RIKEN BIORESOURCE CENTER
EXPERIMENTAL PLANT DIVISION
実験植物開発室

植物リソースリスト

1．リストの見方

2010 年春現在、実験植物開発室から提供するリソースは合計 50 万系統を越えております。本書ではこれらのリソースの概要について説明いたします。個別のリソースの詳細情報につきましては当室ホームページにてご確認をお願いいたします。

リソース番号について： 当室より提供するリソースには固有のリソース番号が付与されております。通常リソースには系統名がつけられますが、リソース番号をつけることにより、(1)リソースをカテゴリー別に仕分けできる、(2)l(英文字)と**1**(数字)などまぎらわしい名前を持つリソースを区別することができる、(3)野生株のライン化等、理研BRCにおいて派生的なリソースを整備する際に対応しやすい、などの利点があります。当室のリソース番号はリソースのカテゴリーを表すアルファベット3文字(下記表を参照ください)と5桁の数字から成ります。

リソースの付加情報について： カタログではリソース付加情報として寄託者から得た情報と理研BRCで新たに取得した情報を表示しております。例えばシロイヌナズナ完全長cDNAの場合、クローンの塩基配列がシロイヌナズナゲノムの塩基配列と完全一致しない場合もありますが、理研BRCではクローンの配列が寄託者の解析した結果と一致することをもって提供可としております。付加情報については必ずホームページのカタログ等により確認されてから提供申込みを行ってください。

シロイヌナズナ種子

pst	シロイヌナズナトランスポゾンタグライン(ホモ/ヘテロ未判別)
psh	シロイヌナズナトランスポゾンタグライン(ホモ種子系統)
pss	シロイヌナズナアクティベーションタグラインまたは FOX ライン(20 プールのセットの番号)
psp	シロイヌナズナアクティベーションタグラインまたは FOX ライン(50 系統を混合したプールの番号)
psa	シロイヌナズナアクティベーションタグライン(理研 BRC で樹立した個別の系統の番号)
psm	シロイヌナズナアクティベーションタグライン(理研 GSC で樹立した個別の系統の番号)
psx	シロイヌナズナ FOX ライン(シロイヌナズナ遺伝子過剰発現系統の種子プールを構成する個別の系統)
psr	シロイヌナズナ FOX ライン(イネ遺伝子過剰発現系統の種子プールを構成する個別の系統)
psi	個別のシロイヌナズナ変異体・形質転換体
sja ほか sj で始まる系統	シロイヌナズナ野生株、変異体及び近縁種の系統(SASSC 由来系統含む)

植物遺伝子材料

pda	シロイヌナズナ完全長 cDNA クローン(全長塩基配列解析済み)
pdx, pdy, pdz	シロイヌナズナ完全長 cDNA クローン(原則端読み配列のみ)
pdp, pdr	ヒメツリガネゴケ完全長 cDNA クローン
pds	ポプラ完全長 cDNA クローン
pdm	キャッサバ完全長 cDNA クローン
pby	タバコ BY-2 培養細胞由来 EST クローン(完全長 cDNA 含む)
pdc	ハクサイ EST クローン(完全長 cDNA 含む)
pdh	*Thellungiella halophila* の完全長 cDNA クローン
pdw	*Striga hermonthica* の完全長 cDNA クローン
rpd	個別の遺伝子クローン、ベクター

植物培養細胞

rpc	各種植物培養細胞

2. シロイヌナズナ種子

(1)トランスポゾンタグライン

Resource number: pst00001-pst20808

Developer: Drs. Takuya Ito, Takashi Kuromori, Motoaki Seki, Reiko Motohashi, Takashi Hirayama and Kazuo Shinozaki (RIKEN)

Total number of lines: 17,672

Style of distribution:

①Approx. 50 seeds of individual line are provided.

②When homozygous seed stock is requested, we ship approx. 500 homozygous seeds with wild-type Nossen seeds for control.

Number of available lines: 15,267 lines

Background ecotype: Nossen (unknown ecotype for Ds12 and 16)

Name of the vector used for transformation: pCGN derivatives

Selection marker: hygromycin

Specific feature:

①Flanking sequences of transposon have been characterized.

②Homozygous seed stock is available for over 2,700 lines.

Specific terms and conditions:

①When the RECIPIENT has filed a patent application on the invention conceived or made during the course of research studies directly using the BIOLOGICAL RESOURCE, the RECIPIENT agrees to promptly notify RIKEN Plant Science Center (the owner of the BIOLOGICAL RESOURCE) upon filing the application with specifications.

②The recipient can receive up to 50 lines of the BIOLOGICAL RESOURCE in each year.

③The RECIPIENT agrees to expressly describe that “the BIOLOGICAL RESOURCE (the resource name) was developed by the plant genome project of RIKEN Genomic Sciences Center, and provided by the RIKEN BRC through the National Bio-Resource Project of the MEXT, Japan” in Materials and Methods or in the Acknowledgement of any publication reporting the use thereof. The manuscript(s) listed below should be referred in the publication on scientific journal. The RECIPIENT also agrees to send a copy of such publication to the RIKEN BRC. The RIKEN BRC may disclose publicly, copy or otherwise use such publication to demonstrate the contribution by the RIKEN BRC.

References:

①Fedoroff NV. and Smith D. (1993) A versatile system for detecting transposition in Arabidopsis. Plant J. 3: 273-289.

②Smith D., Yanai Y., Liu, Y-G., Ishiguro S., Okada K., Shibata D., Whittier RF. and Fedoroff NV. (1996) Characterization and mapping of Ds-GUS-T-DNA lines for targeted insertional mutagenesis. Plant J. 10: 721-732.

③Ito T., Motohashi R., Kuromori T., Mizukado S., Sakurai T., Kanahara H., Seki M. and Shinozaki K. (2002) Plant Physiol. 129: 1695-1699.

④Kuromori T., Hirayama T., Kiyosue Y., Takabe H., Mizukado S., Sakurai T., Akiyama K., Kamiya A., Ito T. and Shinozaki K. (2004) Plant J. 37: 897-905.

⑤Ito T., Motohashi R., Kuromori T., Noutoshi Y., Seki M., Kamiya A., Mizukado S., Sakurai T. and Shinozaki K. (2005) Plant Cell Physiol. 46: 1149-1153.

Important note:

①AGI codes are frequently changed. Before you make your order, we recommend you to obtain detail information including flanking sequence of the line from RARGE (Riken Arabidopsis Genome Encyclopedia) or T-DNA express.

②The lines marked 'In preparation' are currently unavailable. Do not include those lines in your order. We will make an announcement at the time they are ready for distribution.

③The transposon-tagged lines are categorized to genetically modified organisms. For ordering such materials, the applicants must obtain all of the permission required by any kind of regulation or law before ordering. Also, it is recipient's responsibility to perform customs procedure for importation of biological materials. Please inform us when you need quarantine

certification to import Arabidopsis seeds. Without providing such information, RIKEN BRC cannot guarantee any loss or damage of the materials that is caused during customs procedure.

④Although the background ecotype of this resource has been reported as No-0 (Nossen), we found polymorphisms between the No-0 line from SASSC and the parental lines provided by Dr. Fedoroff. We recommend users to use the parental lines available from ABRC as control plants in your experiments.

Information required by Cartagena Protocol on Biosafety (in part):

This BIOLOGICAL MATERIAL corresponds to Living Modified Organisms destined for contained use. (*Arabidopsis thaliana*)
Requirements for the safe handling, storage, transport and use: ①This BIOLOGICAL MATERIAL is the seeds of *Arabidopsis thaliana*. ②This BIOLOGICAL MATERIAL harbors NPTII, HPT and GUS genes (from *E.coli*), ALS gene (from *A. thaliana*), Ds element (from *Zea mays*), promoter of CaMV 35S RNA and CaMV 19S RNA genes (from califlower mosaic virus), and LB, RB and NOS-terminator sequences of T-DNA (*Agrobacterium tumefaciens*). ③This BIOLOGICAL MATERIAL is for laboratory use (contained use) only. Do not use it for "Intentional introduction into the environment". ④This BIOLOGICAL MATERIAL and its progeny should be inactivated by autoclave or equivalent procedure after use.

バックグラウンドのエコタイプについて:

世界各地で採取されたシロイヌナズナ野生系統を分類するときにエコタイプ（環境型）という言葉が使われます。タグラインがどのエコタイプより作成されたかは重要な意味を持ちます。

アクティベーションタグラインでは、ゲノム塩基配列が解析された Columbia 株に T-DNA を導入して作成されたため、挿入位置の解析には公開されているゲノムの塩基配列が適用でき、ほとんどの場合は一義的に挿入位置を決定することができると考えられます。

一方 Nossen 株にトランスポゾンを導入しているトランスポゾンタグラインの場合、解析した端読み配列と Columbia 株のゲノム塩基配列との間に塩基置換などの多型が存在することがあり、トランスポゾンの挿入位置を100％の確率では決定できない場合がしばしば見られます。このためカタログデータベースでは、挿入位置の候補を2つまで表示しておりますのでご確認をお願いいたします。

トランスポゾンの挿入位置の確認について:

通常挿入位置を確認するためには Tail-PCR などの方法により隣接配列の解析を行います。トランスポゾンタグラインはほとんどの場合、ゲノム上に 1 箇所の挿入がおこるため解析は比較的容易です。当室から提供するトランスポゾンタグラインについては開発者の理研 GSC により決定された挿入位置情報がカタログに掲載され、また遺伝子名を用いてオンライン検索ができるようになっております。なお理研 BRC では提供前にデータベースに記載の位置にトランスポゾンの挿入があることを PCR により確認しています。

一方 T-DNA タグラインではゲノム上の複数の位置に T-DNA の挿入がおこりうるため、挿入位置を決定する際には注意が必要です。タンデムリピートや T-DNA の一部が挿入の際に欠失するなど挿入様式が複雑で解析が困難となる可能性にもご注意ください。

なおトランスポゾンタグライン、T-DNA タグライン両者とも挿入位置と異なる場所に変異が存在することが少なからずあります。このため表現型の解析においては同一遺伝子座に変異のある複数のラインを使用するか、ないしは候補遺伝子の過剰発現株／発現抑制株を用いて表現型を確認されることをお勧めします。

(2) アクティベーションタグライン

Resource number: pss00001-pss00009, developed by RIKEN BRC (The pss00009 contains 17 seed pools. Others contain 20 seed pools.); pss00101-00128, developed by RIKEN GSC (The pss00103 contains 16 seed pools. Others contain 20 seed pools.).

Developers: Drs. Motoaki Seki, Miki Nakazawa, Minami Matsui, Masatomo Kobayashi and Kazuo Shinozaki (RIKEN)

Total number of line: approx. 70,000

Style of distribution: Provided as a seed pool set (equivalent with 1,000 lines). Each seed pool set contains 20 seed pools, and one seed pool contains approx. 400 seeds from 50 lines; that means 8 seeds per line in average. (Please see “Structure of activation tagged-line” shown below.) Seeds for individual lines (psa and psm) that constitute seed pool (psp) are available for the users who obtained desired mutant in the seed pool.

Number of available pool sets: 37 seed pool sets (equivalent with 36, 650 lines)
Background ecotype: Columbia
Name of the vector used for transformation: pPCVICEn4HPT
Selection marker: hygromycin
Specific feature: The 4 x CMV 35S enhancer in T-DNA may promote gene expression near T-DNA insertion site to produce dominant phenotype.
Specific conditions for distribution:
(For pss00001-00009) If the RECIPIENT claims any kind of intellectual property obtained from the use of the BIOLOGICAL RESOURCE, the RECIPIENT is required to notice RIKEN BRC after application.
(For pss00101-00128) When the RECIPIENT has filed a patent application on the invention conceived or made during the course of research studies directly using the BIOLOGICAL RESOURCE, the RECIPIENT agrees to promptly notify RIKEN Plant Science Center (the owner of the BIOLOGICAL RESOURCE) upon filing the application with specifications.
Reference:
①Nakazawa M., Ichikawa T., Ishikawa A., Kobayashi H., Tsuhara Y., Kawashima M., Suzuki K., Muto S. and Matsui M. (2003) Plant Journal 34(5): 741-750.
Information required by Cartagena Protocol on Biosafety (in part):

This BIOLOGICAL MATERIAL corresponds to Living Modified Organisms destined for contained use. (*Arabidopsis thaliana*)
Requirements for the safe handling, storage, transport and use: ①This BIOLOGICAL MATERIAL is the seeds of *Arabidopsis thaliana*. ②This BIOLOGICAL MATERIAL harbor HPT and ampicillin-resistant genes (from *E.coli*), promoter of CaMV 35S RNA gene (from califlower mosaic virus), and LB, RB and NOS-promoter sequences of T-DNA (*Agrobacterium tumefaciens*). ③This BIOLOGICAL MATERIAL is for laboratory use (contained use) only. Do not use it for "Intentional introduction into the environment". ④This BIOLOGICAL MATERIAL and its progeny should be inactivated by autoclave or equivalent procedure after use.

(3)FOX ライン(シロイヌナズナ遺伝子過剰発現系統)

Resource number: pss10001-10011
Developer: Drs. Minami Matsui, Miki Nakazawa and Takanari Ichikawa (RIKEN)
Total number of line: approx. 20,000 (expected)
Style of distribution: Provided as a seed pool set (seed pool contains approx. 400 seeds from 50 lines = 8 seeds per line; one seed pool set contains 20 seed pools = equivalent with 1,000 lines). Seeds for individual lines (psx) that constitute specific seed pool (psp) are available for the users who obtained desired mutant in the seed pool.
Number of lines available: 11seed pool set (equivalent with 10,796 lines)
Background ecotype: Columbia
Name of the vector used for transformation: pBIG2113SF (pBI121 derivative)
Selection marker: hygromycin
Specific feature: Provided as seed pools for screening. Arabidopsis full-length cDNA (RAFL) was introduced with 35S promoter to produce dominant phenotype.
Specific conditions for distribution:
①When the RECIPIENT has filed a patent application on the invention conceived or made during the course of research studies directly using the BIOLOGICAL RESOURCE, the RECIPIENT agrees to promptly notify RIKEN Plant Science Center upon filing the application with specifications.
②When the RECIPIENT publishes his/her research, acknowledge RIKEN PSC and refer designated manuscripts shown below.
Reference:
①Ichikawa T, Nakazawa M, Kawashima M, Iizumi H, Kuroda H, Kondou Y, Tuhara Y, Suzuki K, Ishikawa A, Seki M, Fujita M, Motohashi R, Nagata N, Takagi T, Shinozaki K and Matsui M (2006) Plant J. 48:974-985.

Information required by Cartagena Protocol on Biosafety (in part):

This BIOLOGICAL MATERIAL corresponds to Living Modified Organisms destined for contained use. (*Arabidopsis thaliana*)
Requirements for the safe handling, storage, transport and use: ①This BIOLOGICAL MATERIAL is seed of *Arabidopsis thaliana*. ②This BIOLOGICAL MATERIAL harbor HPT gene (from *E.coli*), promoter of CaMV 35S RNA gene (from cauliflower mosaic virus), cDNA from *Arabidopsis thaliana*, and LB, RB and NOS-terminator sequences of T-DNA (*Agrobacterium tumefaciens*). ③This BIOLOGICAL MATERIAL is for laboratory use (contained use) only. Do not use it for "Intentional introduction into the environment".

(4)FOX ライン(イネ遺伝子過剰発現系統)

Resource number: pss11001, pss11002
Developer: Dr. Minami Matsui (RIKEN PSC)
Total number of line: approx. 20,000 (expected)
Style of distribution: Provided as a seed pool set (seed pool contains approx. 400 seeds from 50 lines = 8 seeds per line; one seed pool set contains 20 seed pools = equivalent with 1,000 lines). Seeds for individual lines (psx) that constitute specific seed pool (psp) are available for the users who obtained desired mutant in the seed pool.
Number of pool sets available: 2 seed pool set (equivalent with 2,000 lines)
Background ecotype: Columbia
Vector for transformation with Agrobacterium: pBIG2113SF(pBI121 derivative)
Selection marker: hygromycin
Specific feature: Provided as seed pools for screening. Rice full-length cDNA was introduced with 35S promoter to produce dominant phenotype.
Specific conditions for distribution:

(1) The RECIPIENT agrees to expressly describe that "the BIOLOGICAL RESOURCE (the resource name) was developed by the RIKEN PSC, NIAS and RIBS through The Special Coordination Fund for Promoting Science and Technology, and provided by the RIKEN BRC through the National Bio-Resource Project of the MEXT, Japan" in Materials and Methods or in the Acknowledgement of any publication reporting the use thereof. The RECIPIENT also agrees to send a copy of such publication to the RIKEN BRC. The RIKEN BRC, RIKEN PSC, NIAS and RIBS may disclose publicly, copy or otherwise use such publication to demonstrate the contribution by the RIKEN BRC.

Information required by Cartagena Protocol on Biosafety (in part):

This BIOLOGICAL MATERIAL corresponds to Living Modified Organisms destined for contained use. (*Arabidopsis thaliana*)
Requirements for the safe handling, storage, transport and use: ①This BIOLOGICAL MATERIAL is seed of *Arabidopsis thaliana*. ②This BIOLOGICAL MATERIAL harbor HPT gene (from *E.coli*), promoter of CaMV 35S RNA gene (from cauliflower mosaic virus), cDNA from *Oryza sativa*, and LB, RB and NOS-terminator sequences of T-DNA (*Agrobacterium tumefaciens*). ③This BIOLOGICAL MATERIAL is for laboratory use (contained use) only. Do not use it for "Intentional introduction into the environment".

(5)野生系統・近縁種及び変異体系統

仙台シロイヌナズナ種子保存センター(SASSC)から寄託された AIS 由来の世界標準となるリソースを中心に提供しています。世界各地の環境に適応した野性のシロイヌナズナは様々な遺伝的変異を持ち、今後の研究に有望なリソースです。そこで当室では遺伝型、表現型に関する情報をカタログに追加するべく準備を進めております。ぜひご活用をお願いいたします。

目次

シロイヌナズナ野生系統の分類について:

野生系統を収集する際には一箇所の生息地から複数の個体を採取することが普通でこれに同一の名称(エコタイプ)をつけて増殖維持するため、個体間に多型が存在する場合があります。理研 BRC では SSLP 解析技術を適用して保有する野生系統の遺伝型情報を収集するとともに、主だった系統より同質系統の確立を進めています。

a. AIS wild type populations
Resource number: SJA00100-SJA26400
(SJAxxx00 means bulk seeds and SJAxxx01-xxx05 means seeds from individual plant.)
Number of available lines: 264
Origin of resource: AIS
Style of distribution: Approx. 50 seeds of individual line are provided.
NOTE: Some of the lines need quite a long period until flowering.

b. AIS form mutants
Resource number: SJF00100-SAJ20500
Number of available lines: 206
Origin of resource: AIS

c. AIS virescent (leaf color) mutant
Resource number: SJV00100-SJV41100
Number of available lines: 321
Origin of resource: AIS

d. AIS metabolic mutants
Resource number: SJE00000-SAJ01300
Number of available lines: 13
Origin of resource: AIS

e. AIS gene marker lines
Resource number: SJM00100-SJM10500
Number of available lines: 106
Origin of resource: AIS

f. AIS trisomic lines
Resource number: SJT00100-SJT02400
Number of available lines: 23
Origin of resource: AIS

g. AIS other species
Resource number: SJS00100-SJS01200
Number of available lines: 12
Origin of resource: AIS

h. Sendai wildtype populations
Resource number: SJW10100-SJW14400
Number of available lines: 45
Origin of resource: SASSC (Dr. Goto)

i. Sendai mutants
Resource number: SJG00100-SJG14000
Number of available lines: 113
Origin of resource: SASSC (Dr. Goto)

j. Mutants from M. Koornneef's collection
Resource number: SJK00100-SJK02400
Number of available lines: 24
Origin of resource: SASSC (Dr. Koornneef)

k. Sendai other species
Resource number: SJO00100-SJO03000
Number of available lines: 28
Origin of resource: SASSC (Dr. Goto)

(6)個別の変異体・形質転換体

論文で発表された変異体、形質転換体を提供します。現在提供可能な系統は以下のとおりです。詳細についてはホームページでご確認ください。

Resource number	Line number	Phynotype	Method for establishment	Reference (PubMed ID)
psi00001	iso-1D	Dwarf	Activation tagging	12787254
psi00002	iso-2D	Dwarf	Activation tagging	12787254
psi00004	iso-4D	Dwarf	Activation tagging	12787254
psi00005	ydk1-D	Dwarf	Activation tagging	14756757
psi00006	lsh1-D	Reduced elongation of hypocotyl	Activation tagging	14871309
psi00007	DFL2OX	Reduced elongation of hypocotyl	Over expression	14581632
psi00008	DFL2AS	Reduced elongation of hypocotyl	Anti-sense	14581632
psi00009	DFL-2GUS	GUS at hypocotyl	Transformation with GUS	14581632
psi00010	pCPC::CPC:GFP	GFP at epidermal cell	Transformation with GFP	12403712
psi00011	stop1	Senstive to acid/Al stress	EMS	17535918
psi00012	stop1-KO	Senstive to acid/Al stress	T-DNA insertion	17535918
psi00013	stop1-comp	Senstive to acid/Al stress (complement line)	Compliment line of stop1	17535918
psi00014	gid1 Aabbcc	Severe dwarf (if homozygous)	Crossig (triple KO)	17521411
psi00015	gid1 bc (AAbbcc)	Mostly normal	Crossing (double KO)	17521411
psi00016	gid1 ac (aaBBcc)	Dwarf	Crossing (double KO)	17521411
psi00017	gid1 ab (aabbCC)	Low fertility	Crossing (double KO)	17521411
psi00018	gid1 a-1 (aaBBCC)	None	Ds insertion	17521411
psi00019	gid1 a-2 (aaBBCC)	None	T-DNA insertion	17521411
psi00020	gid1 b-1 (AAbbCC)	None	Ds insertion	17521411
psi00021	gid1 c-1 (AABBcc)	None	T-DNA insertion	17521411
psi00022	srd2-1	Temperature sensitive	EMS	20965997
psi00023	rid3	Temperature sensitive	EMS	19054368
psi00024	rid5	Temperature sensitive	EMS	14522871
psi00025	rpd1-1	Temperature sensitive	EMS	16407439
psi00026	rpd1-2	Temperature sensitive	EMS	16407439
psi00027	rgd3-1	Temperature sensitive	EMS	19054368

3. 植物培養細胞

2012 年 1 月現在、38 株を提供しています。培養条件の詳細はホームページでご確認ください。

(1)シロイヌナズナ T87 細胞

モデル実験植物シロイヌナズナの代表的な培養細胞です。葉緑体が発達するため緑色をしており、通常明所で培養します。通常より低い温度(22℃)で培養することに注意が必要です。

リソース番号: RPC00008
由来植物名: *Arabidopsis thaliana* L. ecotype Columbia
培養状態: 懸濁培養
培養条件: 明所(連続白色光、40-100 ・E/s/m^2)、22℃、旋回培養(120 rpm)
培地:JPL 培地
寄託者: Micheke Axelos (INRA)
提供条件: 一般 MTA に同じ
参考文献:(1) Axelos M., Curie C., Mazzolini L., Bardet C. and Lescure B. (1992) Plant Physiol. Biochem. 30(1): 123-128 (2) Callard D., Axelos M. and Mazzolini L. (1996) Plant Physiol. 112: 705-715

(2)タバコ BY-2 細胞

増殖が速く同調培養が可能な世界標準の培養細胞株として広く知られています。使用例は細胞増殖機構の研究、タンパクの細胞内局在の解析、物質生産技術の開発等多岐にわたります。

リソース番号: RPC00001
由来植物名: *Nicotiana tabacum* L. cv. Bright Yellow
培養状態: 懸濁培養
培養条件: 暗所、27℃、旋回培養(130 rpm)
培地: Linsmaier and Skoog 改変培地
寄託者: Toshiyuki Nagata (Tokyo Univ.)
提供条件: 一般 MTA に同じ
参考文献: Nagata T., Nemoto Y. and Hasegawa S. (1992) International Review of Cytology 132: 1-30

(3)イネ OS-1 細胞

同調培養可能なイネの培養細胞系として樹立されました。静置培養と懸濁培養の双方で保存しております。提供依頼の際にはどちらかを指定してください。

リソース番号: RPC00020
由来植物名: *Oryza sativa* L.
培養状態: 懸濁培養、静置培養
培養条件: 暗所、27℃、懸濁培養の場合には旋回培養(110 rpm)
寄託者: Yuko Ohashi (NIAS)
提供条件: 一般 MTA に同じ
参考文献: 中曽根正一、南栄一、今井剛、秋山典昭、大橋祐子 (1993) イネの培養細胞における同調培養系の開発および細胞周期の進行に伴うヒストンH3とPCNA遺伝子の発現 農業生物資源研究所報告 8: 1-10

(4)遺伝子組換え植物培養細胞

東京大学の馳澤博士より寄託を受けたタバコ培養細胞株、GV7(rpc00039), GF11(rpc00040), GT16(rpc00041) を提供します。それぞれ液胞膜、アクチン繊維、微小管が GFP により可視化されている細胞株です。ご利用の際には以下の点にご注意ください。

- 本リソースは遺伝子組換え技術を適用して樹立された植物培養細胞ですが、自然条件で個体へと再分化しないため、そのまま実験に使用される場合は法律で定める遺伝子組換え生物に該当しません。ただし何らかの技術を用いて本リソースを含有する組織または個体を作成する場合には法律の対象となりますのでご注意ください。
- 本リソースは GFP 遺伝子を組み込んでいます。利用条件については巻頭の説明もご覧ください。

(5)その他の植物培養細胞

リソース番号	細胞株名	由来植物名	培養状態	備考
RPC00002	Kurodagosun	ニンジン	懸濁培養	
RPC00003	VR	ブドウ	静置培養	
RPC00004	VW	ブドウ	静置培養	
RPC00005	PAR	ヨウシュウヤマゴボウ	静置培養	
RPC00006	PAP	ヨウシュウヤマゴボウ	静置培養	
RPC00007	PAW	ヨウシュウヤマゴボウ	静置培養	
RPC00009	T-13	タバコ	懸濁培養	寄託者の承諾書が必要
RPC00011	Cba-1	スイカ	静置培養	
RPC00012	Sly-1	トマト	静置培養	
RPC00014	CRA	ニチニチソウ	懸濁培養	寄託者の承諾書が必要
RPC00015	V208	ニチニチソウ	懸濁培養	
RPC00016	Spi-WT	ホウレンソウ	懸濁培養	樹立者の承諾書が必要
RPC00017	Spi-I-1	ホウレンソウ	懸濁培養	樹立者の承諾書が必要
RPC00018	Spi-12F	ホウレンソウ	懸濁培養	樹立者の承諾書が必要
RPC00021	Vma-1	ツルニチニチソウ	静置培養	
RPC00022	A.per	アスパラガス	静置培養	
RPC00023	A.pas	アスパラガス	静置培養	
RPC00024	A.plo	アスパラガス	静置培養	
RPC00025	PSB	ゴマ	静置培養	
RPC00026	PSW	ゴマ	静置培養	
RPC00027	PSG	ゴマ	静置培養	
RPC00028	LcyD6	ヘチマ	静置培養	
RPC00029	LcyD7	ヘチマ	静置培養	
RPC00030	ZE3	ヒャクニチソウ	静置培養	
RPC00031	Oc	イネ	懸濁培養	
RPC00032	Lj	ミヤコグサ	懸濁培養	
RPC00033	LjA	ミヤコグサ	静置培養	
RPC00034	Ljm	ミヤコグサ	静置培養	
RPC00035	Xan-1	タバコ	静置培養	
RPC00036	BY-2H	タバコ	静置培養	
RPC00037	M18-1	ムラサキ	静置培養	
RPC00038	OM	ムラサキ	静置培養	

以上の株の詳細はホームページに掲載している植物培養細胞カタログを参照してください。

4. 植物遺伝子

我が国で作成されたモデル植物の完全長 cDNA を中核とした整備を進めています。シロイヌナズナに加えヒメツリガネゴケ(コケのモデル)、ポプラ(樹木のモデル)、キャッサバ(バイオ燃料のモデル)、タバコ(ナス科のモデル)、ハクサイ(アブラナ科作物のモデル)、*Thellungiella halophila*(ストレス研究のモデル)、*Striga hermonthica*(寄生植物のモデル)の完全長 cDNA リソース合計 50 万クローン以上を取り揃え、内外の研究者に提供しております。

完全長cDNAの品質について:

完全長 cDNA の作成には数種のプロトコルが確立されており、プロトコルによって差はあるもののいずれの方法でも完全長率が高いライブラリーを作成することができます。しかし実際にシロイヌナズナの完全長ライブラリーを構成する個々のクローンについて詳しく調べると、ゲノム上に予測されている遺伝子配列と異なる以下のようなクローンを見出すことができます。

(1) 塩基置換があるクローン
Columbia 株の多型によるもの、クローン化過程での変異によるもの等が想定されます。

(2) 転写開始点、エキソンーイントロンの構造が異なるクローン
不完全な転写物より cDNA が作成された可能性もありますが、転写段階において遺伝子機能が調節されている可能性も考えられ、今後の課題です。

(3) 予測された転写領域が存在しない位置や2個の転写領域にまたがるクローン、あるいは1個の転写領域が別々に転写されたクローン
遺伝子予測プログラムの不完全さなどにより差が生じると考えられ、完全長クローンのデータに基づきアノテーションが修正されてきました。

以上のクローンに生物学的意味があるのかどうかについては意見がわかれるところですが、リソースセンターとしては請求があれば提供できるよう体制を整備することが重要と考え、カタログに配列とともに掲載しています。そこでクローンの提供申込み時には必ず配列をご確認いただくようお願いいたします。カタログどおりの配列を持つクローンについては提供後のクレームに応じかねますので、よろしくお願いいたします。

(1)シロイヌナズナ完全長 cDNA (RAFL)クローン

This resource has been developed by RIKEN Genomic Sciences Center (GSC). The clones were deposited after the characterization of their full-length sequence at RIKEN GSC, SSP (Salk/Stanford/PGEC) consortium and National Institute of Genetics (NIG) partially supported by NSF 2010 Project and National Bioresource Project. The clones are called as 'R clone' in the SSP consortium.

Resource number: pda00001- (with full-length sequence), pdx00001-/pdy00001-/pdz00001- (with 5'-and/or 3'-end sequences)
Developers: Drs. Motoaki Seki and Kazuo Shinozaki (RIKEN).
Total number of clones: 251,382 clones
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of available clones: 251,382 clones
Background ecotype: Columbia
Vector: modified pBluescript
Selection marker: ampicillin
Map and restriction site: Shown on our HP.
Specific feature: Full-length sequence and/or 5'-/3'-end sequences have been characterized.
Specific conditions for distribution:
①When the RECIPIENT has filed a patent application on the invention conceived or made during the course of research studies directly using the BIOLOGICAL RESOURCE, the RECIPIENT agrees to promptly notify RIKEN Plant Science Center (the owner of the BIOLOGICAL RESOURCE) upon filing the application with specifications.
②The maximum number of the clones that can be ordered from one laboratory or group in one order is 100.
③When you publish your research, acknowledge RIKEN GSC and refer designated manuscripts.
References:
①Seki, M., Carninci, P., Nishiyama, Y., Hayashizaki, Y. and Shinozaki, K. (1998) Plant Journal 15: 707-720.
②Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A.,

Akiyama, K., Oono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K. (2002) Science 296: 141-145.

NOTE:

①Detailed information including full-length sequence of the individual RAFL clone is available from the following websites:
http://rarge.gsc.riken.jp/
http://signal.salk.edu/cgi-bin/tdnaexpress

②Please examine the sequence of clones that you have interest by yourself.

③Clone numbers pda99001-99400 correspond to RIKEN Arabidopsis Transcription Factor (RARTF) ORF clones. For detail description of this resource, please visit our website, http://www.brc.riken.jp/lab/epd/Eng/catalog/orf.shtml.

(2)ヒメツリガネゴケ完全長 cDNA クローン

This resource has been developed by the collaboration of National Institute for Basic Biology (NIBB) and RIKE GSC, and the sequence was characterized at National Institute of Genetics (NIG).

Resource number: pdp00001-, pdr00001-
Developer: Dr. Mitsuyasu Hasebe (NIBB)
Total number of clones: 149,363
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of available clones: 149,363 clones
Organism: *Physcomitrella patens* (moss)
Vector: modified pBluescript (pFLC-1-E)
Selection marker: ampicillin
Map and restriction site: Please see the figure on our HP.
Specific feature: 5'- and 3'-end sequences have been characterized.
Specific conditions for distribution:

① The manuscript listed below should be referred in the publication on scientific journal.

② This material will not be used for research for commercial parties or otherwise for commercial purposes. For detail please send E-mail to plant@brc.riken.jp.

Reference:

① Nishiyama T., Fujita T., Shin-I T., Seki M., Nishide H., Uchiyama I., Kamiya A., Carninci P., Hayashizaki Y., Shinozaki K., Kohara Y. and Hasebe M. (2003) Comparative genomics of *Physcomitrella patens* gametophytic transcriptome and *Arabidopsis thaliana*: implication for land plant evolution. PNAS 100 (13): 8007-8012.

NOTE: Detailed information on the individual clone is available from the following website:
http://moss.nibb.ac.jp

(3)ポプラ完全長 cDNA クローン

This material has been developed and characterized by National Institute for Basic Biology (FFPRI).

Resource number: pds00001-
Developers: Drs. Tokihiko Nanjo and Kenji Shinohara (FFPRI)
Total number of clones: 23,100
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of available clones: 23,100
Organism: *Populus nigra* var. *italica* (poplar)
Vector: pME18SFL3 (Gene Bank Accession No. AB009864, TOYOBO, Japan)
Selection marker: ampicillin
Map and restriction site: Shown on the catalogue of TOYOBO.
Specific feature: 5'- and 3'-end sequences have been characterized.
Specific conditions in MTA:

① The RECIPIENT should obtain approval of the DEPOSITOR using the APPROVAL FORM prior to entering THE AGREEMENT with the RIKEN BRC.

② The BIOLOGICAL MATERIAL should not be used for any commercial purpose.
③ The manuscript shown below should be referred in the publication on scientific journal.
④ The RECIPIENT can receive up to 10 clones in one order and up to 100 clones in one year as the BIOLOGICAL RESOURCE.
⑤ The RECIPIENT should not distribute or transfer the BIOLOGICAL RESOURCE to any other laboratory or organization.
⑥ Within 6 months after receiving the BIOLOGICAL RESOURCE, the RECIPIENT must sequence the entire length of the insert(s), deposit the sequence(s) into EMBL/GeneBank/DDBJ database, and report the accession number(s) to the depositor via the RIKEN BRC. The RIKEN BRC can use them to improve the catalogue in RIKEN BRC.

Reference:

①Nanjo T., Futamura N., Nishiguchi M., Igasaki T., Shinozaki K. and Shinohara K., Characterization of full-length enriched expressed sequence tags of stress-treated poplar leaves. Plant Cell Physiol. 45 (12): 1738-1748 (2004).

NOTE: More information is available from:
http://www.ffpri.affrc.go.jp/labs/kouho/Press-release/2004/cdna041220.html

(4)キャッサバ完全長 cDNA クローン

This resource has been developed and characterized by RIKEN PSC under the collaboration with CIAT.

Resource number: pdm00001-
Developer: Drs. Motoaki Seki and Kazuo Shinozaki (RIKEN PSC)
Total number of Clones: 19,968
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of clones available: 19,968 clones
Organism: *Manihot esculenta* Crantz.
Vector: pFLCIII
Selection marker: ampicillin
Map and restriction site: Carninci et al. (2001) Genomics 77(1-2): 79-90.
Specific feature: 5'- and 3' -sequences have been characterized.
Specific conditions for distribution:

①The RECIPIENT can use the BIOLOGICAL RESOURCE for research only.
②The RECIPIENT agrees to refer the RIKEN PSC and CIAT as developers and the RIKEN BRC as a provider of the BIOLOGICAL RESOURCE in any publication reporting use of it.
③Following manuscript should be referred in the publication on scientific journal. Sakurai, T., Plata, G., Rodriguez-Zapata, F., Seki, M., Salcedo, A., Toyoda, A., Ishiwata, A., Tohme, J., Sakaki, Y., Shinozaki, K. and Ishitani, M. Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. BMC Plant Biology, 2007, 7:66.
④The RECIPIENT agrees not to use the BIOLOGICAL RESOURCE for constructing microarray or macroarray without the agreement from the RIKEN PSC.
⑤The RECIPIENT should not distribute or transfer the BIOLOGICAL RESOURCE to any other laboratory or organization.
⑥The RECIPIENT can receive up to 10 clones in one order and up to 100 clones in one year as the BIOLOGICAL RESOURCE.

Reference:

① Sakurai, T., Plata, G., Rodriguez-Zapata, F., Seki, M., Salcedo, A., Toyoda, A., Ishiwata, A., Tohme, J., Sakaki, Y., Shinozaki, K. and Ishitani, M. Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. BMC Plant Biology, 2007, 7:66.

NOTE: More information is available from the following website:
http://www.riken.jp/engn/r-world/info/release/press/2007/071206/index.html

(5)タバコ BY-2 培養細胞由来 EST クローン(完全長 cDNA 含む)

This resource has been developed by RIKEN Plant Science Center (PSC). Some of the clones were established as "full-length cDNA clones".

Resource number: pby00101-
Developer: Dr. Ken Matsuoka (RIKEN GSC)
Total number of clones: 22,221
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of available clones: 22,221 clones
Organism: *Nicotiana tabacum* BY-2 cultured cell
Vector: pGEM T-Easy vector (Promega) (pby00101-pby14996); pBluescript II KS+ (Stratagene) (pby21001-35384); pGCAPSP2 (pby40001-)
Selection marker: ampicillin
Map and restriction site: Please see the figure in supplier's catalogue. For pGCASP2, please send your mail to plant@brc.riken.jp.
Specific feature: 5'- and 3'-end sequences have been characterized.
Specific conditions for distribution:
①These materials will be distributed for basic research of no commercial value.
②When result of research using this resource is planned to claim right or to use for industrial purpose, researchers should discuss with RIKEN before starting steps.
③If commercial use of the clone(s) is planned, contact RIKEN to discuss the condition of the commercial use.
④Following manuscripts should be referred in the publication on scientific journal reporting use of it.
References:
①Matsuoka, K., Demura, T., Gális, I., Horiguchi, T., Sasaki, M., Tashiro, G. and Fukuda, H. (2004) A comprehensive gene expression analysis toward the understanding of growth and differentiation of tobacco BY-2 cells. Plant Cell Physiol. 45:1280-1289.
②Gális, I., Šimek, P., Narisawa, T., Sasaki, M., Horiguchi, T., Fukuda, H. and Matsuoka, K. (2006) Tobacco microarray reveals novel MYB transcription factor that selectively activates genes in phenylpropanoid metabolism. Plant J. 43:573-592.
NOTE: Detailed information on the individual clone is available from following website:
http://mrg.psc.riken.go.jp/strc/index.htm

(6)ハクサイ EST クローン(完全長 cDNA 含む)

This resource has been developed by Drs. Hiroshi ABE, Masatomo KOBAYASHI (RIKEN BRC), and Dr. Yoshihiro NARUSAKA (Research Institute for Biological Sciences OKAYAMA).

Resource number: pdc00001-02166 (EST clone), pdc10001-19903 (full-length cDNA clone)
Developer: Drs. Hiroshi ABE and Yoshihiro NARUSAKA
Total number of Clones: 2,166 (EST clone); 9,903 (full-length cDNA clone)
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of clones available: 2,166 (EST clone); 9,903 (full-length cDNA clone)
Organism: *Brassica rapa* subsp. *Pekinensis*
Vector: pBluescript II SK(-) (EST clone); pGCAP10 (full-length cDNA clone)
Selection marker: ampicillin
Map and restriction site: Please see the figure in supplier's catalogue. For pGCAP10, please visit http://dna.brc.riken.jp/pdf3/vector/AB371573.pdf.
Specific feature: 5'-sequences have been characterized (EST clone); 5'- and 3'-sequences have been characterized (full-length cDNA clone)
Specific conditions for distribution: Following manuscripts should be referred in the publication on scientific journal.
(for EST clone)

Narusaka et al. (2006) Comparative analysis of expression profiles of counterpart gene sets between Brassica rapa and *Arabidopsis thaliana* during fungal pathogen *Colletotrichum higginsianum* infection. Plant Biotech. 23: 503-508.

(for full-length cDNA clone)

Abe et al. (2011) Development of full-length cDNAs from Chinese cabbage (*Brassica rapa* subsp. pekinensis) and identification of marker genes for defence response. DNA Res. 18(4): 277-289.

(7) *Thellungiella halophila* 完全長 cDNA クローン

This resource has been developed and deposited by Drs. Motoaki Seki, Tetsuya Sakurai and Kazuo Shinozaki, RIKEN Plant Science Center, Yokohama, Japan. The 5'- and 3'-end sequence information was deposited from Dr. Teruaki Taji, Tokyo University of Agriculture. Full-length sequences were obtained under the support from the National Bio-Resource Project of the MEXT, Japan. .

Resource number: pdh00001-
Developer: Drs. Motoaki Seki, Tetsuya Sakurai and Kazuo Shinozaki (RIKEN PSC)
Total number of Clones: 19,429
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of clones available: 19,429 clones
Organism: *Thellungiella halophila*
Vector: pFLCIII (excersized from lambdaFLCIII)
Selection marker: ampicillin
Map and restriction site: Carninci et al. (2001) Genomics 77(1-2): 79-90.
Specific feature: 5'- and 3' -sequences have been characterized. For some clones, full-length sequence is available.
Specific conditions for distribution:

(1) The RECIPIENT can use the BIOLOGICAL RESOURCE for research only.
(2) The RECIPIENT agrees to refer the RIKEN PSC as a developer and the RIKEN BRC as a provider of the BIOLOGICAL RESOURCE in any publication reporting use of it.
(3) Following manuscript should be referred in the publication on scientific journal.
Taji, T., Sakurai, T., Mochida, K., Ishiwata, A., Kurotani, A., Totoki, Y., Toyoda, A., Sakaki, Y., Seki, M., Ono, H., Sakata, Y., Tanaka, S. and Shinozaki, K. Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, *Thellungiella halophila*.
(4) The RECIPIENT should not distribute or transfer the BIOLOGICAL RESOURCE to any other laboratory or organization.
(5) The RECIPIENT agrees not to use the BIOLOGICAL RESOURCE for constructing microarray or macroarray without the agreement from the RIKEN PSC.
(6) The RECIPIENT can receive up to 10 clones in one order and up to 100 clones in one year as the BIOLOGICAL RESOURCE.
(For detail please send e-mail to plant@brc.riken.jp)

(8) *Striga hermonthica* 完全長 cDNA クローン

This resource has been deposited from Drs. Satoko Yoshida and Ken Shirasu (RIKEN Plant Science Center (PSC)).

Resource number: pdw00001-35198
Developer: Drs. Satoko Yoshida and Ken Shirasu (RIKEN PSC)
Total number of Clones: 37,632
Style of distribution: Approx. 100 ng of lyophilized plasmid is provided.
Number of clones available: 35,198
Organism: *Striga hermonthica*
Vector: pAL17.3

Selection marker: ampicillin
Map and restriction site: Please visit website http://brc.riken.jp/lab/epd/Eng/catalog/pAL17-3-1.pdf.
Specific feature: 5'- and 3'-sequences have been characterized (full-length cDNA clone)
Specific conditions for distribution: Following manuscript should be referred in the publication on scientific journal.
Yoshida et al. (2010) A full-length enriched cDNA library and expressed sequence tag analysis of the parasitic weed, *Striga hermontica*. BMC Plant Biology 10: 55.

(9)その他の遺伝子材料

Most of the materials in this category have been deposited to RIKEN Plant Cell Bank. RIKEN BRC started distribution of the materials from Apr. 2001. The most requested material, pYLTAC7, is explained below. Information for other materials is on our HP.

Resource number: rpd00105
Resource name: pYLTAC7
Developer: Dr. Daisuke Shibata
Depositor: Mitsui Chemical Co.
Type of resource: vector DNA (TAC vector)
Size: 22.5 kbp
Style of distribution: Approx. 1 micro gram of lyophilized DNA is provided.
Selection marker: kanamycine
Map and restriction site: Please see the figure in the manuscript below.
Accession no.: AB020028
Specific feature: Able to accept and maintain large genomic DNA fragment in both *E. coli* and *Agrobacterium tumefaciens*.
Specific conditions for distribution:
①The recipient should obtain approval of the depositor using the approval form prior to entering the agreement with the RIKEN BRC.
②The BIOLOGICAL MATERIAL should not be used for any commercial purpose. For detail please send E-mail to plant@brc.riken.jp.
Reference:
①Liu Y-G, Shirano Y., Fukaki H., Yanai Y., Tasaka M., Tabata S. and Shibata D. (1999) PNAS 96 (11): 6535-6540.