

Elucidation of Genetic Mechanism in Resource Animals and Its Application to Animal Breeding & Conservation

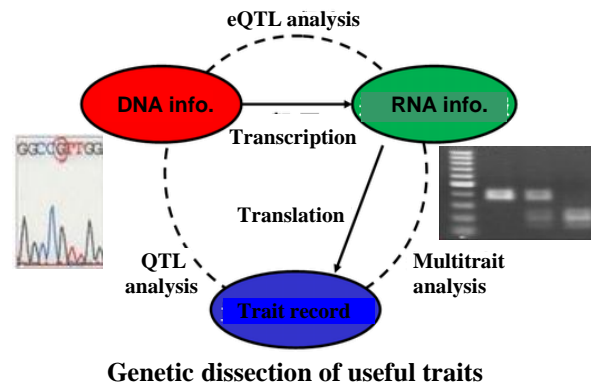
Lab. Animal Breeding and Genetics

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Resource animals provide a variety of useful biological functions and products for human life, and thus large numbers of these animal species are indispensable for human being. We are performing the diversified researches on animal breeding and genetics, which extend from a basic study toward the elucidation of many genetic mechanisms to an applied study toward the establishment of animal breeding strategy for genetic improvement, by utilizing both statistical and molecular genetic approaches. Further, we are carrying out a variety of researches on conservation of endangered animal species, relationship between global warming and microevolution in wild species, and so on.

Elucidation of Genetic Mechanism

We are performing a research on elucidation of molecular mechanisms and gene network for useful traits, through exploration, identification, and functional analysis of genes involved in the traits. Whole genomic sequencing is now ongoing in resource animals. QTL analysis methodology is making remarkable progress, making genetic dissection an interesting task for the future.



Promotion of Animal Breeding in Livestock

Wagyu has been improved by many years of endeavor in Japan, and is established as a unique livestock, resource animal that has a genetic capability to produce high-quality protein. We are performing a research on prediction of the genetic capability for useful traits in various resource animals including Wagyu, and on development of animal breeding strategy for genetic improvement.



Evaluation of Genetic Diversity in Ibis

Captive propagation and tentative release of the endangered crested ibis, *Nipponia nippon*, are now in progress as national project. The information on genetic diversity of captive population in this species is very important for promotion of the project. We are studying development of DNA markers and individual classification utilizing MHC genes in this species.



Photo from Sado Japanese Crested Ibis Conservation Center

Analysis of Global Warming & Microevolution

Evolution theory concerning natural selection plays a pivotal role in contemporary doctrine for adaptive evolution. We are analyzing an effect of global warming on change of gene constitution in animal species, and microevolution due to natural selection.

Keywords

Quantitative genetics, Statistical genetics, Molecular genetics, Population genetics, Conservation genetics, DNA analysis, Bayesian analysis, Gene network system, Genetic diversity, Endangered animals, Wagyu, Animal Breeding

Recent Publications

QTL/microarray approach using pathway information

Matsuda H, Taniguchi Y, Iwaisaki H (2012)
Algorithms Mol Biol 7:1

Changes in agriculture

Itoh R, Okajima T, Fukuyama T, Iwaisaki H (2012)
GIAHS - Encyclopedia of environments in Sado Island:81-90, Sado City Government

Genetic diversity of the current Japanese Crested Ibis population in Japan

Iwaisaki H (2012)
Proceedings of the International Symposium Commemorating the 30th Anniversary of Conservation of Crested Ibis:91-102, P.R. China

Utilization and its future prospects of SNP marker information in beef cattle

Iwaisaki H (2011)
Proceedings of the Nishigo Symposium on DNA in Livestock 5:5-8

Non-invasive sampling technique for DNA extraction from captive Japanese Crested Ibis on Sado Island

Urano K, Yamada T, Taniguchi Y, Iwaisaki H, Sugiyama T, Homma K, Kaneko Y, Yamagishi S (2010)
Anim Sci J 81: 1-4

The Wagyu cattle breeding in Japan: progress and future prospects

Iwaisaki H (2010)
Utilization of native animals for building rural enterprises in warm climate zone,
pp.107-119, FFTC/ASPAC

Genomic selection: some relevant topics

Iwaisaki H, Arakawa A, Matsuda H (2010)
Jpn J Anim Breed Res 18:17-49

Investigation of Gibbs sampling conditions to estimate variance components from Japanese Black carcass field data

Arakawa A, Iwaisaki H, Anada K (2009)
Anim Sci J 80: 491-497

Estimation of breeding values from large-sized routine carcass data in Japanese Black cattle using Bayesian analysis

Arakawa A, Iwaisaki H, Anada K (2009)
Anim Sci J 80: 617-623

Heritability and genetic correlation of abdominal vs. caudal vertebral number in the medaka (*Actinopterygii: Adrianichthyidae*): genetic constraints on evolution of axial patterning?

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Biol J Linn Soc 96: 867-874

A Bayesian approach to the Japanese Black cattle carcass genetic evaluation

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SA J Anim Sci 39: 77-80

Novel SNP in 5' flanking region of EDG1 associated with marbling in Japanese Black beef cattle

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Anim Sci J 80: 486-489

Association of a single nucleotide polymorphism in akirin 2 gene with marbling in Japanese Black beef cattle

Sasaki S, Yamada T, Sukegawa S, Miyake T, Fujita T, Morita M, Ohta T, Takahagi Y, Murakami H, Morimatsu F, Sasaki Y (2009)
BMC Res Notes 2:131

The G allele at the c.-312A>G in the EDG1 gene associated with high marbling in Japanese Black cattle is at a low frequency in breeds not selected for marbling

Watanabe N, Yoshioka S, Itoh M, Satoh Y, Furuta M, Komatsu S, Sumio Y, Fujita T, Yamada T, Sasaki Y (2009)
Anim Genet 40: 579

Genetic mapping found major QTLs for antibody-induced glomerulonephritis in WKY rats

Kose H, Sado Y, Yamada T, Matsumoto K (2009)
Exp Anim 58: 193-198

The use of link provider data to improve national genetic evaluation across weakly connected subpopulations

Nakaoka H, Gaillard C, Fujinaka K, Watanabe N, Ito M, Kawada K, Ibi T, Sasae Y, Sasaki Y (2009)
J Anim Sci 87: 62-71

Association of single nucleotide polymorphisms in the endothelial differentiation sphingolipid G-protein-coupled receptor 1 gene with marbling in Japanese Black beef cattle

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Association of a single nucleotide polymorphism in ribosomal protein L27a gene with marbling in Japanese Black beef cattle

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