

BioResource Now!

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Introduction to Resource Center <NO.42>

Research in Tomato Accelerated by Preparation and Maintenance of Resources

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The Third NBRP Has Begun

The third National BioResource Project (NBRP) on tomato research has begun. The project will use the University of Tsukuba (represented by Hiroshi Ezura) as a central resource center, Osaka Prefecture University (represented by Koh Aoki) as an allocation resource center, and Okayama University (represented by Yasutaka Kobo) and Tohoku University (represented by Yoshinori Kanayama) as backup resource centers. The University of Tsukuba and Okayama University are in charge of resources at the individual level, and Osaka Prefecture University and Tohoku University are in charge of resources at the DNA level. The aim of this term is to improve the quality of resources. Fruit component data will be newly added to the morphological mutant data that are being collected and maintained. These fruit component data contain important information on fruit characteristics; information on these characteristics is often requested by many research communities. Making this information available will improve the quality of the resources available and facilitate increased use of the resources.

Increased Use of Micro-Tom

NBRP Tomato has been preparing and maintaining gamma irradiation-induced mutant lines, mutagenesis lines, full-length cDNA clones, and bacterial artificial chromosome(BAC) clones using the Micro-Tom (a dwarf variety). NBRP has also performed BAC-end sequencing and whole-genome sequencing of Micro-Tom and has continuously published the results. Tomato research communities have developed a TILLING*1 platform to effectively use NBRP resources, supported the creation of transformants by using tomato as an experimental plant (RIKEN Plant Transformation Network), and developed tomato FOX*2-induced mutant lines. NBRP Tomato was established in 2007 and has provided resources and resource-related information to research communities worldwide. Consequently, studies using Micro-Tom, as an experimental material, have been actively performed around the world, particularly since 2009. The number of papers using Micro-Tom and those cited as having used Micro-Tom has rapidly increased since then (Thomson Reuters and Web of Science).

Case Study on the Use of Resources

Two cases have studied important characteristics of fruits using NBRP Tomato resources. The first case is related to long shelf life characteristics (Fig. 1). If the shelf life of a fruit is short, a large amount of the fruit will be abandoned without being consumed in the stages of production, distribution, and consumption. Therefore, studies aimed at developing strategies to prolong the shelf life of fruits are important. TILLING technology, which uses NBRP Tomato resources as many as possible, was developed to identify genes that control important characteristics of tomato, and a new gene mutation that controls the shelf life of fruits was detected. When this mutation is present, the fruits can be stored at room temperature for more than 2 months after harvest. This gene will likely be used in the future to control the shelf life of tomato. The second case is related to fructification of fruits (Fig.2). The tomato is cultured year-round and fructification is an important characteristic in determining its yield throughout the year.

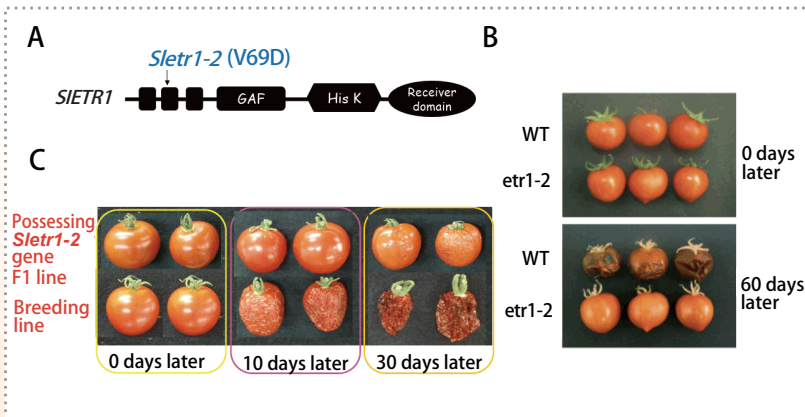


Fig. 1: Selection of a long-shelf-life mutant of Micro-Tom and performance evaluation as a breeding material

A: Primary structure of a protein synthesized from the new gene and the location of the mutation
B: Comparison of the shelf life between a mutant (*Slctr1-2*) and an original line (WT)
C: Comparison of the shelf life of an F1 fruit between a mutant (upper part) and a breeding line (lower part)

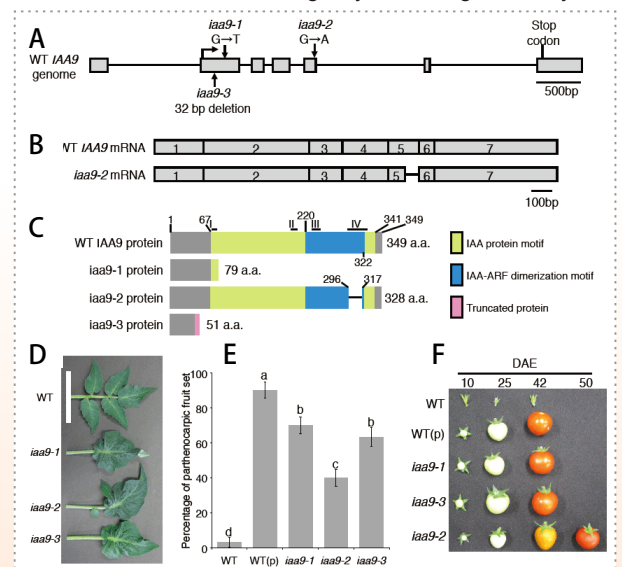


Fig. 2: Selection of Micro-Tom parthenocarpic mutants
A, B, and C: *IAA9* genetic variations of mutants (*iaa9-1*, *-2*, *-3*)
D: Morphologies of the leaves of mutants,
E and F: Fructification of mutants

The tomato fructification rate decreases in winter and summer seasons due to abnormal pollen development. This abnormal pollen development is a great cause of yield decline. Therefore, parthenocarp, which is a characteristic by which fructification can be achieved, is an important factor in preventing yield loss. As a result, parthenocarp has been extensively studied. Parthenocarpic mutants have been selected from NBRP Tomato resources, and research on these mutant genes is now being pursued. It is expected that these studies will help elucidate the molecular mechanism underlying parthenocarp^{*3} and facilitate the development of technologies that control it.

Research Acceleration Due to Genome Sequencing

This year, an international consortium published detailed whole-genome sequencing information from tomato. Use of this data will allow the whole-genome sequencing information of Micro-Tomato to be published soon. Tomato mutants have been analyzed using these 2 types of information in combination with a next-generation sequencer. The genes with important characteristics will then be successively explicated. The development of a new genome-editing technology using artificial nucleases^{*4}, which has attracted attention as a new plant breeding technology, has begun for tomato.

Research using tomato as an experimental plant will thus be accelerated.

- *1 This is an abbreviation of targeting induced local lesions in genomes, a method to detect genomes and gene substitution. By specifically cleaving a mutation site that cannot form a base pair, the location of a base, which is different from that of the wild type, can be detected.
- *2 FOX is an abbreviation of full-length cDNA over-expressing, and it is a mutation that occurs by over-expressing the target gene.
- *3 This means that an ovary wall or a receptacle is swollen to form a fruit without pollination. Fruits are generally asperous.
- *4 These are chimeric proteins, in which a domain specifically bound to DNA is joined to a DNA-cleavage domain. Zinc-finger nuclease (ZFN) and transcription activator-like effector nuclease (TALEN) are typical artificial nucleases. When 2 artificial nucleases are bound to an adjacent target sequence, a DNA-cleavage domain becomes a dimer that cleaves the DNA. The cleaved DNA is repaired by homologous recombination or non-homologous end-joining. The target gene can then be modified.

Using Google's Data Storage Service

Google provides many useful services, such as Google Drive, a data storage service similar to SkyDrive that was introduced in the 69th Ongoing Column. You can use Google Drive to manipulate files more intuitively using drag and drop.

In addition, the steps to begin using the service are very easy.

Installation

- 1) Install Google Drive from the following URL:
<https://www.google.com/intl/en/drive/start/download.html>
On clicking this link, the screen shown in Fig.1 will appear.
- 2) We will use the Windows version as an example. Clicking on the [Download Google Drive] button will take you to a page displaying the Terms of Service. Click on the [Accept and Install] button after carefully reading the terms (Fig. 2).
- 3) Next, a form will be displayed where you can enter your account information and sign in.
- 4) On signing in, the "Getting Started" dialog will be shown (Fig. 3).



Fig. 1. Download page

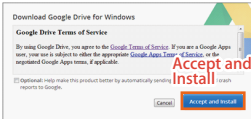


Fig. 2. Terms of Service

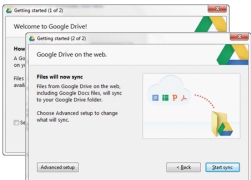


Fig. 3. Getting Started

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On the second page of the Getting Started dialog is an option to select folders for synchronization. Open the [Advanced Setup] and specify the location of the folder for synchronization. There are also other configurable options that you should consider setting as required (Fig. 4).

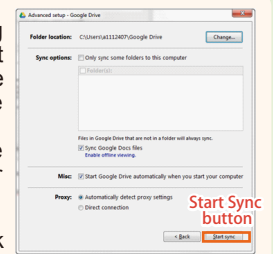


Fig. 4. Advanced Setup screen

Installation is complete once you click on the [Start Sync] button.

Logon using your Google account

After installation is completed, go to the Google website and sign in, and you will see that a new Google Drive menu has been added, allowing you to access the service online (Fig. 5).

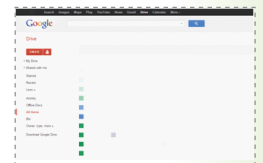


Fig. 5. Google Drive user interface

As mentioned above, you can drag and drop to upload or download files from Google Drive. I recommend that you try using this service by all means. (Atsuki Aiba)

Important Note about Google Drive

Please understand the Terms of Service that states, in short, that there is a possibility that the confidentiality of uploaded data is not guaranteed. Please be careful when dealing with highly confidential data.

Recommended Book ! <NO.10>



"Tree of Knowledge"

Written by H. Maturana and F. Valena
Translated by Keijiro Suga (Chikuma Gakugei Bunko, 1997)

This book is an attempt of "biology of recognition" by 2 Chilean biologists who proposed autopoiesis (self-creation) (from the translator's afterword). Unlike general biology, this book scarcely describes DNA and genes, but describes the cell as an autonomous system. A cell arises by its own strength, it is separated from the environment by its own dynamics, and it creates its own boundary (membrane). If a system separated by a boundary is called a unit, a cell will be a typical autopoietic unit. This idea is a kind of organismism on the basis of a cell and its activities. The idea that the cell is an autopoietic unit is in contrast to the mechanistic understanding of molecular biology which is focused on genetic information of DNA and functions of protein. For example, the phenomenon of "inheritance" is defined as conservation of some kinds of structural features through generations in a historically joined group of units. Biological evolution is understood as a natural drift. Adaption (normal interactions between living things and environments) and selection (destructive interactions between living things and environments) are acceptable, but "natural selection" is a subjective interpretation of an observer. Moreover, objects to be examined include neural systems, recognition, and linguistics.

This book is written in a friendly and simple style, and its content appears to have the profound "wisdom" told by an ancient sage. This book is recommended for persons who want to redefine their understanding of the phenomena of life. (K.N.)

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Editor's Note

Tomato was introduced in this newsletter in volume 3 (No.1). This year is a commemorative one for tomato researchers, since it is the year in which whole-genome sequencing of tomato was completed. It is worth noting that Japanese researchers greatly contributed to whole-genome sequencing of tomato. Tomato research will certainly be accelerated in the future as a result of this achievement, and the demands for tomato genetic resources will continue to increase. (Y. Y.)

BioResource Information

(NBRP) www.nbrp.jp/
(SHIGEN) www.shigen.nig.ac.jp/
(WGR) www.shigen.nig.ac.jp/wgr/
(JGR) www.shigen.nig.ac.jp/wgr/jgrUrlList.jsp

