Editorial

Darwinism to Breeding

Year 2009 is a commemorative year for evolutionary biology marking the 150th year since the publication of Charles Darwin's landmark book entitled "*On the Origin of Species*". The book presented observations made during his voyage to the Galapagos Islands via HMS Beagle. Among other things, Darwin described how the appearance of several organisms such as giant tortoise and finch differed depending on their habitat and the environmental conditions. His extensive observations and speculations provided compelling evidence on the idea of evolution through the process he called natural selection. This theory provides insight on how current living species including human beings evolve and diversify since their appearance on earth. The essence of evolution by natural selection is often caricatured as a monkey gradually evolving into a human being. However, we all know by now that behind the simple explanation proposed by Darwin lies a complicated biological basis that extends to the most fundamental component of life. In the late 1960s, Motoo Kimura proposed the neutral theory of molecular evolution based on nucleotide sequence analyses. He presented statistical evidence that mutation in the DNA occurs randomly and survival after mutation results from luck in adapting to the environment. Although it was initially perceived as an argument against the theory of natural selection, the compatibility of both theories later became the underlying principle of adaptive evolution.

In principle, breeding technology developed by human beings does not depend on natural selection or neutral mutation. Breeders simply identify a favorable phenotype for cultivation irrespective of a mutation in nucleotide sequence. However, a favorable or unfavorable phenotype must be a reflection of some mutation or variation in the nucleotide sequence, which has been generated either spontaneously or artificially. In case of spontaneous mutation, available

breeding resources should be the same as the resources observed by evolutionary geneticists. Success in theoretical and applied utilization of these resources depends on the abundance of genetic diversity in target species.

Rice provides a concrete example of a crop with a wide range of genetic diversity. Allelic diversity of 236 accessions Japanese domesticated rice landrace, *Oryza sativa*, has been characterized using SSR polymorphism by Ebana *et al.* (*Breeding Science* 58: 281–291). This article was awarded one of the best papers published in *Breeding Science* for 2008. Genetic association analysis of a phenotype with diversity using this core collection could identify significant information that could be used for breeding. Rice landraces are old cultivars established in isolated communities and adapted to the natural and cultural environment in which they originate, thereby possessing diverse phenotypes and genotypes.

This diversity in rice landraces is similar to the diversity of plants and animals inhabiting the Galapagos Islands. The relationships between non-biased, spontaneous variation of nucleotide sequence and corresponding phenotypes must be analyzed from a large collection of rice landraces including wild rice species such as *O. rufipogon*. More than 150 years ago, such kind of research has been greatly facilitated by the HMS Beagle. With all available genomic tools as the modern version of HMS Beagle, geneticists and breeders can achieve a lot more in characterizing diversity of cereal crops and applying this diversity in breeding important traits such as high yield or grain size.

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