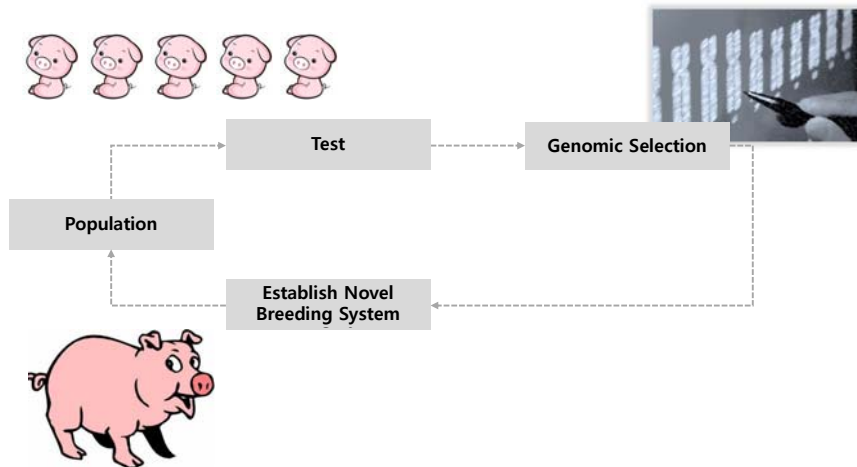
| Trait | Only Pedigree | Pedigree + Genomic Data | Increase Accuracy |
|--------------------|---------------|-------------------------|-------------------|
| TBN | 0.248 | 0.353 | 10.5% |
| TBN(contain mummy) | 0.259 | 0.363 | 10.4% |
| NBA | 0.246 | 0.347 | 10.1% |

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▪ Pig Genomic Selection



▪ Total Strategy of Pig Genomic Selection



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▪ Pig Genomic Selection



▪ Strategy of Pig Genomic Selection 1 : “Development of genomic selection for improvement pig”

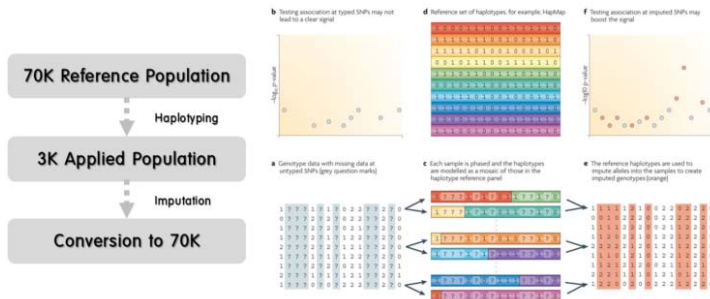
- 1) Establishment of fitted genomic selection model based on reference population
- 2) Selection of useful marker and estimation of genomic breeding value
- 3) Evaluation selection response and efficiency of genomics selection comparing pedigree method with genomic selection

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▪ Pig Genomic Selection



▪ Strategy of Pig Genomic Selection 2 : "Development of low density chip for industrial application"

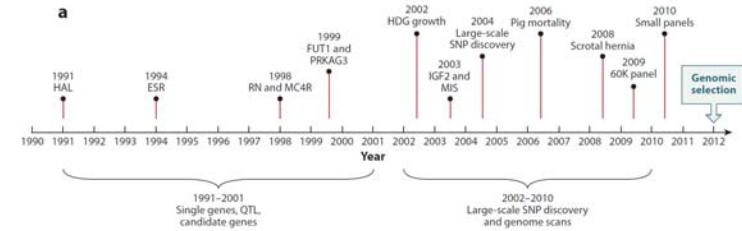


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▪ Pig Genomic Selection



- Because previous genome study was based on identification of functional gene, we have difficulties of application to industry.
- We can apply result of genomic select, directly.
- Global company in animal industry increased level of genomic selection technic to practical use.



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▪ The End

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