

**“Biological Production and Biological Environment” field**

**Achievement : Contribution to modern crop breeding through research on development of molecular genetic analysis**

**Dr. Steven D. Tanksley** (USA)

Born: April 7, 1954 (Age 61)

Professor Emeritus, Cornell University

**Summary**

Since the beginning of agriculture, mankind has practiced selective breeding in search of crops with enhanced traits. For most of that time, the methods practiced relied on experience and intuition. From the 1980s, however, rapid advancements in genomic analysis techniques brought about significant changes. The pioneering figure who continuously led this field was Dr. Steven Tanksley.

Dr. Tanksley created chromosomal maps of crops by molecular genetic analysis and went on to identify genes that are related to agricultural productivity, such as fruit size, thereby developing a genomic analysis technique that is instrumental for selective breeding. His research, which combines genetic information and breeding techniques, has contributed enormously to increasing selection accuracy and reducing the amount of time required to breed new crop varieties.

**Selective breeding, from reliance on experience and intuition to application of molecular genetics**

It is believed that agriculture began 10 to 20 thousand years ago. Humans took their staple wild plants and began intentionally cultivating them as crops. Through a long course of trial and error, humans bred diverse varieties of “crops” by selectively cultivating those individual crops that had higher yields and were more resistant to diseases and pests. “Selective breeding,” in which superior individuals are crossbred, was also developed.

Most traditional selective breeding relied on experience, intuition and luck, but in the 19th century, a “scientific perspective” was brought into this field. Gregor Johann Mendel revealed that when two strains of pea plants were crossbred, traits (properties and characteristics of an organism) inherited by the offspring followed a certain fixed pattern. It’s famously known as “Mendel’s laws of inheritance.”

Mendel’s laws led to the adoption of a scientific approach to selective breeding. His laws, however, only applied to traits related to genes that determine “qualitative” differences amongst individuals, such as “the color of the peas being green/yellow” and “the peas being round or wrinkled,” most of which were caused by single genes.

In contrast, many of the traits we desire in crops, such as “larger size,” “greater yields” and “faster flowering,” cannot be determined in the “black and white” manner of qualitative traits. These traits are determined by a complex interaction of multiple genes on the chromosome and environmental factors. Genes of this nature are called “Quantitative Trait Loci (QTL).”

Even into the 20th century, traits determined by QTL were being selectively bred based only on experience and intuition. However, following the discovery of restriction enzymes which cut double-stranded DNA containing the genes, selective breeding entered a new era in the 1980s with rapid advancements in the molecular genetic analysis of crops.

**Creation of the tomato chromosomal map Elucidation of QTL genes responsible for fruit size**

During the 1980s, Dr. Steven Tanksley was the first to make a major breakthrough in this field. He was involved in research on plant molecular genetics and selective breeding at New Mexico State University (1981-1985) and Cornell University (1985 onwards). Using the Restriction Fragment Length Polymorphism (RFLP) method, which had been developed at the time, Dr. Tanksley undertook the challenge of creating “chromosomal maps” for the tomato and rice crops, which mark the location of important genes on DNA.

The RFLP method enables the analysis of a chromosome’s characteristics on the “individual level” by the fragment length of DNA when it is cut using a restriction enzyme. This method centered on the fact that when the base sequence is identical, the fragment length is also identical, and when the gene differed, the fragment length also differed.

First, Dr. Tanksley successfully created a chromosomal map of tomato plant by the RFLP method. He then analyzed the location of fragments where length differed across individual plants (gene mapping) and discovered six QTLs related to the fruit size of tomatoes.

When his research achievements were published in the “Nature” in 1988, a ripple of excitement ran through researchers around the world engaged in the study of selective breeding, whether for animals or plants. His research paper revealed that, by regarding QTLs related to important traits as “DNA markers,” the selection of individuals during selective breeding could now be backed by scientific evidence. In recognition of his innovative research, Dr. Tanksley was elected a member of the U.S. National Academy of Sciences in 1995.

**Application of DNA markers leads to realization of efficient selective breeding**

Throughout the 1990s to 2000s, Dr. Tanksley continues to lead the field of selective breeding and plant genetics. One of his research themes was to elucidate which genes of wild plant species mankind had taken advantage of in order to create the modern species.

For example, Dr. Tanksley points out in his paper that when comparing the wild ancestor of tomatoes, which originated in South America, with the modern species, fruit size has increased several hundred-fold. Dr. Tanksley conducted research in which he crossbred tomatoes that differed in fruit size and mapped out the major QTLs that determine tomato fruit size. As a result, he revealed that the modern species with larger fruit size had a decreased amount of transcription in certain genes, whereas the wild species of tomatoes with smaller fruit size had a large amount of transcription. He believes that such variation occurred during the process of cultivation by humans and was accelerated by intentional selection of larger fruit. Dr. Tanksley’s research also covers a wide variety of themes such as the elucidation of genes for increased resistance to diseases and pests.

Led by Dr. Tanksley’s research, selective breeding using DNA markers began to spread around the world. In Japan, where rice is the staple crop, new varieties have been developed using DNA markers that influence agriculturally important traits, such as “resistance to diseases and pests like the rice blast fungus,” “cold tolerance,” “variations of heading time (early or late)” and “taste,” some of which have turned out to be exceptionally successful breeds.

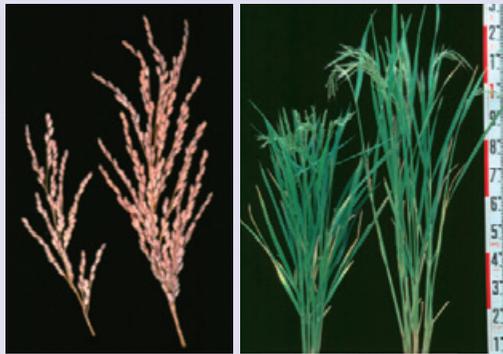
Today, one of the most important themes surrounding selective breeding is the challenge of adapting to global warming. Mankind will face serious food shortages if agriculture is unable to adapt to the rapidly changing climate. Therefore, the prompt and precise development of species adapted to the warming climate is essential. In facing this challenge, the “development and application of DNA markers for breeding” (Marker Assisted Selection), led by Dr. Tanksley, is playing a crucial role.

In this manner, Dr. Steven Tanksley’s research has brought us to a new age in breeding techniques, which are contributing towards solutions such as the realization of a stable and increased production of food, and have become one of the most important technologies for mankind in building a prosperous future.

**QTL**  
Quantitative Trait Loci

The gene cluster that influences the height, the yield, and the flowering period of a crop (right)

Qualitative Trait Loci : Mendel's principles of inheritance determines whether peas will be "green/yellow" and "round/wrinkled"



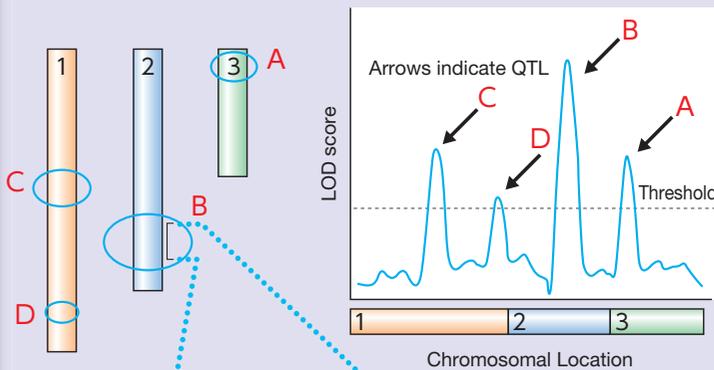
Size of ears

Size of the whole crops

QTLs are found across multiple chromosomes

The size of the circle indicates the contribution rate of each gene to a quantitative trait.

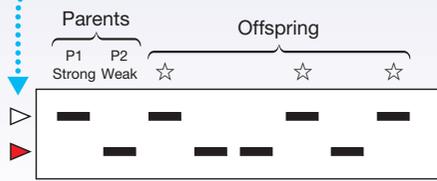
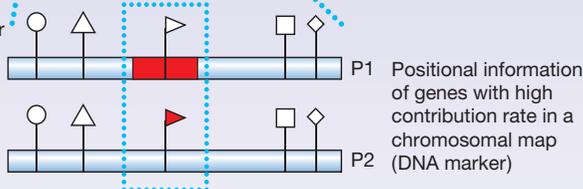
LOD score; The statistical score that estimate the positional relation of phenotype to DNA marker.



Genes with high contribution rates are selected by DNA markers

The DNA marker that's strongly influential in the improvement of crops

A DNA marker with little influence



☆ Offspring that carry strongly influential DNA marker

Selection of superior offspring by DNA markers (MAS) : Allows fast and accurate determination of which parent the offspring inherited its chromosome fragment from