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Japanese Cedar as a Forest Genetic Resource in Japan — P1–2

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Japanese Cedar as a Forest Genetic Resource in Japan

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Outline of the history and current situation

Japanese cedar (*Cryptomeria japonica*) is a conifer peculiar to Japan. It is a tree species adaptable to a wide range of climates from that of Yakushima Island in the south to that of Aomori in the north. Japanese cedar has been used in timber production as can be seen from its afforestation records in the Kamakura period (1185–1333). Presently, Japanese cedar continues to remain invaluable and ranks first in timber production in Japan .

According to Japanese history, timber consumption rapidly increased following war, reconstruction, and prosperity in the Sengoku (Warring States) period (1467–1567), the Edo period (1603–1868), and the Meiji period (1868–1912). This rapid increase in timber consumption often resulted in large-scale deforestation and environmental degradation. In the aftermath of World War II, there was largescale deforestation in Japan due to the post-war reconstruction. As a countermeasure, a large number of Japanese cedar trees were planted under the "expansive afforestation policy."

During this period, there was vigorous forest tree-breeding activity carried out, with excellent individuals selected from either natural or artificial forests and an experimental station (test forest) established to evaluate the qualities of the individuals selected. In the test forest, evaluation took more than 40 years. In recent times, these excellent individuals have finally been crossbred to create the next generation of trees.

Evaluation of Japanese cedar elite trees as genetic resources

Excellent individuals selected in the forest tree breeding are first-generation elite trees. Until now, approximately 3,700 lines have been collected and preserved (Fig.1). The characteristics of these first-generation elite trees, such as tree height, trunk thickness, wood quality, and male flower mating patterns, were evaluated.

Japanese cedar forests were lost due to historical reasons but re-created by the expansive afforestation policy. At present, only a small number of natural cedar forests remain. These first-generation elite trees exhibit not only the characteristics of the breeder population but also of a population of genetic resources that reflect the genetic composition of Japanese cedar before the afforestation policy was enforced.

Considering these first-generation elite trees as a population of genetic resources we evaluated tree breeding based on the following three points (Ref.1): (1) the distance between two selected elite trees, (2) the ratio of the distributional areas under various environmental conditions, and (3) a diversity assessment made using simple sequence repeat markers. Consequently, a first-generation elite tree was selected every 20 km in the forest tree-breeding site. The distributional areas in the forest tree-breeding site accounted for approximately 80% of the entire distributional area in Japan and the genetic diversity in the tree-breeding site was similar to that of the existing natural forests.

Accumulation of molecular data and its use

Timber production is possible mainly from plants belonging to the division Coniferophyta. Plants belonging to the family Pinaceae are often used as research subjects for breeding and in thremmatology worldwide. The genome sizes of the plants in the division Coniferophyta are generally large, so their genome sequencing is apparently difficult. However, the genome sequence of Norway spruce (*Picea abies*) was determined in 2013 and that of loblolly pine (*Pinus taeda*) was determined in 2014. With these data of genomics and genome information, plants in the division Coniferophyta are now being used for tree breeding.

To perform molecular breeding, we collected the expressed sequence tags (ESTs) and the single nucleotide polymorphisms (SNPs) from various organs of the Japanese cedar (shoot, xylem, male flower, and root) using a next-generation sequencer (unpublished). We examined the collected information about ESTs, including organ specificity, and found that the ESTs of a Japanese cedar converged to 34,731 isotigs. We also collected approximately 500,000 SNPs and developed around 50,000 SNP markers (equivalent to approximately 10% of the SNPs). These markers were used for linkage analysis. As a result, the basis was established for performing molecular breeding. The collected genetic data were subjected to microarray analysis (Fig.2) and the analytical results were published in the form of gene expression profiles regarding xylem formation and photoperiodic response (Ref. 2, 3). We believe that organ- specific genetic information and gene expression profiles can be used in not only molecular breeding but also as fundamental data in elucidating biological processes that are developed to cope with environmental changes such as climate change due to global warming and the environmental responsiveness of an organism at its habitat. In future, we expect organ-specific genetic information and gene expression profiles to be used for evolutional research on plants in the family Pinaceae in which genomic analysis has seen major advancements (Fig. 3).

Future directions in Japanese cedar collection

The sufficient data generated from this study on first-generation Japanese cedar elite trees as a genetic resource can be used by the international community to propel further research on conifers.
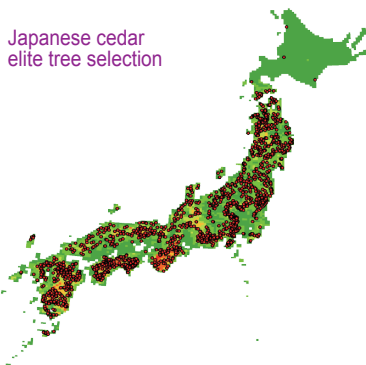

Japanese cedar elite tree selection

Fig. 1. Areas from where the first-generation Japanese cedar elite trees were selected
Fig. 1 depicts the areas from where the first generation of Japanese cedar elite trees were selected in the tree-breeding project launched during the second half of the 1950s. As can be seen from the figure, elite trees were selected from all over Japan. A total of 3,669 lines have been selected until now.
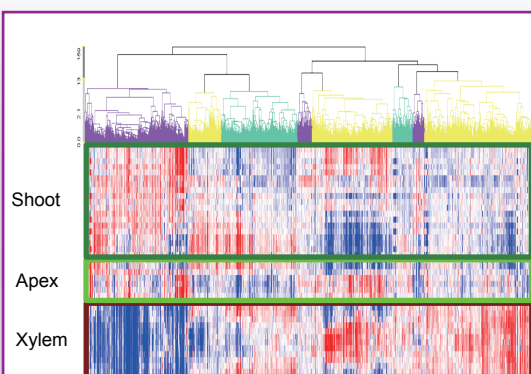

Shoot

Apex

Xylem

Fig. 2. Analytical results obtained using a microarray equipped with 19,304 probes
We find from Figure 2 that the gene expression intensity is higher at the areas marked in red and lower in the areas marked blue. Although continuity was observed in the morphologies of the organs, different genes were expressed in different organs at the same time.
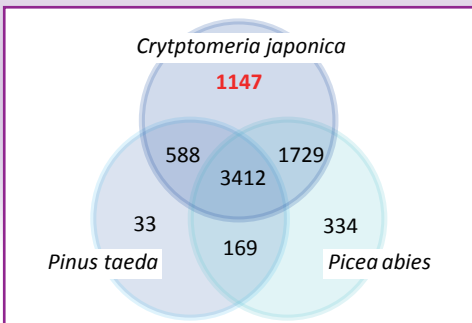
Cryptomeria japonica

1147

588   1729

3412

33   334

169

Pinus taeda   *Picea abies*

Fig. 3. Comparison of the gene group of Japanese cedar (conifer II) with that of plants in the family Pinaceae (conifer I)
Fig. 3 shows the results obtained by comparing gene groups using the Markov cluster algorithm. As shown in the figure, the specificity of genetic data obtained from Japanese cedar is high and therefore it can be used as fundamental information for further research on conifers.

The growth period of breeding plants belonging to the division Coniferophyta is generally 10 years; flower setting is sometimes rich and sometimes not. Flower setting is generally a difficult procedure to perform artificially. Clonal expansion using plant cutting is also difficult in many cases. In contrast, flower setting is easy to perform for even a three-year-old Japanese cedar using gibberellin treatment; clonal expansion using plant cutting is also easily carried out on these plants. Therefore, Japanese cedar possesses various advantages by which it can be considered a model plant for conifers. All possible efforts must be made to give worldwide recognition to this plant collection while comparing it with other species.

References

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Introducing PubMed Commons

Have you ever noticed the link to the "PubMed Commons" feature at the top of the PubMed homepage[1](Fig. 1, highlighted by the red rectangle)? Did you know that comments may be posted on articles registered with PubMed (Fig. 2, highlighted by the red rectangle)? These comments are the core feature of PubMed Commons. In this article, I would like to introduce PubMed Commons and its functionality.
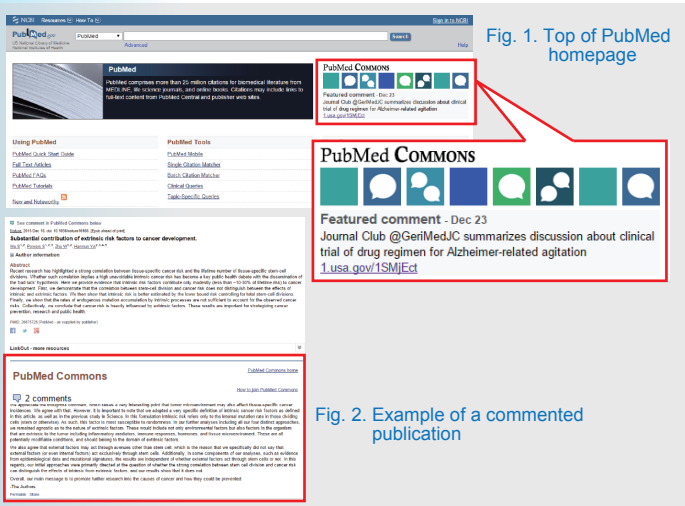

Fig. 1. Top of PubMed homepage

Fig. 2. Example of a commented publication

PubMed Commons is a system that enables authors who have publications registered with PubMed to share their opinions and other information. A pilot version of this new feature was released in October 2013 to members registered with PubMed, and comments were made available for viewing by the public starting December 2013.

Posted comments can be viewed by anyone. Users can search for publications that have been commented on by simply entering the keyword "has_user_comments [filter]" in the search box (Fig. 3). The number of comments posted on each article is displayed with the search result (red rectangle in Fig. 3). By specifying the search term "Chimenko I [author] AND has_user_comments[filter]" you can search for specific publications by an author whose work has been commented on[2].

Fig. 3. Result of searching for commented articles displaying the number of comments per article

Not everyone is eligible to post comments—the function is only authrized for use by authors who have publications registered with PubMed. You can post comments on Pub Med Commons by inviting yourself, which you can do by searching for your email address in the list of email addresses maintained in the NIH database, or by obtaining an invitation from a member already registered with PubMed Commons. You can check whether you can register yourself by visiting the webpage shown in Fig. 4.
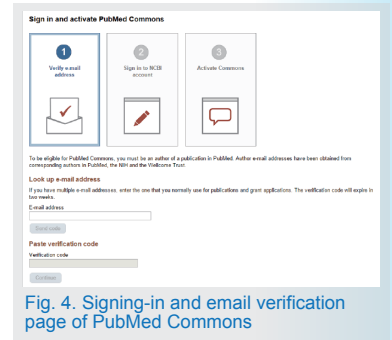

Fig. 4. Signing-in and email verification page of PubMed Commons

According to a PubMed Commons blog post published in December 2015[3], there have been more than 4,000 comments posted on 3,300 publications. Although the same blog post mentions that the number of comments may have reached a plateau, users continue to post valuable comments. Approximately half of the commented articles relate to clinical and healthcare.

Approximately 20% of authors have posted comments on their own articles, and about a third of these are in response to comments or questions submitted by others. The start of a service whereby an email notification is sent to an author whose articles have attracted comments has enabled the PubMed Commons administration to achieve an increase in the percentage of author comments. However, the response rate remains lower than 10%, prompting them to continue their endeavour to promote author responses.

PubMed will celebrate its 20th anniversary since its inauguration in January 1996. It has grown to become a giant publication search database with more than 2.7 billion searches performed during the past year alone. In comparison to this number, the speed at which the PubMed Commons service is being taken up can be said to be rather slow. However, the number of visitors to the PubMed Commons website has increased from 1.2 million in the first half of 2014 to 2.3 million during the same time span in 2015, which indicates a heightened interest in posted comments.

Why not try using PubMed Commons to help search for articles of interest, to collect additional information, provide online feedback, and engage in discussions?

(Gaku Kimura)

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Editor's Note

For the past 10 years, this newsletter has provided information on the genetic resources of various species. This is the first time we are publishing an article on forest resources. Although forest resources have had a long history in Japan and have been a familiar topic of research, they were accepted by the Genetic Resources Committee only in the year 2015. As the time required for the growth of trees differs greatly from that of other species and since the use of trees was limited earlier, there were very few opportunities to examine trees along with other species. Presently, however, since trees are not only used as construction materials but also have drawn international attention as resources to study environmental response and biomass energy, there has been a rapid increase in the accumulation of genome information and molecular data on forest resources. As Associate Professor Watanabe writes in his article, a Japanese cedar is a conifer peculiar to Japan. I hope that by understanding its advantages, it will be adopted as a model organism (Y. Y.).