

 **Support for Genomic Studies in Animals and Plants** 

Explosion of the world population, diversification of the needs by consumers and the decision by our government to participate in the negotiation about Trans-Pacific Strategic Economic Partnership Agreement (TPP) are all likely to give large impacts on the food production in Japan. It is one of the most important issues in the future Japanese society to promote efficient food production under the limited resources and to increase the competitiveness of the Japanese agricultural products in the international market through the diversification and quality-improvement of various agricultural products

One of the tools to improve the productivity and quality is breeding, i.e. genetic improvement. In the past, selection and mating have been performed only based on trait measurement and pedigree information. Recently, however, DNA polymorphisms such as microsatellites and SNPs are used as markers for a more efficient breeding strategy. This field has entered a new era when we can observe big-size DNA polymorphism information in various species with reasonable prices and within short period of time using high-density SNP arrays and next-generation sequencers. However, most of the indexes of the productivity and quality are quantitative traits whose measurements distribute continuously. Each trait is complicated and associated with multiple loci (QTLs) as well as non-genetic factors. In addition, because of errors in SNP arrays and NGS, it is possible that the data may lead to incorrect interpretations and conclusions.

DNA polymorphism data themselves do not solve any problem. It is important to manage, control and analyze the large-size data efficiently and reflect the results in the mathematical models for the evaluation and prediction of genetic ability. Statistical genetics plays a key role in that process. StaGen Co. Ltd evaluates and predicts the genetic ability based on sophisticated statistical genetics using QTL data from various agricultural products, cattle and experimental animals. We have already contributed the analysis of Okinawa Agu pig and citrus genomes. We also provide other services such as making GUI for the software currently installed as command line operation.