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Hot News — Kazuhiro Sato (Institute of Plant Science and Resources, Okayama University)
Publication of Barley Genome Information P1 - 2

Ongoing Column No.77 — **Windows 8′ s picture password** P2

New Series: Database of This Month — **Integrated Rice Science Database "Oryzabase"** P2

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Publication of Barley Genome Information

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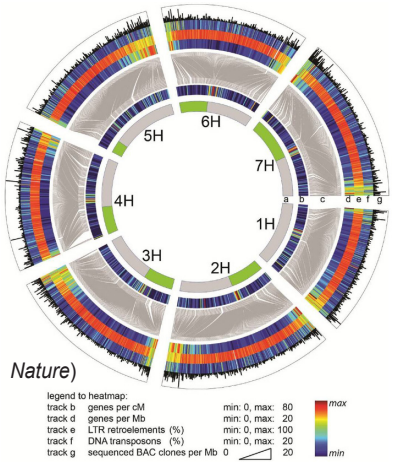
Barley is an important grain crop, and its global production ranks after wheat, rice, soybean, and corn. A paper on the barley genome sequence was published in the November 29, 2012 issue of *Nature*. The size of the barley genome (5.1 billion base pairs [bp]) is approximately 13 times that of the rice genome (400 million bp), and most of the barley genome consists of repetitive sequences, which are technically difficult to decode. Therefore, only a small part of the barley genome sequence has been deciphered. As demonstrated from the resources conserved in the National BioResource Project (NBRP), foreign and domestic barley researchers have analyzed expressed sequence tags (ESTs) and developed bacterial artificial chromosome (BAC) libraries to prepare barley genome resources similar to those of other species. In 2006, the International Barley Genome Sequencing Consortium (IBSC), comprising 6 countries, including Japan, was established. Since then, full-scale barley genome sequencing has been underway at institutes of participant countries. In Japan, Okayama University and the National Institute of Agrobiological Sciences (NIAS) are the participating institutes of the IBSC.

Between 2009 and 2011, IBSC participants Germany and the US analyzed the genome sequence of Morex, a US standard variety of barley used for beer making, by utilizing high-speed genome sequencers. This analysis took 3 years and entailed (1) arrangement of DNA clones that included the whole genome; (2) whole-genome shotgun analysis, which fragmented and analyzed the whole genome at once; and (3) location determination of genes using genetic maps.

The size of the barley genome is estimated to be approximately 5.1 billion bp, of which 4.98 billion bp (98%) was identified in the genome region of the cultivar Morex recently. A detailed analysis revealed that 84% of the determined genome sequence consisted of transposable elements and specific sequences such as simple sequence repeats, repeated in the range of several thousand times. Generally, genes are not considered to exist in repetitive regions. Therefore, genes that determine the characteristics of barley likely exist in the remaining 16% of the genome. The first crop plant genome to be sequenced was that of rice, for which the International Rice Genome Sequencing Project took 7 years. Since then, sequencing technologies have advanced greatly, leading to shorter sequencing time.

Next, Japan and Germany compared the genome sequence of Morex with the genetic information of other crops and identified 26,159 genes in barley. In the present study, Okayama University and NIAS created full-length cDNA of Haruna Nijo, *Hordeum vulgare* subsp. *vulgare* cv., and compared it with the genome sequence of Morex. Consequently, gene locations were precisely determined. This determination greatly contributed to gene identification.

Finally, the participating countries determined the genome sequences of 4 cultivated barley varieties and 1 wild barley species, compared the determined genome sequences with the genome sequence of Morex, and identified more than 15 million single nucleotide polymorphisms. These polymorphisms can be used as genomic markers for gene isolation and barley breeding with DNA markers in the future. When the locations of these 15 million polymorphisms were compared with those of 26,159 genes, 350,000 polymorphisms were found to exist in the genes. Some of these 350,000 polymorphisms were suggested to determine the differences in the morphology and characteristics of barley. In the present study, Okayama University determined the genome sequence of Haruna Nijo, a high-yielding variety of barley in Japan, and compared it with the genome sequences of Morex and other varieties to contribute to the detection of polymorphisms. The obtained results may result in the development of DNA markers useful for the improvement of barley varieties in Japan.



(IBSC 2012 *Nature*)

Number of identified base pairs
4.98 billion (98%)

Number of identified genes
26,159

Ratio of transposable elements
84%

a: Chromosome
Green: Short arm
Grey: Long arm

b: Gene density (Genetic map)

d: Gene density (Physical map)

e: LTR retroelements

f: DNA transposons

g: Sequenced BAC clones

Figure: Outline of the genome sequence of Morex (a US barley variety)

↳To the next page

Such detailed barley genome sequencing was attempted for the first time in the world. How have crops belonging to the wheat family evolved from the common ancestor of gramineous crops? This mysterious question is expected to be solved by comparing the genome sequence of barley with the genome sequences of other gramineous crops such as rice and corn.

The barley genome sequencing being performed so far is incomplete; therefore, the IBSC will continue its activities to determine the complete barley genome sequence. A high similarity is considered to exist in the base sequence of each gene among crops belonging to the wheat family, such as bread wheat, durum wheat, barley, and rye. Therefore, the results obtained in this research are expected to contribute to the elucidation of the structures and functions of genes in crops belonging to the wheat family, including barley.

Because many DNA makers necessary for gene isolation and genomic breeding can be generated based on the information of many polymorphisms, the mechanisms underlying disease resistance and high yield are attempted to be elucidated, and new wheat varieties that can be stably produced are expected to be developed using DNA makers.

References:
The International Barley Genome Sequencing Consortium. (2012) A physical, genetic and functional sequence assembly of the barley genome. *Nature* DOI:10.1038/nature11543

Windows 8's picture password

Ongoing Column [No. 77] 10min.

Windows 8, which was released in October 2012, features a new authentication system called "picture password." It combines three types of actions—"taps (clicks)," "straight lines," and "circles"—to authenticate a user login. User authentication by traditional text input via a touch panel operation is slightly cumbersome, but it can be improved using "picture password," in which the action set for authentication is to be reproduced, which increases login convenience significantly (Note 1). In this article, I will introduce how to set the picture password.

Steps to set up a picture password

1) Swipe your finger from the right edge of the screen to the left; the Charms bar appears subsequently. Tap "Setting," and then tap "Change PC settings" (Fig.1). Tap "Change PC settings" again (Fig.2).

Fig.1: Charm (Setting)

Fig.2: Charm (Change PC settings)

2) Under the "Sign-in option" of "User," tap "Create a picture password" (Fig.3).

3) Enter the current password, and tap "OK."

4) Tap "Select a picture."

5) Select a picture, and tap "Open" (Fig.4). In this article, we will use a picture of the NBRP logo, "R-kun" (Fig.5).

Fig.3: PC settings screen

Fig.5: R-kun (Information ver.)

6) Tap "Use this picture" if the displayed picture is acceptable.

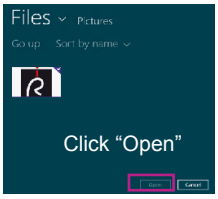


Fig.4: Picture selection screen

7) Set a gesture by combining the three actions, "A: Tap," "B: Draw a line," and "C: Draw a circle" (Fig.6). The direction and size of your gesture become part of the picture password. You might want to make use of the outline and position of the images when drawing your gesture.

8) Input the gesture again for confirmation.

9) Tap "Close."

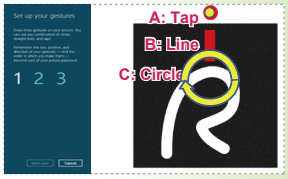


Fig.6: Example of a gesture input

Once you set a picture password, the registered picture will appear on the login page thereafter. Input the gesture you have set on the screen, and then you can login without inputting any text password. If you are in public where it is possible for someone to view your gesture, or if you forget your gesture, you can login via traditional text input as well.

The picture password system divides the picture into grids and evaluates the operations by position, direction, and type at every coordinate. A slight difference between the operation and the registered one is acceptable as long as the calculated score is 90% or higher (Note 2). Choosing a slightly complicated picture is recommended so that the action cannot be guessed easily (e.g., a landscape or a group picture with multiple objects).

It is possible to obtain flexible security measures by using both a picture password and a traditional text password. It is advisable to use this system if you intend to upgrade to Windows 8.

(Kyohei Matsuno)

Note 1 You can use not only the touch panel but also the mouse to set and authenticate the picture password.
Note 2 Please refer to the below site for more information.
Blog by Windows engineering team
http://blogs.msdn.com/b/b8_ja/archive/2011/12/22/signing-picture-password.aspx

Database of This Month

Integrated Rice Science Database "Oryzabase"

- Number of strains: 17,497
- Number of genes: 5,670
- Number of papers: 6,382

(As of January, 2013)

DB name: Oryzabase
URL : http://www.shigen.nig.ac.jp/rice/oryzabaseV4/
Language: Japanese, English
Original contents:
Rice resources for research (wild strains, mutants other strains)
Reports of the study tours, list of stages in each organ, Dictionary of genes, registration site of gene symbols,
Literature information on rice
MAP tool, ID checker, Sequence cutter, etc.
Other contents:
Genome information, linkage maps, tools including BLAST
Features: Resources can be ordered. Complete image information.
Provision of wild rice locality: Google maps
Cooperative DB: Gramene, RAP
DB construction group: NBRP-Rice, NBRP Information
Management organization:
Center for Genetic Resource Information, NIG
Year of DB publication: 1996 Year of last DB updated: 2013

Comment from a practicing developer: Last year, we finally completed a large-scale update. During its 17-year history, this database had become complicated, and it was difficult to keep the resources ordering system and registration site of gene symbols operational while development work was undertaken. The update took 4 years from planning to completion. Regarding literature search and the ID checker, since the search functions were greatly expanded compared to the previous version, we recommend that they be tried out. Please do not hesitate to express your comments, questions,

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Editor's Note

Topics on the barley genome that have been analyzed by an international consortium were explained by Professor Sato of Okayama University, a member of the consortium. The difficulty in analyzing the gigantic genome of barley was overcome; therefore, research on crops belonging to the wheat family seems to be rapidly advancing. From this year onwards, this newsletter will provide "Database of This Month" instead of "Recommended Book." We will wait for your requests (Y. Y.).

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