BioResource Now !

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Entire Japanese morning glory genome decoded !

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Introduction

NBRP(National BioResource Project) -Morning Glory collection comprises more than 1,500 mutant strains of Japanese morning glory (*Ipomoea nil*). Many mutant strains were isolated in the late Edo era (1806-1860) and are caused by transposons in the transport of pyridoxine protein 1 gene (*Tpn1*) family. The first study of *I. nil* was reported in 1916. Since then, *I. nil* has been studied in Japan and other countries by taking advantage of its unique characteristics. Recently, the challenge of decoding the complete genome sequence of *I. nil* has required the most effective use of the NBRP's well-prepared resources. That challenge has been overcome with support from a Grant-in-Aid for Scientific Research on Innovative Areas "Genome Science" (representative: Project Professor Yuji Kohara of the National Institute of Genetics) (A. Hoshino *et al., Nat. Commun.* 7, 13295 (2016)).

Outline of genome sequences

Ipomoea nil has 2n = 30 chromosomes, and its genome is estimated to comprise 750 Mb. Table 1 presents an outline of the decoded genome sequence. Each contig (a set of DNA segments aligned without any space between them) is extremely long; in fact, they are among the longest found in any plant genome sequence recently published. A high-density genetic linkage map has also been created based on 3,700 single-nucleotide polymorphism markers. The sequences of 15 pseudo-molecules have been obtained by aligning genome sequences on the map. These pseudo-molecules contain 91.4% of the genome sequence and 95.7% of 42,783 putative genes. Of the 15 pseudo-molecules, 8 correspond to linkage groups 1–6 and 10 on the traditional genetic linkage map created in 1956. Therefore, pseudo-molecules are assigned numbers according to the number of their corresponding linkage group. There are only 10 linkage groups on the traditional genetic linkage map and 2 pseudo-molecules correspond to linkage group 3. Therefore, those pseudo-molecules were defined as pseudo-molecules 3 and 11.

The *Tpn1* family comprises 339 non-autonomous transposons*1, *TpnA1*, which seems to be an autonomous transposon*2, and *TpnA2*, which cannot be transposed because a part of the corresponding autonomous transposon has been lost.

A standard strain of *I. nil* and the decoding of its genome

The genome of Tokyo Kokei Standard (Photo 1), a strain of *I. nil*, has been decoded. This strain was obtained by Dr. Yo Takenaka (1903–1966) of the National Institute of Genetics, who preserved the strains of *I. nil* for the first time. Dr. Takenaka found a strain of *I. nil* with similar traits to the wild type cultivated in a downtown area of Tokyo, and established the Tokyo Kokei Standard strain, which was used in a study of genetic tumors in *I. nil* conducted in 1962, (Takenaka and Yoneda, *Japanese Journal of Genetics* Vol. 40 (1965), pp. 141–145). Because the traits of Tokyo Kokei Standard are similar to those of the wild type, and its *Tpn1* family transposons are inactive, Tokyo Kokei Standard is considered a descendant of a strain that was introduced into Japan, the transposons of which are also inactive. Although Violet is also a famous standard strain, its activated transposons might affect the sequencing of its genome. Because many researchers use Violet in their studies, it is expected that its genome sequence will be decoded.

Photo 1. Tokyo Kokei Standard, the complet genome sequence of which was decoded

Gene cloning using genome sequences

Gene cloning can be carried out using genome sequences and a traditional genetic linkage map. Linkage group 5 contains mutation *a3*, the causative gene of which has been identified. A gene called *ROTUNDIFOLIA3 (ROT3)* causes the *contracted* mutation, which has been mapped 1.2 centimorgan (cM) away from the *a3* mutation; *ROT3* codes an enzyme called CYP90C1, which is involved in the biosynthesis of brassinosteroids, (a type of plant hormone). The leaves and petals of the contracted mutant are thickened and shrunken. Following an investigation of 42 strains other than Tokyo Kokei Standard, transposons in the *Tpn1* family were inserted into the *contracted* gene of 19 strains, which were said to have *contracted* the mutation.

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	Number of sequences	N50 (Mb)	Total length (Mb)	Ratio (%)
Contig	3,865	1.87	734.6	
Scaffold	3,416	2.88	734.8	100
Scaffold on pseudo-molecule	321	3.14	671.7	91.4
Putative gene	42,783		182	24.8
Repetitive sequence			465	63.3

Table 1. Outline of genome sequences
A scaffold is a DNA sequence that consists of overlapping contigs separated by gaps of unknown sequence but known length (up to 1,000 nucleotides). N50 indicates the length of a DNA sequence obtained by sequentially adding longer DNA sequences until half the total length of the genome has been reached. The length of a DNA sequences increases as the value of N50 increases.

*1 A non-autonomous transposon does not encode a transferase, and is transposed by an enzyme encoded by an autonomous transposon.
*2 An autonomous transposon is transposed by an enzyme that it encodes itself.

A double mutant caused by the *contracted* and *star* mutations, which lacks another enzyme used to synthesize brassinosteroids (DET2), is the source of a famous strain called Uzukobito, which is very small and has an unusual shape (Photo 2).

Photograph 2. Uzukobito (strain number: Q837)
Uzukobito is a double mutant caused by the *contracted* and *star* mutations. The *contracted* gene can be cloned using genome sequences and a genetic linkage map. The size marker in the photograph is an AA battery.

Genome sequencing and bioresources

DNA clones produced from Tokyo Kokei Standard were also used to decode the whole genome of *I. nil.* A total of 93,691 expressed sequence tags (ESTs) were obtained from 61,126 complementary DNA (cDNA) clones. The sequences of 99.1% of these ESTs were mapped to the genome sequence. The bacterial artificial chromosome (BAC)-end sequences of 23,424 BAC clones were also obtained. Subsequently, the sequences of 94.9% of these clones at both terminals were mapped to the genome sequence at intervals of 100 kb on average (corresponding to the insert size). The results of the EST and BAC-end mapping verified the accuracy of the genome sequence. Moreover, some of the BAC clones were derived from the genomes of mitochondria and chloroplasts, and were used to decode these genomes. The NBRP-Morning Glory collection provided the strains and DNA clones introduced in this article.

NBRP-Morning Glory and genome sequences in the future

At present, NBRP-Morning Glory is building a genome browser in cooperation with information centers, etc. NBRP-Morning Glory will create an environment in which not only cDNA and BAC clones but also information on strains can be accessed through the sequences of alleles. We presume that in the future, the genome sequences of typical strains such as Violet, information on epigenomes, and the sequences of the alleles in each strain will rapidly accumulate. We hope that NBRP-Morning Glory will adopt these sequences and information, create an environment for resources that are relevant to *I. nil,* and form the basis of research on Japanese morning glory in the next century.

LastPass: A password management tool

Ongoing Column [No. 110] 10min.

The number of websites that require user registration for accessing them has increased. Users can access such websites by entering their user ID and password after registration; however, for security reasons, users have recently been suggested to setup much more complex passwords without using the same password used on other websites. Complicated and long passwords are difficult to memorize and users tend to use much simpler passwords. An announcement on frequently used passwords in 2015 stated that "123456" is the most commonly used password.
I can understand the feelings, but it is still scared. It is useful to have a tool that allows users to conveniently manage complicated passwords without memorizing them. There are various password management tools, and the tool called LastPass, which has been incorporated into a Microsoft Edge extension, is introduced in this document.

LastPass can be installed from Microsoft Edge's [details> Extension function> get extension from store]. Search for LastPass on the Microsoft store and install it (Fig. 1). When the installation is complete, the LastPass page will open. From now, can confirm the installation and settings of the tool by clicking on Microsoft Edge details. Here, you will need to create an account to use LastPass (Fig. 2). The password that you set when creating the account is the master password for managing other passwords.

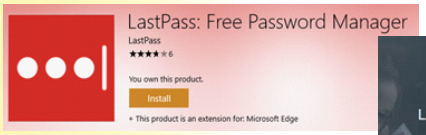

Fig. 1 LastPass

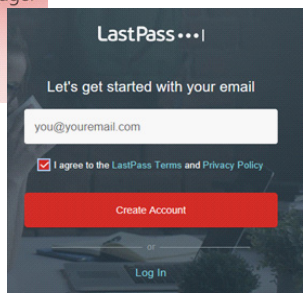

Fig. 2. Creating an account

After the account has been created, you can save your login information for various websites. Click on the "Add site" button on the top of the LastPass page (Fig. 3). Enter the URL and user name, and click on the save button (Fig. 4). If you check the "Require Password Reprompt" option, you will have to authenticate your credentials using the master password (Fig.5). Login information can also be registered to LastPass from each login screen.

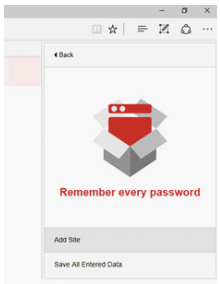

Fig. 3 LastPass management

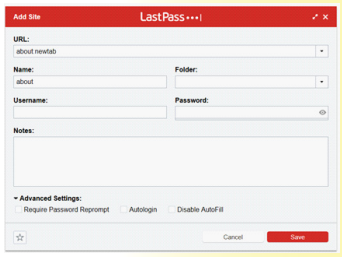

Fig. 4 Adding a website

LastPass not only functions as a means of automatic login to websites, and supplements the password input form, but it also has the capability of creating complicated passwords.
Because the saved password is managed in the cloud, the password can also be accessed from other browsers and devices. Even if you forget your master password, you can use reminders or reset the master password. By using cloud management, you can prevent the loss of the file with passwords saved or the loss caused by the theft of your personal computer.
The way of managing passwords depends on each individual's decision, and using such a tool would provide users with more options.

(Haruka Kouyama)

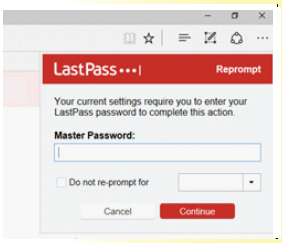

Fig. 5 Authentication using master password

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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/jgr/jgrUrlList.jsp

Editor's Note

The news that the complete genome sequence of Japanese morning glory (*Ipomoea nil*) has been decoded using the latest technologies is a memorable and pleasant event for researchers and hobbyists alike, particularly since it comes 100 years after scientific research on *I. nil* first began. Assis. Prof. Hoshino, the first author, and Lecturer Nitasaka, the representative of the resource organization, kindly contributed this explanatory article to our newsletter. There are many familiar varieties of *I. nil,* and I am excited to hear that the genes that produce these beautiful mutants will be elucidated one after another. The genome browser will be opened to the public soon; please check the homepage of the NBRP-Morning Glory website (Y. Y.).

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