The National BioResource Project (NBRP) *Lotus* and *Glycine* in Japan

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The objective of the National BioResource Project (NBRP) in Japan is to collect, conserve and distribute biological materials for life sciences research. The project consists of twenty-eight bioresources, including animal, plant, microorganism and DNA resources. NBRP *Lotus* and *Glycine* aims to support the development of legume research through the collection, conservation, and distribution of these bioresources. *Lotus japonicus* is a perennial legume that grows naturally throughout Japan and is widely used as a model plant for legumes because of such advantages as its small genome size and short life cycle. Soybean (*Glycine max*) has been cultivated as an important crop since ancient times, and numerous research programs have generated a large amount of basic research information and valuable bioresources for this crop. We have also developed a “LegumeBase” a specialized database for the genera *Lotus* and *Glycine*, and are maintaining this database as a part of the NBRP. In this paper we will provide an overview of the resources available from the NBRP *Lotus* and *Glycine* database site, called “LegumeBase”.

Key Words: NBRP, *Lotus japonicus*, *Glycine max*, *Glycine soja*, LegumeBase, bioresource.

Introduction

Leguminosae is an enormous plant family consisting of 20,000 species divided into 700 genera with high diversity in morphology (Doyle and Luckow 2003). This family includes important plant species used for grain, feed and oil due to their rich seed composition, plants of medicinal value, and those that can be used as fertilizers. Some examples include soybean (*Glycine max*), alfalfa (*Medicago sativa*), peanut (*Arachis hypogaea*), kudzu (*Pueraria lobata*) and sesbania (*Sesbania aculeata*). *Lotus japonicus* has been promoted as a model legume in the past two decades due to its short life cycle (2–3 months), self-fertility, diploidy (n = 6), small genome size (472.1 Mb), small plant size, ease of hand pollination, and amenability to *Agrobacterium*-mediated transformation (Handberg and Stougaard 1992). Moreover, the first whole genome sequencing of a legume was reported using *L. japonicus* Miyakojima MG-20 (Sato et al. 2008). Soybean (*Glycine max*) is the most important grain legume crop worldwide for its useful seed components such as protein, oil and secondary metabolites and consequently, has been utilized for a large number of basic and applied research investigations. Recently, a soybean whole-genome shotgun sequence of *G. max* var. Williams 82 was published (Schmutz et al. 2010). Another genome sequence project for Japanese soybean (*G. max* var. Enrei) has been conducted in Japan since 2007. Due to the significant numbers of investigations on these two species, we expect research on *Lotus* and *Glycine* to continue being at the forefront of plant science research in the future.

Currently, large numbers of important bioresources such as experimental strains, mutants, DNA libraries, etc., have been developed through numerous independent research programs and scientific research projects. These bioresources will continue to serve as valuable materials for basic and applied studies. The National BioResource Project (NBRP) was launched by the Japanese government in 2002 with the objective of collecting, conserving and distributing such valuable, independent resources and making them easily available to the larger research community. At present, the NBRP is a consortium of twenty-eight core facilities of animal, plant, microorganisms and DNA resources, and an information center (Yamazaki et al. 2010). The NBRP plant consists of nine resources: *Arabidopsis* (*Arabidopsis thaliana*), rice (*Oryza sativa*), Lotus/Glycine, wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), tomato (*Solanum lycopersicum*), *Chrysanthemum*, morning glory (*Ipomoea nil*) and algae (Kurata et al. 2010). As part of this...
project, the _L. japonicus_ and _G. max_ program has been developed since the end of 2003. In this paper, we provide an overview of the extensive resources available for _L. japonicus_ and _G. max_ from our resource center.

**Lotus resource**

**Experimental strains**

Gifu B-129 is the first established experimental _L. japonicus_ strain, collected by Hirayoshi in Gifu Prefecture Japan, named Gifu B-129 by Grant and self-pollinated 9 times by Stougaard (Handberg and Stougaard 1992, Stougaard and Beuselinck 1996). Secondly, Kawaguchi (2000) established the accession Miyakojima MG-20 by self-pollinating _L. japonicus_ strains from Miyakojima Island, Okinawa Prefecture, Japan. This accession is characterized by a short generation time and easily flowers under fluorescent lights. Another strain, _Lotus burttii_ B-303, was established as the third _Lotus_ experimental strain, collected in Pakistan and named by Burtt (Sz.-Borsos et al. 1972) and self-pollinated 9 times by Kawaguchi et al. (2005). There is a great demand for these experimental strains that have played central roles in studying legume-specific characteristics such as noduleation, and large numbers of mutants have been isolated in the past two decades (Charpentier and Oldroyd 2010, Kawaguchi et al. 2002, Novák 2010, Popp and Ott 2011, Szczygłowski et al. 1998). All of these experimental strains are available from LegumeBase (Table 1).

**Wild accessions**

_L. japonicus_ ecotype is distributed across East and Central Asia, including Japan, Korea, and China, extending to West Asia into Afghanistan (Pajuelo and Stougaard 2005). Since _Lotus_ adapts readily to diverse environmental conditions, such as temperature or soil type, it is thought to possess a broad range of genetic variations. The strains that we

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**Table 1. _L. japonicus_ and _G. max/soja_ resources preserved in LegumeBase**

| Name of resource                            | No. of stocked resources | Depositor                      | Reference                  |
|---------------------------------------------|--------------------------|--------------------------------|----------------------------|
| **Lotus resource**                          |                          |                                |                            |
| Wild accessions                             | 180                      | _Lotus_ research community, NBRP| Sugino et al. 1988         |
| Core collectiona                            | 20                       | NBRP                           | Kawaguchi et al. 2001      |
| Experimental strains (Gifu B-129, Miyakojima MG-20, _L. burttii_ B-303) | 3                       | M. Kawaguchi, W. Grant         | Stougaard and Beuselinck 1996 |
| RILs (Gifu B-129 × Miyakojima MG-20)        | 205                      | Kazusa DNA research institute  | Hayashi et al. 2001        |
| EMS mutants                                 | 171                      | RIKEN                          |                            |
| Superroot                                    | 1                        | University of Miyazaki         | Akashi et al. 1998         |
| _M2_ bulked seeds                           | 162³                     | NBRP                           |                            |
| Activation tag linesa                       | 960                      | Nihon University               | Imaizumi et al. 2005       |
| _M. loti_ STM mutants                       | 6,671                    | Kazusa DNA research institute  | Shimoda et al. 2008        |
| TAC clones                                   | 72,192                   | Kazusa DNA research institute  | Sato et al. 2001           |
| BAC clones                                   | 14,976                   | Kazusa DNA research institute  | Sato et al. 2007, 2008     |
| cDNA clones                                 | 140,544                  | Kazusa DNA research institute  | Asamizu et al. 2004        |
| Binary vectors                               | 6                        | M. Hayashi                     | Maekawa et al. 2008        |
| Full-length cDNA clones                     | 104,064                  | Kazusa DNA research institute  |                            |
| **Glycine resource**                        |                          |                                |                            |
| Wild accessions                             | 1,159                    | Hokkaido University            | Hong et al. 2003           |
| Cultivars                                    | 205                      | Hokkaido University            | Xu et al. 2002             |
| RILs (Misuzudaizu × Moshidou Gong 503)       | 167                      | Chiba University               | Abe et al. 2003            |
| RILs (TK780 × B01176)                       | 96                       | Hokkaido University            | Tajuddin et al. 2003       |
| Edamame (cultivars)                         | 8                        | Yamagata University            | Watanabe et al. 2004       |
| Fatty acid mutants                          | 21                       | Saga University                | Liu et al. 2007            |
| _M1_ bulked seeds¹                          | 1³                       | Saga University                | Akazawa and Egashira 2005  |
| Full-length cDNA clones                     | 37,890                   | _Glycine_ full-length cDNA consortium, RIKEN | Umezawa et al. 2008 |

a This resource is in preparation.

b Number of batches. We provide seed sets containing of 10–20 batches. Each set consists of 5,000–9,000 _M2_ seeds derived from 1,000–2,000 _M1_ plants.

c Number of batches. One batch containing 250 g; approximately 1,000 grains. The _M2_ seed set was derived from approximately 5,000 _M1_ plants.
currently maintain and distribute at LegumeBase were collected across several climatic zones from as far north as Rebun Island, Hokkaido (45°17′46″ N) to Miyakojima Island, Okinawa (24°43′57″ N) to the south. These strains were collected mainly for three purposes: first, to evaluate the potential of *L. japonicus* as a pasture plant by Shimada in 1979 and for the Gene Bank Project of the Ministry of Agriculture, Forestry and Fisheries of Japan in 1981 (Suginobu et al. 1988); second, to assess the suitability of this plant species to serve as a model organism for leguminous plants by Kawaguchi and Aoki since 1996 (Kawaguchi et al. 2001); and third, to collect *L. japonicus* bioresources for NBRP. At present, 180 accessions are stocked and 108 accessions are available via LegumeBase.

After the launch of NBRP, we studied variations in nine morphological characteristics of *L. japonicus* wild accessions (Hashiguchi et al. 2011). Recently, Kai et al. (2010) selected 20 accessions to serve as a representative core collection based on SSR (Simple Sequence Repeats) polymorphisms (Table 1). The range of morphological traits in the core collection was representative of that found in the entire collection. This core collection will be useful for genomewide studies and data obtained for this model species should lead to numerous practical applications for crop legumes.

### Recombinant inbred lines (RIL)

A total of 205 “LjMG RI Lines” (Table 1) were derived from an *F*2 seed cross between Miyakojima MG-20 and Gifu B-129, and were established at the Kazusa DNA Research Institute by eight times self-pollination. A total of 96 SSR markers were mapped on the chromosomes of *L. japonicus* using the *F*2 generation (Hayashi et al. 2001), and AFLP and SSR marker-based high-density linkage maps of *L. japonicus* were constructed (Wang et al. 2008). Gondo et al. (2007) reported the first quantitative trait locus (QTL) analysis of 13 phenotypic traits in two consecutive years in *L. japonicus*, and the data evaluated in this study are available at LegumeBase. In addition, macrosynteny between soybean and *L. japonicus* was analyzed with the objective of applying genomic information of the model legume *L. japonicus* to soybean (Tsubokura et al. 2008).

### EMS mutants and M2 bulked seeds

Ethyl methanesulfonate (EMS)-treated mutants of *L. japonicus* were isolated from Miyakojima MG-20 at the RIKEN Plant Science Research Center. There are two kinds of mutants: above-ground mutants (plantlet, leaf, stem, flower etc.) and root morphological mutants (root elongation, root thickness, root hair length and the number of root hairs etc.). At present, 98 homozygous mutants are available, as well as 78 heterozygous mutants. In addition, we have prepared 10 sets of EMS-treated bulked seeds of *L. japonicus* Miyakojima MG-20 (Table 1). Each set consists of 5,000–9,000 M2 seeds derived from 1,000–2,000 M1 plants treated with a 0.4% EMS solution for 8 to 10 hours. Users may screen the mutants themselves and use the screened mutants for their research. Once their study is published, users are required to deposit the isolated mutant lines derived from this resource with our resource center.

### Activation tag lines

Activation tagging is a method to produce gain-of-function mutants by random insertion of tandemly repeated CaMV 35S enhancer sequences into the plant genome. This method allows the analysis of functionally redundant gene families and essential genes, whose knockout mutants cannot be obtained. Although this powerful approach has been used in *Arabidopsis thaliana* (Weigel et al. 2000), its application to leguminous plants was not popular because of the difficulty in genetic transformation of legumes. Imaizumi et al. (2005) improved the transformation technique for *L. japonicus* and produced more than 3,500 T-DNA insertional lines, demonstrating the possibility of activation tagging with *L. japonicus*. Activation-tagged populations of this model legume should provide a powerful tool for identifying novel genes involved in morphology, accumulation of seed storage proteins, biosynthesis of legume-specific natural products, symbiotic nitrogen fixation, and mycorrhizal formation. These activation tagged lines will also serve as suitable materials for post-genomic analyses, such as transcriptomics, proteomics and metabolomics, and will be available via LegumeBase in the future (Table 1).

### Root culture (superroot)

We discovered super-growing roots (superroot: SR) from *Lotus corniculatus* L. that grow efficiently after removal of the above-ground organs and when cultured in a medium containing no plant hormones (Akashi et al. 1998) (Table 1). SRs are highly competent for plant regeneration. Moreover, protoplasts can be easily obtained from SRs that proliferate well in vitro. These characteristics are still maintained 14 years after the discovery of SR (Akashi et al. 1998, 2003). SRs can be used in physiological research as well as in functional analysis of genes using *A. tumefaciens* (Tanaka et al. 2008) or *A. rhizogenes*-mediated transformation (Jian et al. 2009). Himuro et al. (2011) developed 130 *Arabidopsis* full-length cDNA overexpressor (FOX)-superroot lines using the FOX hunting system. FOX-superroot lines provide a new tool for genetic analysis and control of root growth in leguminous plants.

### cDNA, TAC and BAC clones

Sato et al. (2008) sequenced the entire genome of *L. japonicus* genome using the Miyakojima MG-20 strain. Various material resources such as transformation-competent artificial chromosome (TAC) (Asamizu et al. 2003, Kaneko et al. 2003, Kato et al. 2003, Nakamura et al. 2002, Sato et al. 2001), bacterial artificial chromosome (BAC) (Sato et al. 2007, 2008) and cDNA libraries (Asamizu et al. 2000, 2004) were developed during the genome sequencing projects. These important products of *L. japonicus* genome sequence projects are exceedingly...
valuable tools for genetic and physiological studies and/or synteny analysis of leguminous plants. These resources have been deposited with our resource center and are available from LegumeBase for researchers (Table 1).

Full-length cDNA
Full-length cDNAs are useful resources for the functional analysis of genes or proteins and are available for several plants, such as Arabidopsis (Seki et al. 1998), rice (Kikuchi et al. 2003), wheat (Ogliara et al. 2004), soybean (Umezawa et al. 2008), maize (Zea mays; Soderlund et al. 2009), tomato (Aoki et al. 2010) and barley (Matsumoto et al. 2011). L. japonicus full-length cDNAs were deposited at the Kazusa DNA Research Institute and have been deposited with LegumeBase (Table 1). There are approximately 100,000 L. japonicus cDNA clones from a full-length enriched cDNA library, including 3,874 full read sequences that were derived from plants and roots, as well as from in vitro cultured cells of L. japonicus that were cultured under diverse chemical treatment conditions (Sakurai et al. unpublished).

Binary vectors
Promoter analysis studies have demonstrated that the polyubiquitin promoter from L. japonicus plants (Ljubq1) possesses higher activity than the CaMV35S promoter in L. japonicus leaves, stems, roots, nodules, and pollen (Maekawa et al. 2008). The GATEWAY conversion technology-compatible binary vectors that were constructed in this study for overexpression and RNAi under the control of the Ljubq1 promoter provide alternative choices for studies in L. japonicus. For one of these vectors, Nakagawa et al. (2011) investigated expression profiles for the Nod factor (NFs) receptor gene in roots of L. japonicus through a complementation test using Agrobacterium rhizogenes-mediated transgenic L. japonicus with pUB-GW-GFP. In LegumeBase, six kinds of vectors are now available for research (Table 1).

Mesorhizobium loti STM mutants
The mutant library of M. loti was developed by the Kazusa DNA Research Institute through transposon mutagenesis. These transposon insertion mutants were generated using the signature-tagged mutagenesis (STM) technique (Shimoda et al. 2008). At present, 6,671 STM M. loti mutants are available from LegumeBase (Table 1). Detailed information about M. loti ORFs, such as the operon structure, predicted protein domains and orthologous protein groups, is available at RhizoBase (http://bacteria.kazusa.or.jp/rhizobase/Mesorhizobium/index.html), a database constructed by the Kazusa DNA Research Institute. The M. loti mutant STM5 that contains an inserted transposon at 738 bp of the 1,602-bp PHGDH (3-phosphoglycerate dehydrogenase) gene plays an important role in the development of an effective symbiosis between M. loti and L. japonicus (Thapanapongworakul et al. 2010).

Glycine Resource
Wild accessions
Wild soybean (Glycine soja) is the ancestor of the cultivated soybean (G. max) and is distributed widely in East Asia, growing in riverbanks, open areas and the peripheries of agricultural fields, and is a prostrate or a twining tall herb. Molecular assays have revealed that the wild soybean possesses rich genetic variability compared to cultivated soybean (see Xu et al. 2002, Hyten et al. 2006). In fact, the wild soybean germplasm often has provided unique variants not observed in the cultivated germplasm in seed chemical compositions, such as a storage protein variant lacking all sub-units of the 7S-globulin and a variant lacking soyasapogenol A (Hajika et al. 1998, Tsukamoto et al. 1993). The wild soybean collection in LegumeBase consists of samples collected by Hokkaido University and their collaborators from various regions of Japan (Table 1) and has been used in genetic studies of seed compositions (Fukuda et al. 2005, Kanamaru et al. 2008, Shibata et al. 2008), stress tolerance studies (Hamwich and Xu 2008) and evolutionary studies (Abe et al. 1999, Hong et al. 2003, Tozuka et al. 1998, Xu et al. 2002).

Cultivars
Cultivated soybean, G. max, is the most important leguminous crop in the world due to the high quality of protein, lipid and functional components in its seeds. Nuclear SSR marker analyses have revealed that the Asian cultivated soybean population mainly consists of two sub-populations, the Chinese and Japanese populations, suggesting that genetic resources from different sub-populations could widen the genetic variability of cultivated soybeans (Abe et al. 2003). Around 200 accessions of G. max introduced from China and Korea are available from LegumeBase (Table 1), and have been evaluated for seed coat color, and fatty acid and seed isoflavone compositions.

Recombinant inbred lines
Two sets of soybean recombinant inbred lines (RILs) are available from LegumeBase (Table 1). The first set was developed by the single seed descent method (SSD) from an F₂ population of a cross between Misuzudaizu and Moshidou Gong 503 at Chiba University (Tajuddin et al. 2003, Yamanaka et al. 2000). Misuzudaizu (Norin 51) was released in 1968 from the Nagano Prefectural Agricultural Experimental Station and has a determinate habit, tawny pubescence, white flowers and large and yellow seeds. Moshidou Gong 503 was developed as a forage crop at the Jilin Agricultural Experimental Station, China, and has a semi-determinate habit, tawny pubescence, purple flowers, and small brownish compressed seeds. A total of 1,131 markers were mapped in the RIL population (Hisano et al. 2007, Xie et al. 2007) that have been used for QTL analyses for agronomical traits (Watanabe et al. 2004, Yamanaka et al. 2001, 2005) and for gene isolation (Watanabe et al. 2009,
2011). Presently, 165 lines are available via LegumeBase.

Another set of RILs, RIL MsXs, was developed by SSD from an F2 population of a cross between TK780 (G. max parent) and B01167 (Hidaka 4) (G. soja parent) at Hokkaido University. The G. max parent has a determinate habit, tawny pubescence, and large and yellow seeds. The G. soja parent is an inbred pureline selection from a wild population near the Saru River in Hokkaido and has an indeterminate and twining habit, tawny pubescence, and small and black compressed seeds. A total of 282 markers were mapped for 98 RILs, and QTL analyses for agronomic traits have been carried out (Liu et al. 2007). This RIL population has also been used for mapping genes isolated through the use of the high level of genetic polymorphism between the max and soja parents (Kong et al. 2010, Liu et al. 2008, 2010, Matsuura et al. 2009).

**Fatty acid mutants**

A total of 21 mutants for fatty acid compositions of seed oil are available from LegumeBase (Table 1). These mutants were developed by X-ray mutagenesis from a cultivar “Bay” at Saga University. The mutants include low-α-linolenic acid mutants (Anai et al. 2005, Takagi et al. 2000) and high-oleic acid mutants (Anai et al. 2008). All of the lines were confirmed to be homozygous for their respective genes by progeny tests. A mutant line for high oleic acid content, M23, possesses a dysfunctional allele of GmFAD2-1A that results in a higher level of oleic acid and a reduced level of linolenic acid (Anai et al. 2008). M23 has been used to develop a high-oleic acid line (with a seed oleic acid content greater than 80%) in combination with a dysfunctional allele GmFAD2-1B in another copy of the FAD2 gene, through the use of genetic resources (Pham et al. 2010, 2011) and a reverse genetic approach using mutagenesis (Hoshino et al. 2010). These mutant lines that have variable fatty acid compositions are valuable in soybean breeding for improving seed oil quality.

**M2 bulked seeds**

EMS-treated bulked seeds of G. max were developed from a cultivar “Fukuyutaka” at Saga University. The M2 seed set is derived from approximately 5,000 M1 plants. Part of this M2 population was used in a reverse genetic screening technique called TILLING (Hoshino et al. 2010). Users could screen the mutants themselves for use in their research. After their studies are published, users are required to deposit the isolated mutant lines derived from this resource in our resource center. These soybean M2 bulked seeds will be available from LegumeBase in the near future.

**Edamame (vegetable soybean)**

LegumeBase includes a list of characteristics affecting the quality of edamame, vegetable soybean, for 39 accessions collected in Yamagata Prefecture in northern Japan (Akazawa and Egashira 2005). A local variety of edamame named ‘Dadachamame,’ which was established in Yamagata Prefecture not less than 150 years ago, has a particular aroma, sweetness, and tastiness. The sweetness and tastiness are due to high contents of sucrose, alanine and glutamine. Different Dadachamame varieties vary in the amount of these constituents and in the dates of their harvest, thereby providing edamame varieties from summer to early fall and supporting a traditional local culture in areas where these varieties are cultivated. At present, eight edamame strains are available from LegumeBase (Table 1).

**Full-length cDNA**

The Soybean Full-Length cDNA Research Consortium has assembled a large-scale collection of full-length cDNA clones derived from the Japanese soybean cultivar, Nourin No. 2. This Consortium developed approximately 40,000 soybean cDNA clones from a full-length enriched cDNA library, including 4,711 full-read sequences, which were obtained from soybean plants grown under various developmental and environmental conditions (e.g., flower buds, roots, nodules, developing seed, drought stress, salt stress, chilling stress, low temperature, etc.) (Umezawa et al. 2008). All of clones are available from LegumeBase (Table 1).

The list of stock and their depositors in LegumeBase for Lotus and Glycine are summarized in Table 1, including resources that are in preparation.

**Database**

We have constructed a web page for NBRP Lotus and Glycine “LegumeBase” (http://www.legumebase.brc.miyazaki-u.ac.jp/) at our resource center, that is composed of two databases, the “Lotus japonicus database” (http://www.legumebase.brc.miyazaki-u.ac.jp/lotus/) and the “Glycine max/soja database” (http://www.legumebase.brc.miyazaki-u.ac.jp/glycine/) (Table 2). In this database, users may pick the strains of interest by passport data, morphological data, meteorological data of the collecting site, and seed components or genotype. Sequence data for DNA resources are also available for each database: L. japonicus Genomic clone: miyakogusa.jp, L. japonicus cDNA: Lotus japonicus EST index and G. max full-length cDNA clone: soybean full-length cDNA database (Table 2). In addition, there are several related websites, such as the social bookmark site “Worldwide Legume Science Information Desk” or sites providing lists of relevant papers in the research area, such as Research Resource Circulation lotus/glycine that was established by the NBRP Information Center at the National Institute of Genetics (Yamazaki et al. 2010) (Table 2). The latter site provides useful information about legume research using the resources of NBRP Lotus and Glycine.

**Conclusions**

We have developed extensive resources for two important leguminous plants, Lotus japonicus and Glycine max, and
have constructed a database called LegumeBase at our resource center for researchers. NBRP Lotus and Glycine aims to facilitate rapid progress in legume research by collecting research materials and resources readily available to the legume research community. We make all efforts to collect valuable resources for legume research, maintain them in good condition and provide superior quality resources. When using our resources, the user is required to sign a material transfer agreement (MTA) and to explicitly acknowledge our resource center as the source in any publication that ensues from the study. We started collecting handling fees for providing resources in April, 2010. The fees can be paid online using credit cards or by transferring funds to a bank account. Care will be taken to adhere to the protective conditions that were recommended by the depositor when distributing the bioresources. Previously, researchers wasted a lot of time with labor costs for procuring and maintaining their resources. NBRP Lotus and Glycine LegumeBase will alleviate these problems by accepting valuable research materials, maintaining the resources and distributing them as and when needed.

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**Table 2.** NBRP Lotus and Glycine-related websites and databases

| Name of database                  | Contents                                                                 | URL                                          |
|-----------------------------------|---------------------------------------------------------------------------|----------------------------------------------|
| LegumeBase                        | Main page of NBRP Lotus and Glycine                                        | http://www.legumebase.brc.miyazaki-u.ac.jp/   |
| Lotus japonicus database          | Database for L. japonicus in NBRP                                          | http://www.legumebase.brc.miyazaki-u.ac.jp/lotus/ |
| Glycine max/soja database         | Database for G. max and soja in NBRP                                       | http://www.legumebase.brc.miyazaki-u.ac.jp/lotus/ |
| NBRP Information Site             | Website of NBRP                                                           | http://www.nbrp.jp/                          |
| Worldwide Legume Science Information Desk | Social bookmark site of legume-related webpage                           | http://www.shigen.nig.ac.jp/infodesk/topSpeciesAction.do?speciesId=4 |
| Research Resource Circulation lotus/glycine | Database of papers related to the NBRP resources                      | http://www.shigen.nig.ac.jp/rrc/gatewayAction.do?speciesId=17 |
| RIKEN Bioresource Center          | Distribution of L. japonicus culture cell lines                           | http://www.brc.riken.jp/lab/epd/Eng/species/lotus |
| Miyakogusa.jp                     | Genetic map and clone list of L. japonicus                                  | http://www.kazusa.or.jp/lotus/               |
| Lotus japonicus EST index         | EST information for L. japonicus                                        | http://est.kazusa.or.jp/en/plant/lotus/EST/  |
| Rhizobase                         | Database for Rhizobium genome                                              | http://genome.kazusa.or.jp/rhizobase/        |
| Marker BD-Glycine max/soybean-    | Linkage map and marker information of G. max                               | http://www.kazusa.or.jp/soymarker/           |
| Soybean Full-Length cDNA Database | Information for full-length cDNA clones of G. max                         | http://rsoy.psc.riken.jp/                    |

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