

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO	
RAD: 14-188876- -3	FECHA: 2016-04-13 12:44:13
DEP: 2020 DIRECCION DE NUEVAS CREACIONES	EVE: 378 FASE NACIONAL INCLUIDO CAPITULO I
TRA: 11 PCT-PATENTE DE INVENCION CAPITULOS I Y II	FOLIOS: 9
ACT: 519 TRASLADOINFORME	

DIRECCIÓN DE NUEVAS CREACIONES

2020
Bogotá, D.C.,

Abogado(a)/Señor(a)
LUZ CLEMENCIA DE PÁEZ

Asunto: Radicación: 14-188876- -3
Trámite: 11
Evento: 378
Actuación: 519
Oficio: 4190
Folios: 9

Patente de Invención	X			Patente de Modelo de Utilidad	
Vía Nacional					
Vía PCT (Fase Nacional)	X	Capítulo I	X	Capítulo II	
No. Solicitud Internacional	PCT/US2013/024498				
Fecha de Presentación Internacional	01/02/2013				

Como resultado del examen de fondo realizado, con fundamento en el Artículo 45 de la Decisión 486 de la Comisión de la Comunidad Andina, se comunica:

1. Documentos estudiados

Descripción:	Radicado N° 14-188876-00000-0000	28/Agosto/2014
Reivindicaciones:	Radicado N° 14-188876-00000-0000	28/Agosto/2014
Dibujos:	Radicado N° 14-188876-00000-0000	28/Agosto/2014
Secuencias:	Radicado N° 14-188876-00000-0000	28/Agosto/2014
Prioridad:	US61/593,555	01/Febrero/2012
	US61/625,222	17/Abril/2012

2. Análisis de la Prioridad

Se acepta la reivindicación de prioridad porque ésta solicitud fue presentada dentro del plazo establecido (Art. 9 D 486) y su contenido técnico corresponde con el de la prioridad reivindicada.

3. Objeto de la invención

De acuerdo con lo establecido en el numeral 1.2.2.2 del Título 10 de la Circular Única para efectos del examen de patentabilidad, se tendrá en cuenta la tasa pagada por el solicitante al momento de comenzar el examen para las reivindicaciones adicionales; esto es que cuando la solicitud contenga más de diez (10) reivindicaciones y no se haya pagado la tasa complementaria, sólo se estudiarán las cubiertas por la tasa pagada. En el presente caso se estudiarán las reivindicaciones 1 a 52 del capítulo reivindicatorio del Radicado N° 14-0188876-00000-0000.

Título de la solicitud: "PÉPTIDO DE TRÁNSITO AL CLOROPLASTO"

El problema planteado en esta solicitud consiste en la necesidad continua de desarrollar mecanismos que permitan la obtención de plantas transformadas de interés agronómico tolerantes a herbicidas.

Para resolver este problema técnico la solicitud en estudio proporciona moléculas de ácidos nucleicos que codifican péptidos de tránsito TraP14 y TraP24, que pueden usarse para dirigir cualquier polipéptido a un plastidio en un amplia gama de especies de plantas.

El objeto de la presente solicitud se relaciona con la Clasificación Internacional de Patentes (CIP): A01H 5/00, C12N 15/29 // 15/63 // 15/82.

4. No es una invención (Art 15 D 486 literal (b))

El objeto de las reivindicaciones 1 a 13 no se considera una invención, por cuanto en su encabezado a pesar de reclamar una molécula de ácido nucleico aislada, su única característica técnica esencial corresponde al péptido codificado por dicha molécula de ácido nucleico según las secuencias de aminoácidos SEC ID NO: 1, 2 y 4, las cuales como se indica en el capítulo descriptivo corresponden a un péptido de tránsito aislado de la proteína deshidrogenasa de glicerol-3-fosfato (GPDH) de *Dunaliella salina* (Pág. 6, Párr. [0017]); una proteína 3-enolpiruvilsiquimato-5-fosfato sintetasa (EPSPS) de *Dunaliella salina* (Pág. 6, Párr. [0017]); y una proteína EPSPS de *Chlamydomonas reinhardtii* (Pág. 7, Párr. [0018]) respectivamente, tal y como se encuentra en la naturaleza o aquel que pueda ser aislado (ver alineamientos). Cabe resaltar que dichas reivindicaciones hacen referencia al enlace gramatical "contiene", el cual es un termino no limitativo el cual puede incluir cualquier otro elemento no mencionado en la reivindicaciones tal como el resto de la proteína EPSPS. Por lo anterior no pueden ser objeto de patente de conformidad con lo dispuesto en el artículo 15 lit. b) de la referida Decisión 486.

Query: SEC ID NO: 1

Sbjct: gb|ACD84643.1| glycerol-3-phosphate dehydrogenase [*Dunaliella*]

Range 1: 1 to 47 GenPept Graphics ▼ Next Match ▲ Previous Match				
Score	Expect	Identities	Positives	Gaps
153 bits(342)	9e-39	47/47(100%)	47/47(100%)	0/47(0%)
Query 1	MILGSSPTLPHASHPARPGPARPDRAAALAGSTRQLLRGTFRPNPAP			47
	MILGSSPTLPHASHPARPGPARPDRAAALAGSTRQLLRGTFRPNPAP			
Sbjct 1	MILGSSPTLPHASHPARPGPARPDRAAALAGSTRQLLRGTFRPNPAP			47

Query: SEC ID NO: 2

Sbjct: gb|ABM68632.1| plastid EPSP synthase [*Dunaliella salina*]

Range 1: 1 to 71 GenPept Graphics ▼ Next Match ▲ Previous Match				
Score	Expect	Identities	Positives	Gaps
229 bits(516)	2e-63	71/71(100%)	71/71(100%)	0/71(0%)
Query 1	MLARQGGSLRASQCNAGLARRVEVGALVVPRPISVNDVVPHVYSAPLSVARRSCSKSSIR			60
	MLARQGGSLRASQCNAGLARRVEVGALVVPRPISVNDVVPHVYSAPLSVARRSCSKSSIR			
Sbjct 1	MLARQGGSLRASQCNAGLARRVEVGALVVPRPISVNDVVPHVYSAPLSVARRSCSKSSIR			60
Query 61	STRRLQTTVCS	71		
	STRRLQTTVCS			
Sbjct 61	STRRLQTTVCS	71		

5. Excepción a la Patentabilidad (Art 20 D 486 literales (b) y (c))

El objeto de las reivindicaciones 31 a 37, 45 a 51 no es patentable de acuerdo con el Art citado, ya que hacen referencia a un material de planta seleccionado del grupo que consiste de una célula de una planta, un tejido de una planta, un cultivo de tejidos de plantas, un cultivo de callo, una parte de la planta, y una planta entera. Se entiende que las células vegetales, hacen parte de una planta completa, comprendiendo dicha planta de cultivo una pluralidad de células vegetales, por lo cual el alcance de estas reivindicaciones es una excepción a la patentabilidad.

El objeto de las reivindicaciones 38 a 43 y 52 no es patentable de acuerdo con el Art citado, ya que hacen referencia a un método para producir un material de una planta transgénica seleccionado del grupo que consiste de una célula de una planta, un tejido de una planta, un cultivo de tejidos de plantas, un cultivo de callo, una parte de la planta, y una planta entera; los cuales son procesos esencialmente biológicos. Si bien el solicitante obtuvo una planta modificada la cual presenta resistencia a a los herbicidas, los pasos esenciales de “plantar, cultivar, producir una planta, cosechar” corresponden a procesos esencialmente biológicos.

6. De la solicitud de patente

Reivindicaciones (Art 30 D 486, Art 22 PCT)

- 1- Las reivindicaciones 14 a 17 no son claras porque no definen una molécula de ácido nucleico en términos sus características técnicas esenciales, especificando la secuencia de polinucleótidos completa con su respectivo SEC ID No.
- 2- La reivindicación 14 no es clara ni concisa porque define una molécula de ácido nucleico en términos de que esta codifica un péptido que contiene una primera y una segunda secuencia de aminoácidos contiguas, en donde dicho péptido se encuentra definido en términos de porcentajes de similitud respecto a la SEC ID NO: 2, por lo cual se podría obtener un gran numero de ácidos nucleicos, los cuales no se encuentran comprendidos dentro del objeto de la solicitud, ni presentan sustento en la descripción de que cualquier

modificación en la molécula de ácido nucleico resulte en una estructura con la actividad deseada. Se sugiere a la solicitante especificar la secuencia de nucleótidos que codifica dicho péptido y caracterizar las posibles variantes estructurales de la secuencias citadas en esta reivindicación por sus secuencias completas, las cuales además debe ser adjuntadas en un listado aparte con su respectivo SEQ ID NO, dichas variantes deben estar completamente sustentadas en la descripción. Por último se recuerda a la solicitante que no es correcto hacer definiciones indicando porcentajes de similitud, puesto que esta definición no permite establecer la secuencia aminoácida exacta a la que se refiere. Adicionalmente no se indica la secuencia de nucleótidos de interés que se une operativamente a la secuencia de nucleótidos que codifica el péptido. Se le sugiere a la solicitante definir la invención en la reivindicación independiente, en términos de un sistema de expresión de plantas transgénicas, tal como un evento de transformación estable que contiene un elemento de expresión génica fusionada a una secuencia de un transgén importante desde el punto de vista agronómico, que comprenda por ejemplo las secuencias de aminoácidos de los péptidos de tránsito al cloroplasto quiméricos TraP14 (SEC ID NO: 3) y Tra P24 (SEC ID NO: 6), o las secuencias de nucleótidos que codifica un péptido TraP14 etiquetado como TraP14v2 (SEC ID NO: 7), y un péptido TraP24 etiquetado como TraP24v2 (SEC ID NO: 8); los cuales se encuentran fusionados a rasgos tolerantes a los herbicidas por ejemplo los genes *dgt-32* y *dgt-33*, tal y como se evidencia en los múltiples ejemplos de producción de eventos de plantas transgénicas con constructos de expresión, en el capítulo descriptivo.

- 3- La reivindicación 14, no es clara porque el término “*por lo menos*”, es impreciso, por lo cual no permite distinguir la invención del estado de la técnica. Se sugiere sustituirlo por un término preciso o un rango concreto.
- 4- La reivindicación 15 no es clara porque no define una molécula de ácido nucleído en términos de sus características técnicas esenciales, sino que se reclama en función de la secuencia de aminoácidos contigua de un péptido de tránsito al cloroplasto distinta de la SEC ID NO: 2. En este caso, se sugiere modificar dicha reivindicación especificando la secuencia de la molécula de ácido nucleído completa con su respectivo SEC ID No.
- 5- Las reivindicaciones 18 a 29 no son claras porque no definen un polipéptido en términos de sus características técnicas esenciales, sino que se reclaman en función de la ruta metabólica o de sus posibles transformaciones. En este caso, se sugiere modificar dichas reivindicaciones especificando la secuencia de aminoácidos para cada polipéptido con su respectivo SEC ID No.
- 6- La reivindicaciones 19 a 29 no son claras porque definen un polipéptido codificado por la molécula de ácido nucleico, en términos de su resultado alcanzar que da cuenta de su mecanismo de acción, al indicar que está dirigido a un plastidio en una célula que contiene plastidios; que contiene un péptido de tránsito al cloroplasto que se elimina cuando el polipéptido está dirigido al plastidio, o que permanece cuando el péptido de tránsito al cloroplasto se retira, en el que el péptido dirigido al cloroplasto está codificado por la secuencia de nucleótidos codificantes de interés; que codifica un péptido biológicamente activo fluorescente que es una enzima seleccionado de un grupo de ocho opciones, el cual está implicado en un proceso de resistencia a herbicidas entre otros. En este caso las reivindicaciones incluirían no sólo la solución propuesta por el solicitante, sino todas las alternativas presentes o futuras que lleguen a ese resultado. Se le

recomienda a la solicitante definir el polipéptido codificado por la molécula de ácido nucleico, exclusivamente en términos de sus características técnicas esenciales.

- 7- La reivindicación 30 no es clara porque no define el vector especificando el tipo de vector y la secuencia recombinante que contiene. Se sugiere a la solicitante modificar la redacción de la reivindicación mencionada y proveer la secuencia de polinucleótidos completa con su respectivo SEQ ID No.
- 8- La reivindicación 44 no es clara porque se define un producto de un commodity en términos del método de producción de un material de una planta transgénica, y no se define a partir de sus características estructurales. Adicionalmente no se presenta sustento en la descripción con pruebas técnicas para la obtención de productos destinados a uso comercial derivados de una planta transgénica.

7. Unidad de invención (Art 25 D 486)

La solicitud no cumple con el requisito de unidad de invención porque se refiere a 2, grupos inventivos.

Los grupos inventivos están definidos por las siguientes características esenciales

- I. Moléculas de ácido nucleico aisladas que codifican péptidos de transito al cloroplasto, que están operativamente ligadas a una secuencia de nucleótidos de interés agronómico (Reivindicaciones 14 - 30).
- II. Un producto de un commodity producido a partir del material de una planta transgénica (Reivindicación 44).

Cabe resaltar que no existe unidad de invención porque los dos grupos pertenecen a campos técnicos distintos. Además el grupo inventivo II no tiene sustento en la descripción, porque no se divulga la obtención con pruebas técnicas de productos de uso comercial a partir de dichas plantas.

Se sugiere presentar las respectivas solicitudes divisionales para cada uno de los grupos inventivos presentados en esta solicitud, o se sugiere al solicitante restringir la materia a patentar en un solo grupo inventivo, eliminando de la solicitud los otros grupos inventivos.

8. Determinación del Estado de la Técnica

El estado de la técnica se determinó con base en la fecha de presentación de la solicitud de prioridad: 1 de febrero de 2012, y se encontraron los siguientes documentos que anticipan el objeto de esta solicitud:

Ítem	Documento	Título	Fecha de Publicación
D1	US20110023179	"Plastid transit peptides derived from lower photosynthetic eukaryotes and methods"	27/Enero/2011
D2	WO2010078156	"Genetically engineered herbicide resistant algae"	22/Diciembre/2009

El documento D1¹ divulga constructos de ADN que comprenden una secuencia de nucleótidos que codifica para péptidos de transito a plastidios, los cuales se encuentran unidos operativamente a una secuencia de nucleótidos que codifica un péptido de interés. Se presentan composiciones que comprenden casetes de expresión, útiles en la transformación de un material de una planta (Abstract).

El documento D2² divulga un polinucleótido aislado útil para la transformación de un alga, donde dicho polinucleótido comprende una o más secuencias de ácido nucleico que codifican para una proteína que confiere resistencia a herbicidas (Pág. 1, Párr. [0006]). Adicionalmente el polipéptido comprende una secuencia que codifica un péptido de tránsito al cloroplasto (Pág. 4, Párr. [0017]).

9. Examen de Patentabilidad (Art 14 D486)

Nivel inventivo (Art18 D486)

La reivindicación 14 consiste en *“Una molécula de ácido nucleico aislada que contiene: una secuencia de nucleótidos que codifica un péptido que contiene una secuencia de aminoácidos contigua que es, por lo menos, un 80% idéntica a una secuencia de aminoácidos contigua dentro de la SEC ID NO: 2, en el que el péptido contiene además una segunda secuencia de aminoácidos contigua que es, por lo menos, un 80% idéntica a una secuencia de aminoácidos contigua de un péptido de tránsito al cloroplasto distinto a la SEC ID NO: 2, en el que la secuencia de nucleótidos que codifica el péptido está operativamente unido en marco a una secuencia de nucleótidos de interés”* (Radicado N° 14-0188876-00000-0000).

Comparación de las características técnicas esenciales, con las del estado de la técnica:

Características esenciales	D1	D2
Molécula de ácido nucleico aislado contiene:	Constructo de ADN que comprende (Pág. 2, Párr. [0018] - Pág. 24, Rv. 1).	Polinucleótido aislado (Pág. 94, Rv. 1).
Secuencia de nucleótidos que codifica un péptido que contiene una secuencia de aminoácidos contigua que es, por lo menos, un 80% idéntica a una secuencia de aminoácidos contigua dentro de la SEC ID NO: 2.	Secuencia de nucleótidos que codifica un péptido dirigido a un plástido (Pág. 2, Párr. [0018] - Pág. 24, Rv. 1). Secuencia de nucleótidos SEC ID NO: 20 la cual presenta un 100% de identidad y cobertura con la SEC ID NO: 2 de la solicitud (ver alineamientos).	Comprende una secuencia de ácidos nucleicos que codifican una proteína que confiere resistencia a herbicidas (Pág. 94, Rv. 1).
Contiene además una segunda secuencia de aminoácidos contigua que es, por lo menos, un 80% idéntica a una secuencia de aminoácidos contigua de un péptido de tránsito al cloroplasto distinto a la SEC ID NO: 2.	Secuencia de nucleótidos que codifica un polipéptido heterólogo (Pág. 2, Párr. [0018]), el cual comprende un elemento regulatorio para facilitar la transcripción, traducción o el transporte del polipéptido de interés (Pág. 7, Párr. [0047]).	Comprende una o mas secuencias de ácidos nucleicos que codifican una proteína que confiere resistencia a herbicidas (Pág. 94, Rv. 1).
Secuencia de nucleótidos que	Secuencia de nucleótidos que se encuentra operativamente ligada a	Constructos de ADN recombinantes que comprenden

1<http://worldwide.espacenet.com/publicationDetails/biblio?CC=US&NR=2011023179A1&KC=A1&FT=D>

2<http://worldwide.espacenet.com/publicationDetails/biblio?CC=WO&NR=2010078156A1&KC=A1&FT=D>

codifica el péptido, está operativamente unida a una secuencia de nucleótidos de interés	una secuencia de polinucleótidos que codifica un péptido de interés (Pág. 24, Rv. 1).	marcadores seleccionables y uno o mas genes de interés para la transformación del cloroplasto (Pág. 28, Párr. [00166]).
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El documento D1 se considera el estado de la técnica cercano a la invención definida en la reivindicación 14 porque divulga un constructo de ADN que comprende elementos regulatorios para facilitar la transcripción, traducción o el transporte del polipéptido de interés; una secuencia de nucleótidos que codifica un péptido dirigido a un plástido, la cual se encuentra operativamente ligada a una secuencia de nucleótidos que codifica un polipéptido de interés (Pág. 7, Párr. [0047]). El péptido de transito a cloroplastos es derivado de un organismo eucariótico fotosintético inferior seleccionado del grupo que comprende algas verdes de los géneros *Chlamydomonas* y *Dunaliella* (Pág. 2, Párr. [0015]). En realizaciones específicas los péptidos de transito a cloroplastos pueden ser encontrados en genes, de los cuales se sabe están codificados en el núcleo de una célula huésped, y que después de la traducción pueden ser orientados a organelos fotosintéticos de la célula huésped, entre los que se destacan la proteína deshidrogenasa glicerol-3-fosfato (GPDH) y la proteína 3-enolpiruvilsiquimato-5-fosfato sintetasa (EPSPS) de las especies *Chlamydomonas reinhardtii* y *Dunaliella salina* respectivamente (Pág. 3, Párr. [0019]). Además se divulga el desarrollo de un método de de expresión de un polipéptido de interés en una planta monocotiledónea o dicotiledónea, que comprende introducir en dicha planta, un constructo de ADN que contiene una secuencia de polinucleótidos que codifica un péptido de transito a un plástido, la cual se encuentra unida operativamente a un gen tolerante a herbicidas (Pág. 9, Párr. [0063 - 0068]).

Cabe resaltar que el documento D1 divulga la secuencia de aminoácidos SEC ID NO: 20 correspondiente a un péptido de transito a cloroplasto derivado de la proteína EPSPS de *Dunaliella salina*, la cual presenta un 100% de identidad y cobertura (ver alineamientos) respecto a la SEC ID NO: 2 reclamada en la solicitud.

CLUSTAL O(1.2.1) multiple sequence alignment

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US_2011_0023179_A1_20      MLARQGGSLRASQCNAGLARRVEVGALVVPRPISVNDVVP HVYSAPLSVARRSCSKSSIR
WO_2013_116773_2          MLARQGGSLRASQCNAGLARRVEVGALVVPRPISVNDVVP HVYSAPLSVARRSCSKSSIR
                           *****

US_2011_0023179_A1_20      STRRLQTTVC SATLAHSA
WO_2013_116773_2          STRRLQTTVC -----
                           *****
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La diferencia entre la molécula de ácido nucleico aislado, definida en la reivindicación 14 y el constructo de ADN divulgado en el documento D1, consiste en que la molécula de ácido nucleico aislado contiene además una secuencia de polinucleótidos que codifica una segunda secuencia de aminoácidos contigua a un péptido de tránsito al cloroplasto distinta de la SEC ID NO: 2, mientras que el constructo divulgado en el documento D1, comprende elementos regulatorios para facilitar la transcripción, traducción o el transporte del polipéptido de interés; y una secuencia de nucleótidos que codifica un péptido dirigido a un plástido, operativamente ligada a una secuencia de nucleótidos que codifica un polipéptido de interés.

El efecto que logra el introducir una secuencia de polinucleótidos que codifica una segunda secuencia de aminoácidos contigua de un péptido de tránsito al cloroplasto, consiste en dirigir una molécula que comprende un péptido de tránsito, unida operativamente a un péptido biológicamente activo (implicado en un proceso de resistencia a herbicidas de interés), a plástidos tales como un cloroplasto, en una célula de una planta monocotiledónea o dicotiledónea. Cabe resaltar que el documento D1 demuestra a partir de pruebas técnicas, la importación de proteínas heterólogas a los cloroplastos de células de plantas monocotiledóneas (maíz) y dicotiledóneas (tabaco), por medio del desarrollo de un constructo de expresión que comprende una secuencia de polinucleótidos que codifica un péptido de tránsito al cloroplasto, y un gen tolerante a herbicidas (Párr. [0110 – 0122], Ejemplo 4 y 5; Pág. 24, Rv. 6 – 10); por lo cual no hay evidencia de un efecto técnico inesperado ni sorprendente a la luz de las enseñanzas del documento D1.

Por lo tanto, el problema técnico objetivo que pretende resolver esta invención se puede formular así: Cómo modificar el constructo de ADN divulgado en D1, para producir un polinucleótido que permita la obtención de plantas de interés agronómico tolerantes a herbicidas.

Sin embargo el documento D2 ya sugería el desarrollo de un polinucleótido que comprende una o mas secuencias de ácidos nucleicos que codifican para la proteína 3-enolpiruvilsiquimato-5-fosfato sintetasa (EPSPS), que confiere resistencia a herbicidas tales como el glifosato (Pág. 8, Párr. [0036]), donde dicho polinucleótido además comprende una secuencia que codifica un péptido de tránsito al cloroplasto, útil para la transformación de organismos eucarióticos fotosintéticos (Pág. 94, Rv.1 - Pág. 98, Rv.27). Adicionalmente se afirma que la molécula de ADN recombinante comprende elementos regulatorios de la transcripción para la expresión del polinucleótido, y secuencias que codifican polipéptidos reporteros detectables tal como una proteína verde fluorescente (Pág. 35, Párr. [00193] - Pág. 101, Rv.47).

Por lo tanto, la persona del oficio normalmente versada en la materia, incluiría las secuencias de polinucleótidos que codifican para la proteína EPSPS que confiere resistencia a herbicidas tales como el glifosato divulgadas en el documento D2, en el constructo de ADN que comprende una secuencia de nucleótidos que codifica un péptido dirigido a un plástido, unida operativamente a una secuencia de polinucleótidos que codifica un péptido de interés divulgado en el documento D1, para llegar así al objeto de la solicitud, por lo cual se considera obvia.

En consecuencia, la reivindicación 14 de acuerdo con lo divulgado en los documentos D1 y D2, carece de nivel inventivo.

Las reivindicaciones dependiente 15 a 30 no mencionan alguna característica que haga inventiva la molécula de ácido nucleico aislada de la reivindicación 14, por lo cual se considera que tampoco tienen nivel inventivo.

10. Conclusión

Los requisitos de Patentabilidad de la presente solicitud están afectados así:

Ítem	Documento	Reivindicaciones afectadas	Requisito que afecta
D1	US20110023179	14 - 30	Nivel inventivo
D2	WO2010078156	14 - 30	Nivel inventivo

En cumplimiento del artículo 45 de la Decisión 486 de la Comisión de la Comunidad Andina, se le indica que debe dar respuesta dentro del término de sesenta (60) días contados a partir de la fecha de notificación de la presente comunicación. En caso de no dar respuesta al presente requerimiento, o si a pesar de la respuesta subsistieran los impedimentos para la concesión, se denegará la patente.

Si como respuesta a este requerimiento el solicitante llegara a modificar: i) el capítulo reivindicatorio, ii) la descripción de la invención a proteger, iii) o presente un nuevo capítulo reivindicatorio, y desee que se realice un nuevo examen de patentabilidad a esta modificación, no deberá pagar la tasa de modificación voluntaria pero sí la correspondiente a la tasa de examen de patentabilidad. En todo caso, el número de requerimientos por no patentabilidad estará supeditado a que el término del estudio de patentabilidad no sea superior a 18 meses, contados desde la publicación de la solicitud de patente de invención. Adicionalmente, se le recuerda al solicitante que si como respuesta a este requerimiento llegara a modificar el capítulo reivindicatorio y éste contenga más de diez (10) reivindicaciones deberá pagar la tasa por reivindicación adicional.

Notifíquese el presente oficio conforme a lo dispuesto en el numeral 5.2, literal e), del capítulo quinto del título primero de la Circular Única No. 10 de 2001.



JOSÉ LUIS SALAZAR LÓPEZ
Director de Nuevas Creaciones (c)

El anterior requerimiento fue notificado por fijación en lista, de fecha 2016-04-19

Elaboró: Mario Andres Forero

Revisó: Dayron Alexander Ramirez Reyes

INFORME DE BÚSQUEDA DE PATENTES PARA EL Radicado N° 14-0188876-00000-0000

CRITERIOS PARA LA BÚSQUEDA (anexar pantallazo o reporte en PDF, junto con los boleanos utilizados)

Palabras clave utilizadas	Polynucleotide comprising chloroplast transit peptide, recombinant nucleic acid molecule, chloroplast and/or other plastid transformation, EPSPS.
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CLASIFICACIONES INTERNACIONALES UTILIZADAS PARA LA BÚSQUEDA	A01H 5/00, C12N 15/29 // 15/63 // 15/82.
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BASES DE DATOS CONSULTADAS.

Patentscope	Google/patents		
NCBI	PatBase		
Espacenet	ScienceDirect		
Lens			

INFORMES DE EXÁMENES REALIZADOS EN OTRAS OFICINAS (documentos patentes, literatura no patente etc...)

Oficina	Fecha del examen o de reporte de búsqueda de documentos	Anterioridades encontradas para el examen o reportados en el examen de búsqueda(relacionarlos todos)	Reiv. afectadas	RELEVANCIA (requisito que afecta)	FUERON TENIDOS EN CUENTA PARA EL EXAMEN EN LA OFICINA COLOMBIANA	
					SI	NO
INTERNATIONAL SEARCH REPORT KOREAN INTELLECTUAL PROPERTY OFFICE	02/Junio/2013	NCBI, GENE BANK ACCESSION NO. ABM68632	1 - 7, 10 - 15, 17 - 19, 22 - 52 / 8, 9, 16, 20 - 21	Nivel inventivo/ Documento tipo A		X
		WO2010078156	1 - 7, 10 - 15, 17 - 19, 22 - 52	Nivel inventivo	X	
		US20100029485	1 - 52	Documento tipo A		X
		US20030077801	1 - 52	Documento tipo A		X

DOCUMENTOS ADICIONALES ENCONTRADOS POR EL EXAMINADOR DE ACUERDO A LOS CRITERIOS DE BÚSQUEDA.

US20110209246
US7517684
WO2009099580
US7507875
US2009093366
US2007300326
US7169970
US5510471
US20110023179
US5633435
WO2007053482
US2003009783
WO0012732
WO0031282
US2006242727
US2010186125
US2011321187

BÚSQUEDA DE SECUENCIAS					
Número de depósito / patente y N° de secuencia					
% de identidad					
SEQ ID NO (de la solicitud)	NCBI	The Lens	EMBL-EBI	DDJB	Genome Quest
SEC ID NO: 1	gb ACD84643.1 100% de identidad y cobertura				
SEC ID NO: 2	gb ABM68632.1 100% de identidad y cobertura				

Búsqueda de Secuencias

SEC ID NO: 1

Alignments Download GenPept Graphics Distance tree of results Multiple alignment							
	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycerol-3-phosphate dehydrogenase [Dunaliella viridis]	153	153	100%	9e-39	100%	ACD84643.1
☐	transcriptional regulator [Streptomyces griseoaurantiacus]	43.2	43.2	65%	0.050	56%	WP_006142902.1
☐	MULTISPECIES: peptidase S41 [Streptomyces]	41.9	41.9	42%	0.13	71%	WP_039654429.1
☐	hypothetical protein [Methylobacterium sp. 4-46]	41.5	41.5	42%	0.16	67%	WP_012336288.1
☐	two-component sensor histidine kinase [Enterorhabdus caecimuris]	41.5	41.5	82%	0.19	51%	WP_022926700.1
☐	hypothetical protein C811_02435 [Enterorhabdus caecimuris B7]	41.5	41.5	82%	0.19	51%	EOS49970.1
☐	hypothetical protein [Georgenia sp. SUBG003]	41.0	41.0	42%	0.25	70%	WP_043497685.1
☐	40-residue YVTN family beta-propeller repeat-containing protein [Catenulispora acidiphila]	40.6	40.6	51%	0.35	72%	WP_015793333.1
☐	PREDICTED: LOW QUALITY PROTEIN: serine palmitoyltransferase small subunit B [Microcebus murinus]	40.1	40.1	70%	0.46	58%	XP_012638233.1
☐	serine/threonine protein kinase [Frankia sp. DSM 45899]	40.1	40.1	46%	0.50	63%	CUU56462.1

SEC ID NO: 2

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	plastid EPSP synthase [Dunaliella salina]	229	229	100%	2e-63	100%	ABM68632.1
☐	histidine kinase [Frankia sp. QA3]	40.1	40.1	29%	1.1	64%	WP_051054678.1
☐	histidine kinase [Frankia sp. Avcl1]	40.1	40.1	29%	1.1	64%	WP_055750399.1
☐	histidine kinase [Frankia sp. ACN1ag]	40.1	40.1	29%	1.1	64%	WP_055407881.1
☐	MULTISPECIES: histidine kinase [Frankia]	40.1	40.1	29%	1.1	64%	WP_044888196.1
☐	histidine kinase [Frankia alni]	40.1	40.1	29%	1.1	64%	WP_041939674.1
☐	osmosensitive K+ channel histidine kinase [Frankia sp. QA3]	40.1	40.1	29%	1.1	64%	EIV96348.1
☐	sensory histidine kinase in two-component regulatory system with KdpE, regulation of potassium translocation [Frankia alni ACN14a]	40.1	40.1	29%	1.1	64%	CAJ63937.1
☐	hypothetical protein M770_34855 [Pseudomonas aeruginosa VRFA03]	37.5	37.5	32%	6.9	65%	EQL42751.1
☐	sugar phosphotransferase [Streptomyces aurantiacus]	37.1	37.1	47%	9.6	56%	WP_055507269.1

SEC ID NO: 3

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	plastid EPSP synthase [Dunaliella salina]	135	135	66%	2e-31	100%	ABM68632.1
☐	glycerol-3-phosphate dehydrogenase [Dunaliella viridis]	77.5	77.5	37%	1e-12	100%	ACD84643.1
☐	LacI family transcriptional regulator [Frankia sp. EUN1f]	40.1	40.1	37%	0.83	71%	WP_006540825.1
☐	salinity inducible transcription factor ERF4 [Triticum aestivum]	37.9	37.9	24%	3.8	80%	AFN02502.1
☐	VWA domain-containing protein [Rhizoctonia solani AG-1 IA]	37.5	37.5	62%	5.7	52%	ELU39304.1
☐	PREDICTED: LOW QUALITY PROTEIN: signal peptide, CUB and EGF-like domain-containing protein 1 isoform X1 [Ovis aries]	37.5	37.5	22%	5.8	86%	XP_014949490.1
☐	hypothetical protein [Streptomyces almqvistii]	37.1	37.1	25%	7.0	75%	WP_055496190.1
☐	hypothetical protein [Streptomyces albus]	37.1	37.1	25%	7.7	75%	WP_052439612.1
☐	hypothetical protein ADL27_51855 [Streptomyces sp. NRRL F-6602]	37.1	37.1	25%	7.7	75%	KPC73681.1
☐	MULTISPECIES: hypothetical protein [Streptomyces]	37.1	37.1	25%	7.7	75%	WP_051719333.1

Alignments  Download  GenPept  Graphics  Distance tree of results  Multiple alignment 						
Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 111602 from patent US 7214786	32.7	32.7	24%	1.9	73%	ABT24132.1
☐ Sequence 1744 from patent US 8362325	32.2	32.2	29%	2.8	61%	AGF07890.1
☐ Sequence 27481 from patent US 7517684	30.9	30.9	30%	7.0	63%	ACQ34967.1
☐ Sequence 26330 from patent US 7517684	30.9	30.9	29%	7.1	65%	ACQ33816.1
☐ Sequence 18656 from patent US 7517684	30.9	30.9	27%	7.3	65%	ACQ26142.1
☐ Sequence 991 from patent US 7507875	30.5	30.5	20%	9.7	71%	ACQ14120.1
☐ Sequence 221556 from patent US 9029636	30.5	30.5	30%	9.9	68%	AMJ00323.1

SEC ID NO: 4

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus palmeri]	218	218	100%	7e-60	100%	ACV53022.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus palmeri]	214	214	100%	1e-58	99%	ACV53021.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus spinosus]	213	213	98%	4e-58	100%	AHL4484.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus spinosus]	206	206	98%	8e-56	97%	AHL44843.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus spinosus]	206	206	98%	8e-56	97%	AHL44842.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus tuberculatus]	201	201	100%	5e-54	93%	ACV67277.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus tuberculatus]	195	195	100%	1e-51	91%	ACV67278.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus palmeri]	188	188	88%	2e-49	98%	AGE94064.1
☐ 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus palmeri]	183	183	88%	1e-47	97%	AGE94065.1
☐ hypothetical protein SOVF_063390 [Spinacia oleracea]	124	124	100%	1e-27	69%	KNA19236.1

SEC ID NO: 6

Alignments  Download  GenPept  Graphics  Distance tree of results  Multiple alignment 						
Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 7 from patent US 8426204	99	99	72%	2e-22	68%	AGM78067.1
☐ Sequence 10 from patent US 8426204	99	99	72%	9e-22	68%	AGM78070.1
☐ unnamed protein product [synthetic construct]	99	99	72%	1e-21	68%	CAZ39522.1

SEC ID NO: 7

Alignments  Download  GenBank  Graphics  Distance tree of results 						
Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Sequence 41 from Patent EP2846623	344	344	100%	4e-92	100%	LP631909.1
☐ Sequence 38 from Patent EP2846623	344	344	100%	4e-92	100%	LP631906.1
☐ KR 1020150008120-A/41: SYNTHETIC BRASSICA-DERIVED CHLOROPLAST TRANSIT PEPTIDES	344	344	100%	4e-92	100%	LG018565.1
☐ KR 1020150008120-A/38: SYNTHETIC BRASSICA-DERIVED CHLOROPLAST TRANSIT PEPTIDES	344	344	100%	4e-92	100%	LG018562.1
☐ JP 2015514426-A/36: SYNTHETIC BRASSICA DERIVED CHLOROPLAST TRANSIT PEPTIDES	344	344	100%	4e-92	100%	HZ099113.1
☐ JP 2015514426-A/33: SYNTHETIC BRASSICA DERIVED CHLOROPLAST TRANSIT PEPTIDES	344	344	100%	4e-92	100%	HZ099110.1
☐ JP 2015511815-A/41: NOVEL CLASS OF GLYPHOSATE RESISTANCE GENES	344	344	100%	4e-92	100%	HZ042302.1
☐ JP 2015511815-A/38: NOVEL CLASS OF GLYPHOSATE RESISTANCE GENES	344	344	100%	4e-92	100%	HZ042299.1
☐ JP 2015511126-A/41: GLYPHOSATE RESISTANT PLANTS AND ASSOCIATED METHODS	344	344	100%	4e-92	100%	HZ041138.1
☐ JP 2015511126-A/38: GLYPHOSATE RESISTANT PLANTS AND ASSOCIATED METHODS	344	344	100%	4e-92	100%	HZ041135.1

Documento por fuera de la fecha de prioridad

Alignments							 Download	 GenBank	 Graphics	 Distance tree of results		
Description							Max score	Total score	Query cover	E value	Ident	Accession
☐	Sequence 42 from Patent EP2846623						383	383	100%	9e-104	100%	LP631910.1
☐	Sequence 40 from Patent EP2846623						383	383	100%	9e-104	100%	LP631908.1
☐	KR 1020150008120-A/42: SYNTHETIC BRASSICA-DERIVED CHLOROPLAST TRANSIT PEPTIDES						383	383	100%	9e-104	100%	LG018566.1
☐	KR 1020150008120-A/40: SYNTHETIC BRASSICA-DERIVED CHLOROPLAST TRANSIT PEPTIDES						383	383	100%	9e-104	100%	LG018564.1
☐	JP 2015514426-A/37: SYNTHETIC BRASSICA DERIVED CHLOROPLAST TRANSIT PEPTIDES						383	383	100%	9e-104	100%	HZ099114.1
☐	JP 2015514426-A/35: SYNTHETIC BRASSICA DERIVED CHLOROPLAST TRANSIT PEPTIDES						383	383	100%	9e-104	100%	HZ099112.1
☐	JP 2015511815-A/42: NOVEL CLASS OF GLYPHOSATE RESISTANCE GENES						383	383	100%	9e-104	100%	HZ042303.1
☐	JP 2015511815-A/40: NOVEL CLASS OF GLYPHOSATE RESISTANCE GENES						383	383	100%	9e-104	100%	HZ042301.1
☐	JP 201551126-A/42: GLYPHOSATE RESISTANT PLANTS AND ASSOCIATED METHODS						383	383	100%	9e-104	100%	HZ041139.1
☐	JP 201551126-A/40: GLYPHOSATE RESISTANT PLANTS AND ASSOCIATED METHODS						383	383	100%	9e-104	100%	HZ041137.1

Documento por fuera de la fecha de prioridad

Búsqueda en PatBase



Menu - Search - History - Session - Folder - Order Help - Logoff

#	Search query	Results	Options
3	TAC=(((CHLOROPLAST~ AND TRANSIT~ AND PEPTIDE~) AND (ALS~ AND EPSPS~)))	25	View Browse Hits Optimise more...
2	TAC=(((PLASTID~ AND TRANSIT~ AND PEPTIDE~) AND (EXPRESSION~ AND CASSETTES~)))	56	View Browse Hits Optimise more...
1	TAC=(((CHLOROPLAST~ TRANSIT~ PEPTIDE~) AND (DNA~ CONSTRUCT~)))	39	View Browse Hits Optimise more...

8) Family number: 14923366 (US2003077801A)

Similar • Translate • Full-text • Status • Citations    

Title: [EN] Herbicide resistant plants

Abstract: Source: US2003077801A [EN] The present invention provides, inter alia, an isolated polynucleotide comprising a region encoding a **chloroplast transit peptide** and a glyphosate resistant 5-enolpyruvylshikimate phosphate synthase (**EPSPS**) 3' of the **peptide**, the said region being under expression control of a plant operable promoter, with the proviso that the said promoter is not heterologous with respect to the said region, and the **chloroplast transit peptide** is not heterologous with respect to the said synthase. The polynucleotide may comprise the following components in the 5' to 3' direction of transcription: (i) at least one transcriptional enhancer being that enhancing region which is upstream from the transcriptional start of the sequence from which the enhancer is obtained and which enhancer per se does not function as a promoter either in the sequence in which it is endogenously comprised or when present heterologously as part of a construct; (ii) the promoter from the rice **EPSPS** gene; (iii) the rice genomic sequence which encodes the rice **EPSPS chloroplast transit peptide**; (iv) the genomic sequence which encodes the rice **EPSPS**; (v) a transcriptional terminator; wherein the rice **EPSPS** coding sequence is modified in that a first position is mutated so that the residue at this position is Ile rather than Thr and a second position is mutated so that the residue at this position is Ser rather than Pro, the mutations being introduced into **EPSPS** sequences which comprise the following conserved region GNAGTAMRPLTAAV (SEQ ID NO:56) in the wild type enzyme such that modified sequence reads GNAGIAMRSLTAAV (SEQ ID NO:57).

Classifications: [Classification Explorer](#)

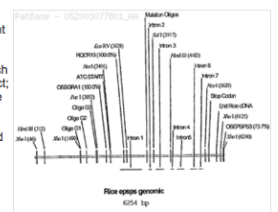
International [IPC s-a](#): A01H5/00 A01N57/20 C12N15/09 C12N15/29 C12N15/31 C12N15/54 C12N15/82 C12N5/10 C12N9/10 (Advanced/Invention); A01H5/00 A01N57/00 C12N15/09 C12N15/29 C12N15/31 C12N15/54 C12N15/82 C12N5/10 C12N9/10 (Core/Invention); A01H C12N (Subclass/Invention)

International [IPC t-n](#): A01H A01H5/00 A01H5/10 A01N57/20 C07H21/04 C12N15/09 C12N15/29 C12N15/31 C12N15/54 C12N15/82 C12N5/04 C12N5/10 C12N9/10 C12N9/16 C12P21/02

CPC: C12N9/1092 C07K2319/00 C12N15/8209 C12N15/8216 C12N15/8275 C12Y205/01019

European: C12N15/82A8 C12N15/82B C12N15/82C8B4A C12N9/10E19 C12Y205/01019 M07K319/00 M12N207/00

US: 435/198 435/196P 435/320.1 435/320.100S 435/410 435/410S 435/69.1 435/69.100S 536/23.2 536/23.200S 536/23.6 536/23.7 536/23.72 536/24.1 536/24.2 800/278 800/278S



44) Family number: 48202245 (US2011023179A)

Similar • Translate • Full-text • Status • Citations    

Title: [EN] **PLASTID TRANSIT PEPTIDES** DERIVED FROM LOWER PHOTOSYNTHETIC EUKARYOTES AND METHODS

Abstract: Source: US2011023179A [EN] Compositions and methods for targeting polypeptides to **plastids** are provided. Compositions comprise **plastid transit peptides** as well as nucleotide sequences encoding such **transit peptides** and variants thereof. Compositions further comprise DNA constructs comprising a nucleotide sequence encoding the **plastid transit peptide** operably linked to a nucleotide sequence encoding a polypeptide of interest. These DNA constructs find use in **expression** and targeting of the polypeptide of interest to a **plastid**. Compositions also comprise **expression cassettes**, vectors, transformed plants, transformed plant cells, and stably transformed plant seeds wherein a polypeptide of interest is targeted to a **plastid** by the **plastid** targeting **peptide** of the invention.

Classifications: [Classification Explorer](#)

International [IPC s-a](#): A01H5/00 C07H21/04 C07K14/195 C07K14/405 C12N15/00 C12N15/31 C12N15/63 C12N15/82 C12N5/10 C12Q1/68 (Advanced/Invention)

CPC: C07K14/405 C12N15/8214 C12N15/8221

European: C07K14/405

US: 435/320.1 435/320.100S 435/419 435/419S 530/324 530/324S 536/23.1 536/23.100S 800/278 800/278P 800/298 800/298S 800/312 800/312S 800/320.1 800/320.100S 800/320.2 800/320.200S

Family: [Family Explorer](#)

Publication number	Publication date	Application number	Application date	Links
AU2010274177 AA	20110127	AU20100274177	20100709	 
CA2768125 AA	20110127	CA20102768125	20100709	 
CN102471778 A	20120523	CN201080032079	20100709	 
EP2456875 A1	20120530	EP20100802659	20100709	 
EP2456875 A4	20130320	EP20100802659	20100709	 
RU2012105754 A	20130827	RU20120105754	20100709	 
US2011023179 AA	20110127	US20100833253	20100709	 
WO11011210 A1	20110127	WO2010US41469	20100709	 

43) Family number: 4268534 (US2011321187A)

Similar • Translate • Full-text • Status • Citations

Title: [EN] PLANT **PLASTID** TRANSFORMATION METHOD

Abstract: Source: US2011321187A [EN] Method for heterologous protein production in plant cell **plastids** comprising introducing into plant cells nucleic acid components that encode heterologous proteins under the control of promoters operative in **plastids**, vectors, host cells, plants and uses thereof.

Classifications: [Classification Explorer](#)

International *IPC* 8-9: A01H1/06 A01H5/00 C07K14/195 C07K14/415 C07K19/00 C12N15/11 C12N15/113 C12N15/62 C12N15/82 C12N15/90 C12N5/10 C12N9/12 (Advanced/Invention);

A01H5/00 C12N15/82 (Core/Invention)

CPC: C07K14/195 C07K14/415 C07K19/00 C12N15/113 C12N15/625 C12N15/8221 C12N15/902 C12N15/8214 C12N15/8216 C12N15/8217 C12N15/8257 C12N9/1276

European: C12N15/82A12 C12N15/82B C12N15/82B2 C12N15/82C4D

US: 435/317.1 435/317.100S 435/320.1 435/320.100S 435/411 435/411S 435/412 435/412S 435/414 435/414S 435/415 435/415S 435/416 435/416S 435/417 435/417S 435/419 435/419S 435/468 435/468S 800/278 800/278P 800/298 800/298S 800/305 800/305S 800/306 800/306S 800/309 800/309S 800/312 800/312S 800/314 800/314S 800/317.1 800/317.100S 800/317.2 800/317.200S 800/317.3 800/317.300S 800/317.4 800/317.400S 800/320 800/320.1 800/320.100S 800/320.2 800/320.200S 800/320.3 800/320.300S 800/320S 800/322 800/322S

Family: [Family Explorer](#)

Publication number	Publication date	Application number	Application date	Links
AU2009321351 AA	20100603	AU20090321351	20091125	  
AU2009321351 AB	20110616	AU20090321351	20091125	  
CA2781900 AA	20100603	CA20092781900	20091125	  
CA2781900 AA	20120524	CA20092781900	20091125	  
EP2367942 A2	20110928	EP20090795795	20091125	  
GB200821516 A0	20081231	GB20080021516	20081125	  
GB2465749 A1	20100602	GB20080021516	20081125	  
GB2465749 B2	20130508	GB20080021516	20081125	  
IN03584CN2011 A	20120907	IN2011CN03584	20110525	  



35) Family number: 34236621 (US2010186125A)

Similar • Translate • Full-text • Status • Citations

Title: [EN] SELECTION METHOD

Abstract: Source: US2010186125A [EN] The invention relates to a method for producing a transformed plant cell. More particularly, the method involves the transformation of a plant cell with a Transformation **Cassette** which is targeted to plant **plastids** and which comprises a selection gene, for example isopentenyl transferase (IPT), and a transgene. After selection for transformed **plastids**, **expression** of a recombinase is induced in the plant cell, which leads to the excision of the selection gene from the **plastid** and the **expression** of the transgene in the **plastid**. The invention also provides cells and plants comprising the Transformation **Cassette**.

Classifications: [Classification Explorer](#)

International *IPC* 8-9: A01G1/00 A01G16/00 A01H5/00 C12N15/09 C12N15/82 C12N5/10 (Advanced/Invention); A01G1/00 A01G16/00 A01H5/00 C12N15/09 C12N15/82 C12N5/10 (Core/Invention)

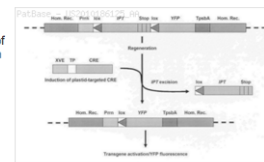
CPC: C12N15/8214 A01H5/00

European: A01H5/00 C12N15/82A12

US: 435/320.1 435/320.100S 435/419 435/419S 435/468 435/468S 800/298 800/298P

Family: [Family Explorer](#)

Publication number	Publication date	Application number	Application date	Links
CA2672710 AA	20090615	CA20072672710	20071214	  
EP2126098 A1	20091202	EP20070848525	20071214	  
EP2126098 B1	20150909	EP20070848525	20071214	  
GB200625076 A0	20070124	GB20060025076	20061215	  
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US2010186125 AA	20100722	US20070448263	20071214	  
WO08071973 A1	20080619	WO2007GB04782	20071214	  



31) Family number: 30665053 (US2006242727A)

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Title: [EN] **EXPRESSION CASSETTE** ENCODING A 5-ENOLPYRUVYL-SHIKIMATE-3-PHOSPHATE SYNTHASE (EPSPS) AND HERBICIDE-TOLERANT PLANTS CONTAINING IT

Abstract: Source: US2006242727A [EN] The present invention relates to a novel **expression cassette** comprising a nucleic acid sequence encoding an EPSPS. In particular, the present invention relates to a novel **expression cassette** comprising, in the direction of transcription, functionally linked to one another, a promoter regulatory sequence which is functional in plant cells or plants, a nucleic acid sequence encoding an EPSPS and a terminator sequence which is functional in plant cells or plants, characterized in that the promoter regulatory sequence is a nucleic acid sequence chosen from the promoter regulatory sequences of the CSMV (Cassava Vein Mosaic Virus) plant virus.

Classifications: [Classification Explorer](#)

International *IPC* 8-9: A01H1/00 A01H5/00 A01H5/10 A01N57/18 A01P13/00 C12N15/54 C12N15/82 C12N15/83 C12N5/04 (Advanced/Invention); A01H1/00 A01H5/00 A01H5/10 A01N57/00 A01P13/00 C12N15/54 C12N15/82 C12N15/83 C12N5/04 (Core/Invention)

International *IPC* 1-7: A01H5/00 A01H5/10 A01N65/00 C12N15/29 C12N15/54 C12N15/82 C12N15/83 C12N15/84 C12N5/10 C12N9/10

CPC: C12N15/8275

European: C12N15/82C8B4A

US: 435/320.1 435/419 435/468 47/58.1R 504/206 536/24.1 800/278 800/280 800/300 800/300S

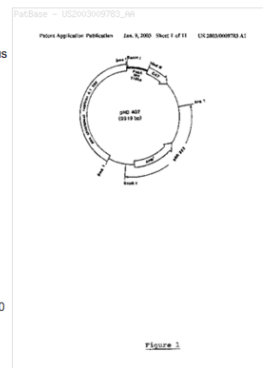
Family: [Family Explorer](#)

Publication number	Publication date	Application number	Application date	Links
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AU2003298258 AA	20040630	AU20030298258	20031210	  
AU2003298258 BB	20091029	AU20030298258	20031210	  
CA2502428 AA	20050414	CA20032502428	20031210	  
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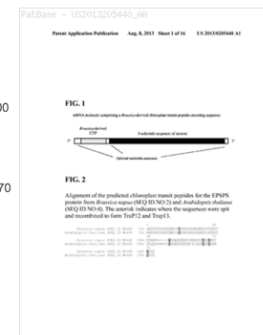
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Abstract: Source: US2003009783A [EN] Novel chimeric constructions and methods for their use are provided for **expression** of exogenous genes in a plant chloroplast. Particularly, **expression** is achieved by the use of a chloroplast or bacterial 5' untranslated region in the **expression cassette**. The **expression cassette** may be integrated into the chloroplast genome by the use of chloroplast DNA flanking sequences, or may replicate autonomously if provided with a chloroplast origin of replication. Plants and cells containing the transformed chloroplasts are also provided. The constructs may be used with both monocotyledonous and dicotyledonous chloroplasts.

[illegible]

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Abstract: Source: US2013205440A [EN] This disclosure concerns compositions and methods for targeting peptides, polypeptides, and proteins to plastids of plastid-containing cells. In some embodiments, the disclosure concerns **chloroplast transit peptides** that may direct a polypeptide to a plastid, and nucleic acid molecules encoding the same. In some embodiments, the disclosure concerns methods for producing a transgenic plant material (e.g., a transgenic plant) comprising a **chloroplast transit peptide**, as well as plant materials produced by such methods, and plant commodity products produced therefrom.

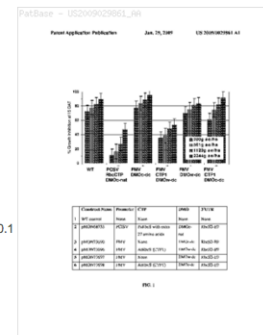
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Publication number	Publication date	Application number	Application date	Links
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AP201407895 A0	20140831	AP20140007895	20130201	
AP201408051 A0	20141130	AP20140008051	20130417	
AR089872 AA	20140924	AR2013P100312	20130201	
AR089873 AA	20140924	AR2013P100313	20130201	

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Abstract: Source: US2009029861A [EN] The invention provides for identification and use of certain **chloroplast transit peptides** for efficient processing and localization of dicamba monooxygenase (DMO) enzyme in transgenic plants. Methods for producing dicamba tolerant plants, methods for controlling weed growth, and methods for producing food, feed, and other products are also provided, as well as seed that confers tolerance to dicamba when it is applied pre- or post-emergence.

International *qpc* s-*g*: A01H10/A01H10/02 A01H50/A01H50/01 A01M2/04 A01N63/32 A01N37/04 **A01P13/00** A01P21/00 A23D9/00 A23J1/00 A23K1/00 A23K1/10 A23L1/10 A23L1/21/20 A23L1/24/20 C07K10/4415 C08B30/00 C10L100 C10L5/00 C11B1/00 C12N1/62 C12N1/63 C12N1/64 C12N1/65 C12N1/66 C12N1/67 C12N1/68 C12N1/69 C12N1/70 C12N1/71 C12N1/72 C12N1/73 C12N1/74 C12N1/75 C12N1/76 C12N1/77 C12N1/78 C12N1/79 C12N1/80 C12N1/81 C12N1/82 C12N1/83 C12N1/84 C12N1/85 C12N1/86 C12N1/87 C12N1/88 C12N1/89 C12N1/90 C12N1/91 C12N1/92 C12N1/93 C12N1/94 C12N1/95 C12N1/96 C12N1/97 C12N1/98 C12N1/99 C12N1/100 C12N1/101 C12N1/102 C12N1/103 C12N1/104 C12N1/105 C12N1/106 C12N1/107 C12N1/108 C12N1/109 C12N1/110 C12N1/111 C12N1/112 C12N1/113 C12N1/114 C12N1/115 C12N1/116 C12N1/117 C12N1/118 C12N1/119 C12N1/120 C12N1/121 C12N1/122 C12N1/123 C12N1/124 C12N1/125 C12N1/126 C12N1/127 C12N1/128 C12N1/129 C12N1/130 C12N1/131 C12N1/132 C12N1/133 C12N1/134 C12N1/135 C12N1/136 C12N1/137 C12N1/138 C12N1/139 C12N1/140 C12N1/141 C12N1/142 C12N1/143 C12N1/144 C12N1/145 C12N1/146 C12N1/147 C12N1/148 C12N1/149 C12N1/150 C12N1/151 C12N1/152 C12N1/153 C12N1/154 C12N1/155 C12N1/156 C12N1/157 C12N1/158 C12N1/159 C12N1/160 C12N1/161 C12N1/162 C12N1/163 C12N1/164 C12N1/165 C12N1/166 C12N1/167 C12N1/168 C12N1/169 C12N1/170 C12N1/171 C12N1/172 C12N1/173 C12N1/174 C12N1/175 C12N1/176 C12N1/177 C12N1/178 C12N1/179 C12N1/180 C12N1/181 C12N1/182 C12N1/183 C12N1/184 C12N1/185 C12N1/186 C12N1/187 C12N1/188 C12N1/189 C12N1/190 C12N1/191 C12N1/192 C12N1/193 C12N1/194 C12N1/195 C12N1/196 C12N1/197 C12N1/198 C12N1/199 C12N1/200 C12N1/201 C12N1/202 C12N1/203 C12N1/204 C12N1/205 C12N1/206 C12N1/207 C12N1/208 C12N1/209 C12N1/210 C12N1/211 C12N1/212 C12N1/213 C12N1/214 C12N1/215 C12N1/216 C12N1/217 C12N1/218 C12N1/219 C12N1/220 C12N1/221 C12N1/222 C12N1/223 C12N1/224 C12N1/225 C12N1/226 C12N1/227 C12N1/228 C12N1/229 C12N1/230 C12N1/231 C12N1/232 C12N1/233 C12N1/234 C12N1/235 C12N1/236 C12N1/237 C12N1/238 C12N1/239 C12N1/240 C12N1/241 C12N1/242 C12N1/243 C12N1/244 C12N1/245 C12N1/246 C12N1/247 C12N1/248 C12N1/249 C12N1/250 C12N1/251 C12N1/252 C12N1/253 C12N1/254 C12N1/255 C12N1/256 C12N1/257 C12N1/258 C12N1/259 C12N1/260 C12N1/261 C12N1/262 C12N1/263 C12N1/264 C12N1/265 C12N1/266 C12N1/267 C12N1/268 C12N1/269 C12N1/270 C12N1/271 C12N1/272 C12N1/273 C12N1/274 C12N1/275 C12N1/276 C12N1/277 C12N1/278 C12N1/279 C12N1/280 C12N1/281 C12N1/282 C12N1/283 C12N1/284 C12N1/285 C12N1/286 C12N1/287 C12N1/288 C12N1/289 C12N1/290 C12N1/291 C12N1/292 C12N1/293 C12N1/294 C12N1/295 C12N1/296 C12N1/297 C12N1/298 C12N1/299 C12N1/300 C12N1/301 C12N1/302 C12N1/303 C12N1/304 C12N1/305 C12N1/306 C12N1/307 C12N1/308 C12N1/309 C12N1/310 C12N1/311 C12N1/312 C12N1/313 C12N1/314 C12N1/315 C12N1/316 C12N1/317 C12N1/318 C12N1/319 C12N1/320 C12N1/321 C12N1/322 C12N1/323 C12N1/324 C12N1/325 C12N1/326 C12N1/327 C12N1/328 C12N1/329 C12N1/330 C12N1/331 C12N1/332 C12N1/333 C12N1/334 C12N1/335 C12N1/336 C12N1/337 C12N1/338 C12N1/339 C12N1/340 C12N1/341 C12N1/342 C12N1/343 C12N1/344 C12N1/345 C12N1/346 C12N1/347 C12N1/348 C12N1/349 C12N1/350 C12N1/351 C12N1/352 C12N1/353 C12N1/354 C12N1/355 C12N1/356 C12N1/357 C12N1/358 C12N1/359 C12N1/360 C12N1/361 C12N1/362 C12N1/363 C12N1/364 C12N1/365 C12N1/366 C12N1/367 C12N1/368 C12N1/369 C12N1/370 C12N1/371 C12N1/372 C12N1/373 C12N1/374 C12N1/375 C12N1/376 C12N1/377 C12N1/378 C12N1/379 C12N1/380 C12N1/381 C12N1/382 C12N1/383 C12N1/384 C12N1/385 C12N1/386 C12N1/387 C12N1/388 C12N1/389 C12N1/390 C12N1/391 C12N1/392 C12N1/393 C12N1/394 C12N1/395 C12N1/396 C12N1/397 C12N1/398 C12N1/399 C12N1/400 C12N1/401 C12N1/402 C12N1/403 C12N1/404 C12N1/405 C12N1/406 C12N1/407 C12N1/408 C12N1/409 C12N1/410 C12N1/411 C12N1/412 C12N1/413 C12N1/414 C12N1/415 C12N1/416 C12N1/417 C12N1/418 C12N1/419 C12N1/420 C12N1/421 C12N1/422 C12N1/423 C12N1/424 C12N1/425 C12N1/426 C12N1/427 C12N1/428 C12N1/429 C12N1/430 C12N1/431 C12N1/432 C12N1/433 C12N1/434 C12N1/435 C12N1/436 C12N1/437 C12N1/438 C12N1/439 C12N1/440 C12N1/441 C12N1/442 C12N1/443 C12N1/444 C12N1/445 C12N1/446 C12N1/447 C12N1/448 C12N1/449 C12N1/450 C12N1/451 C12N1/452 C12N1/453 C12N1/454 C12N1/455 C12N1/456 C12N1/457 C12N1/458 C12N1/459 C12N1/460 C12N1/461 C12N1/462 C12N1/463 C12N1/464 C12N1/465 C12N1/466 C12N1/467 C12N1/468 C12N1/469 C12N1/470 C12N1/471 C12N1/472 C12N1/473 C12N1/474 C12N1/475 C12N1/476 C12N1/477 C12N1/478 C12N1/479 C12N1/480 C12N1/481 C12N1/482 C12N1/483 C12N1/484 C12N1/485 C12N1/486 C12N1/487 C12N1/488 C12N1/489 C12N1/490 C12N1/491 C12N1/492 C12N1/493 C12N1/494 C12N1/495 C12N1/496 C12N1/497 C



Publication number	Publication date	Application number	Application date	Links
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AP201408058 A0	20141130	AP20140008058	20070606	 ☐



US 20110023179A1

(19) **United States**(12) **Patent Application Publication**
NUCCIO et al.(10) **Pub. No.: US 2011/0023179 A1**(43) **Pub. Date: Jan. 27, 2011**(54) **PLASTID TRANSIT PEPTIDES DERIVED
FROM LOWER PHOTOSYNTHETIC
EUKARYOTES AND METHODS**(75) Inventors: **MICHAEL L. NUCCIO,**
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21, 2009.**Publication Classification**(51) **Int. Cl.****A01H 5/00** (2006.01)
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C12N 5/10 (2006.01)(52) **U.S. Cl. 800/278; 800/298; 800/320.1;**
800/320.2; 800/312; 530/324; 536/23.1; 435/320.1;
435/419(57) **ABSTRACT**

Compositions and methods for targeting polypeptides to plastids are provided. Compositions comprise plastid transit peptides as well as nucleotide sequences encoding such transit peptides and variants thereof. Compositions further comprise DNA constructs comprising a nucleotide sequence encoding the plastid transit peptide operably linked to a nucleotide sequence encoding a polypeptide of interest. These DNA constructs find use in expression and targeting of the polypeptide of interest to a plastid. Compositions also comprise expression cassettes, vectors, transformed plants, transformed plant cells, and stably transformed plant seeds wherein a polypeptide of interest is targeted to a plastid by the plastid targeting peptide of the invention.

PLASTID TRANSIT PEPTIDES DERIVED FROM LOWER PHOTOSYNTHETIC EUKARYOTES AND METHODS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 61/227,100, filed Jul. 21, 2009. The above application is incorporated herein by reference.

FIELD OF THE INVENTION

[0002] The present invention relates to the genetic modification of plants, particularly to the transport of polypeptides of interest to plant plastids.

BACKGROUND OF THE INVENTION

[0003] The plastid contains its own genome. However, during evolution many of the plastid genes were transferred to the nuclear genome. Thus, a mechanism for the transport of the nuclear encoded plastid proteins back to the plastid developed. In this manner, the protein products of these nuclear-encoded plastid genes are transferred back to the plastid after expression in the nucleus. The proteins are transported through the use of transit peptide sequences located in the N-terminus of the transported proteins. These peptides direct the proteins to the plastid and are often subsequently removed by specific proteases.

[0004] A fundamental problem in cell biology is the precise and efficient targeting of proteins synthesized by cytoplasmic ribosomes to their appropriate intracellular locations. This is especially true for transgenic higher plants where the transgene product is needed in an appropriate cellular organelle or compartment. The present invention provides a plastid targeting peptide that efficiently transports a heterologous polypeptide into the chloroplast of transgenic higher plants.

BRIEF SUMMARY OF THE INVENTION

[0005] Compositions and methods for targeting polypeptides to chloroplasts are provided. Compositions comprise transit peptides as well as nucleotide sequences encoding a transit peptide (i.e., plastid targeting peptide or transport peptide) and variants thereof. Compositions further comprise DNA constructs comprising a nucleotide sequence encoding the transit peptide operably linked to a nucleotide sequence encoding a polypeptide of interest. These DNA constructs find use in expression and targeting of the heterologous polypeptide to a plastid. Compositions also comprise expression cassettes, vectors, transformed plants, transformed plant cells, and stably transformed plant seeds wherein a polypeptide of interest is targeted to a chloroplast by the plastid targeting peptide of the invention.

DETAILED DESCRIPTION OF THE INVENTION

[0006] Lower photosynthetic eukaryotes include the major lineages of Chlorophytes (green algae such as *Chlamydomonas* and *Dunaliella*), Rhodophyta (red algae), Glaucocystophyta (such as *Cyanophora*), Euglenophyta (such as *Euglena*), Chlorarachniophyta, Heterokonta, Haptophyta, Cryptophyta and the dinoflagellates. The lower photosynthetic eukaryotes do not include Cyanophyta. However, the bacterial phylum Cyanophyta (cyanobacteria such as *Synechococcus* and *Synechocystis*) possess mechanisms for pho-

tosynthesis. Therefore, these photosynthetic bacteria are included as a source of basic photosynthetic mechanisms. The lower photosynthetic eukaryotes are characterized by containing a photosynthetic organelle which is evolutionarily derived from cyanobacteria. The number of membranes surrounding the photosynthetic organelle varies amongst the members of the lower photosynthetic eukaryotes. The photosynthetic organelle may be a primary plastid or a secondary (or tertiary) plastid.

[0007] Primary plastids, or simple plastids, can be found in the chlorophytes, rhodophytes and glaucocystophytes and are identified as having two bounding membranes. The organisms containing primary plastids are thought to be the only descendants of the original endosymbiotic partnership with a cyanobacterium (Harper and Keeling, *Molecular Biology and Evolution* 20(10): 1730-1735 (2003)). The primary plastid containing organisms have been grouped into a single supergroup referred to as the Archaeplastida (Maruyama et al *BMC Evolutionary Biology* 8: 151 (2008)).

[0008] Secondary (and tertiary), or complex plastids, are bounded by three or four membranes and are thought to be derived from secondary endosymbiosis wherein an organism engulfed an alga. Phylogenetic analysis of secondary and tertiary plastids suggests these plastids are derived from several different endosymbiotic events which occurred during evolution (Bhattacharya and Medlin, *Plant Physiology* 116: 9-15 (1998)). The euglenophytes and dinoflagellates are examples of organisms with secondary or complex plastids. See Bhattacharya and Medlin, *Plant Physiology* 116: 9-15 (1998) for a review. Euglenids and chlorarachniophytes have green algal secondary plastids, whereas heterokonts, haptophytes, cryptophytes and dinoflagellates all possess red algal secondary endosymbionts (Harper and Keeling, *Molecular Biology and Evolution* 20(10): 1730-1735 (2003)).

[0009] The plastid targeting or transport peptides of the invention mediate targeting, localization, or transport of operably linked polypeptides into plastids. Plastids are organelles found in plants and algae. Plastids are responsible for photosynthesis, storage of products such as starch, and for the synthesis of many classes of molecules such as fatty acids, terpenes, and other molecules which are needed as cellular building blocks. Plastids have the ability to differentiate, or redifferentiate, into several forms depending upon their role in the cell. Undifferentiated proplastids may develop into any of the following plastids, including, chloroplasts, chromoplasts, leucoplasts, amyloplasts, statoliths, elaioplasts, and proteinoplasts.

[0010] A "chloroplast transit peptide" or "plastid transport peptide" or "plastid transit peptide" or "transit peptide" is necessary and sufficient to facilitate the import of a protein into the plastid of its native host cell. The plastid may be a primary, secondary or tertiary plastid. The plastid may be a chloroplast. Transit peptides are located at the N-terminal end of the proteins imported into the plastids. The transit peptide facilitates co-translational or post-translational transport of an operably linked polypeptide into a plastid. These transit peptides generally comprise between 40 and 100 amino acids. Studies indicate that transit peptides contain common characteristics. These include: they are virtually devoid of negatively charged amino acids, such as aspartic acid, glutamic acid, asparagine or glutamine; the N-terminal region is devoid of charged amino acids, and of amino acids such as glycine or proline; their central region contains a very high proportion of basic or hydroxylated amino acids, such as serine or threo-

nine; and, their C-terminal region is rich in arginine and has the ability to form an amphipathic beta-sheet secondary structure. The transit peptide is cleaved from the operably linked polypeptide, after importation, by specific proteases in the plastid.

[0011] According to one authority (Cline and Henry, *Annual Review of Cellular and Developmental Biology* 12: 1-26 (1996)) chloroplast transit peptides from higher plants share the following characteristics: (1) they have superficially similar properties to mitochondrial transit peptides; that is they are rich in hydroxylated residues and poor in acidic residues, (2) they are 30-120 residues long, (3) the N-terminal 10-15 amino acids are devoid of glycine, proline and charged residues, (4) the variable, middle region is rich in serine, threonine, lysine and arginine, (5) the C-proximal region contains the loosely conserved sequence (Ile/Val-x-Ala/Cys*Ala) for proteolytic processing, (6) there is no extended sequence conservation or conserved secondary structural motifs and (7) they, theoretically, adopt a predominantly random coil conformation.

[0012] Several computational approaches exist which use the above features to predict chloroplast targeting sequences in higher plants. Computational tools include PSORT (Nakai and Kanehisa, *Proteins* 11(2): 95-110 (1991); Horton et al., *Proceedings of the 4th Annual Asia Pacific Bioinformatics Conference APBC06*, Taipei, Taiwan pp. 39-48 (2006); <http://www.psорт.org>), ChloroP (Emanuelsson et al., *Journal of Molecular Biology* 300: 1005-1016 (1999); <http://www.cbs.dtu.dk/services/ChloroP/>) or TargetP (Nielsen et al., *Protein Engineer* 10:1-6 (1997); Emanuelsson et al., *Journal of Molecular Biology* 300: 1005-1016 (2000); <http://www.cbs.dtu.dk/services/TargetP/>).

[0013] In contrast to the higher plants, comparison of transit peptides from organisms like *Chlamydomonas reinhardtii* led to the following characterization: (1) they have a short, uncharged N-terminal region, (2) their central region is rich in arginine, alanine, valine and serine with a high propensity for forming an amphipathic α -helix and (3) they have a C-terminal region that may form an amphipathic β -strand (Franzen et al., *FEBS Letter* 260(2): 165-168 (1990)).

[0014] In one embodiment of the invention, the transit peptide is from a lower photosynthetic eukaryote which when operably linked to a heterologous protein and expressed in a transgenic higher plant, targets the heterologous protein to the chloroplast. The lower photosynthetic eukaryote is selected from the group consisting of Chlorophytes (green algae such as *Chlamydomonas* and *Dunaliella*), Rhodophyta (red algae), Glaucocystophyta (such as *Cyanophora*), Euglenophyta (such as *Euglena*), Chlorarachniophyta, Heterokonta, Haptophyta, Cryptophyta and the dinoflagellates. In another embodiment, the transit peptide is from *Chlamydomonas*. In another embodiment, the transit peptide is from *Chlamydomonas reinhardtii*. In another embodiment, the transit peptide is from *Dunaliella*. In another embodiment, the transit peptide is from *Dunaliella salina*.

[0015] Another embodiment of the invention is a method of targeting a heterologous protein to the chloroplast of a transgenic higher plant comprising the steps of operably linking a transit peptide from a lower photosynthetic eukaryote to a heterologous protein and generating a transgenic plant comprising the heterologous protein wherein the heterologous protein is detected in the chloroplast of the transgenic plant. The transgenic plant may be a higher transgenic plant. The lower photosynthetic eukaryote is selected from the group

consisting of Chlorophytes (green algae such as *Chlamydomonas* and *Dunaliella*), Rhodophyta (red algae), Glaucocystophyta (such as *Cyanophora*), Euglenophyta (such as *Euglena*), Chlorarachniophyta, Heterokonta, Haptophyta, Cryptophyta and the dinoflagellates. In another embodiment, the transit peptide is from *Chlamydomonas*. In another embodiment, the transit peptide is from *Chlamydomonas reinhardtii*. In another embodiment, the transit peptide is from *Dunaliella*. In another embodiment, the transit peptide is from *Dunaliella salina*.

[0016] In one embodiment of the invention, the transit peptide is from a lower photosynthetic prokaryote which when operably linked to a heterologous protein and expressed in a transgenic higher plant, targets the heterologous protein to the chloroplast. The lower photosynthetic prokaryote is selected from the group consisting of Cyanophytes (blue-green bacteria formerly known as "blue-green algae"). In another embodiment, the transit peptide is from *Synechococcus*. In another embodiment, the transit peptide is from *Synechococcus* sp. PCC 7002. In another embodiment, the transit peptide is from *Synechocystis*. In another embodiment, the transit peptide is from *Synechocystis* sp. PCC 6803.

[0017] Another embodiment of the invention is a method of targeting a heterologous protein to the chloroplast of a transgenic higher plant comprising the steps of operably linking a transit peptide from a lower photosynthetic prokaryote to a heterologous protein and generating a transgenic plant comprising the heterologous protein wherein the heterologous protein is detected in the chloroplast of the transgenic plant. The transgenic plant may be a higher transgenic plant. The lower photosynthetic prokaryote is selected from the group consisting of Cyanophytes (blue-green bacteria formerly known as "blue-green algae"). In another embodiment, the transit peptide is from *Synechococcus*. In another embodiment, the transit peptide is from *Synechococcus* sp. PCC 7002. In another embodiment, the transit peptide is from *Synechocystis*. In another embodiment, the transit peptide is from *Synechocystis* sp. PCC 6803.

[0018] The compositions comprise nucleotide sequences encoding a transit peptide as well as variants thereof. In one embodiment the transit peptide comprises the amino acid sequence set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 & 20 or fragments and variants thereof as well as the nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17 & 19 or fragments and variants thereof. Compositions further comprise DNA constructs comprising a nucleotide sequence encoding the transit peptide operably linked to a nucleotide sequence encoding a heterologous polypeptide. These DNA constructs find use in expression and targeting of the heterologous polypeptide to a plastid. Compositions also comprise expression cassettes, vectors, transformed plants, transformed plant cells, and stably transformed plant seeds wherein a heterologous polypeptide is targeted to a plastid by the transit peptide of the invention.

[0019] In another embodiment of the invention, the transit peptide is from a lower photosynthetic eukaryote which when operably linked to a heterologous protein and expressed in a transgenic higher plant, targets the heterologous protein to the chloroplast. Transit peptides are derived from the nucleic acid sequence encoding a protein which is targeted to the photosynthetic organelle. Transit peptides can be found in genes known to be encoded in the nucleus of the host cell but upon translation to be targeted to the photosynthetic organelle of the host cell and can be selected from the group consisting of

ferredoxin-NADP⁺-oxidoreductase, ribulose biphosphate carboxylase/oxygenase, 5-enolpyruvyl-shikimate-3-phosphate synthase, acetolactate synthase, chloroplast ribosomal protein CS17, Cs protein, ferredoxin, plastocyanin, ribulose biphosphate carboxylase activase, tryptophan synthase, acyl carrier protein, plastid chaperonin-60, cyochrome C552, 22-kDa heat shock protein, 33-kDa oxygen-evolving enhancer protein 1, ATP synthase gamma subunit (ATPase gamma), ATP synthase omega subunit, chlorophyll a/b-binding proteinII-1, oxygen-evolving enhancer protein 2, oxygen-evolving enhancer protein 3, photosystem I P21, photosystem I P28, photosystem I P30, photosystem I P35, photosystem I P37, glycerol-3-phosphate acyltransferases, chlorophyll a/b binding protein, CAB2 protein, hydroxymethyl-bilane synthase, pyruvate-orthophosphate dikinase, CAB3 protein, plastid ferritin, ferritin, early light-inducible protein, glutamate-1-semialdehyde aminotransferase, protochlorophyllide reductase, starch-granule-bound amylase synthase, light-harvesting chlorophyll a/b-binding protein of photosystem II, major pollen allergen Lol p 5a, plastid ClpB ATP dependent protease, superoxide dismutase, ferredoxin NADP oxidoreductase, 28-kDa ribonucleotoprotein, 31-kDa ribonucleoprotein, 33-kDa ribonucleoprotein, acetolactate synthase, ATP synthase CFO subunit 1, 2, 3, or 4; cytochrome f, cytochrome c, ADP-glucose pyrophosphorylase, glutamine synthase, glutamine synthase 2, carbonic anhydrase, GapA protein, heat shock protein hsp 21, phosphate translocator, plastid ClpA ATP dependent protease, plastid ribosomal protein CL24, plastid ribosomal protein CL9, plastid ribosomal protein PsCL18, plastid ribosomal protein PsCL25, DAHP synthase, starch phosphorylase, root acyl carrier protein 11, betaine-aldehyde dehydrogenase, GapB protein, glutamine synthase 2, phosphoribulokinase, nitrite reductase, ribosomal protein L12, ribosomal protein L13, ribosomal protein L21, ribosomal protein L35, ribosomal protein L40, triose phosphate-3-phosphoglycerate phosphate translocator, ferredoxin dependent glutamate synthase, glyceraldehyde 3 phosphate dehydrogenase, NADP dependent malic enzyme and NADP

malate dehydrogenase. Table 1 identifies additional nuclear encoded genes containing plastid targeting sequences. In one embodiment of the invention the transit peptide is from *Chlamydomonas reinhardtii*, particularly from *C. reinhardtii* Photosystem I p28 and comprises the amino acid sequence set forth in SEQ ID NO: 2. In another embodiment of the invention the transit peptide is from *Chlamydomonas reinhardtii*, particularly from *C. reinhardtii* Photosystem I p30 and comprises the amino acid sequence set forth in SEQ ID NO: 4. In another embodiment of the invention the transit peptide is from *Chlamydomonas reinhardtii*, particularly from *C. reinhardtii* Photosystem I p35 and comprises the amino acid sequence set forth in SEQ ID NO: 6. In one embodiment of the invention the transit peptide is from *Chlamydomonas reinhardtii*, particularly from *C. reinhardtii* Photosystem I p37 and comprises the amino acid sequence set forth in SEQ ID NO: 8. In another embodiment of the invention the transit peptide is from *Chlamydomonas reinhardtii*, particularly from *C. reinhardtii* ssRubisco and comprises the amino acid sequence set forth in SEQ ID NO: 10. In one embodiment of the invention the transit peptide is from *Chlamydomonas reinhardtii*, particularly from *C. reinhardtii* gamma-ATPase and comprises the amino acid sequence set forth in SEQ ID NO: 12. In one embodiment of the invention the transit peptide is from cyanobacteria, particularly from *Synechococcus* sp. PCC 7002 cytochrome c550 and comprises the amino acid sequence set forth in SEQ ID NO: 14. In one embodiment of the invention the transit peptide is from cyanobacteria, particularly from *Synechocystis* sp. PCC 6803 cytochrome c553 and comprises the amino acid sequence set forth in SEQ ID NO: 16. In another embodiment of the invention the transit peptide is from cyanobacteria, particularly from *Synechocystis* sp. PCC 6803 psaF and comprises the amino acid sequence set forth in SEQ ID NO: 18. In another embodiment of the invention the transit peptide is from *Dunaliella*, particularly from *Dunaliella salina* EPSPS and comprises the amino acid sequence set forth in SEQ ID NO: 20.

TABLE 1

Nuclear encoded genes encoding proteins targeted to the plastid. References are herein incorporated by reference in their entirety.		
Reference	Transit peptides	Organism
WO97/12983	First paragraph, page 17 starting with the text "The following N-terminal sequence . . ."	<i>Chlorella sorokiniana</i> (diatom)
Kilian and Kroth, The Plant Journal 41: 175-183 (2005)	FIG. 3, page 178, part "a" describing chloroplast localizing signals	<i>Phaeodactylum tricornutum</i> (diatom)
Steiner and Löffelhardt, Trends in Plant Science 7(2): 72-77 (2002)	FIG. 2, page 74	<i>Cyanophora paradoxa</i> (glaucocestophyte)
Reyes-Prieto and Bhattacharya, Molecular Phylogenetics and Evolution 45: 384-391 (2007)	Table 1, page 385	Calvin Cycle genes which function in the chloroplast but are encoded in the nucleus
Nassoury et al, J of Cell Science 116(14): 2867-2874 (2003)	Materials and Methods; Luciferase constructs paragraph describing PCP leader sequence	<i>Gonyaulax polyedra</i> (dinoflagellate)
Hackett et al, Current Biology 14: 213-218 (2004)	Table 1, page 214	<i>Alexandrium tamarense</i> (dinoflagellate)
Mishkind et al, J of Cell biology 100: 226-234 (1985)	FIG. 7, page 231	<i>Chlamydomonas reinhardtii</i> (green algae)

TABLE 1-continued

Nuclear encoded genes encoding proteins targeted to the plastid. References are herein incorporated by reference in their entirety.		
Reference	Transit peptides	Organism
Martin et al, Nature 393: 162-165 (1998)	FIG. 2, genes identified in white boxes	Range of lower photosynthetic eukaryotes
Henze et al, Proc natl Acad Sci 92: 9122-9126 (1995)	FIG. 2, page 9124	<i>Euglena gracilis</i> (protist)
Schwartzbach et al Plant Molecular Biology 38: 247-263 (1998)	FIG. 1, page 249	<i>Cyanophora paradoxa</i> (glaucocestophyte)
Steiner et al, The Plant Journal 44: 646-652 (2005)	FIG. 1, page 647	<i>Cyanophora paradoxa</i> (glaucocestophyte)
Kilian and Kroth, J Mol Evol 58: 712-721 (2004)	FIG. 3B, page 717	<i>Phaeodactylum tricornutum</i> (diatom)
Kitao et al Physiology Plantarum 133: 68-77 (2008)	FIG. 1, page 70	<i>Phaeodactylum tricornutum</i> (diatom)

[0020] The targeting sequences of the invention include variant or modified sequences. Such sequences have altered amino acid sequences yet retain the ability to transport a linked polypeptide into a plastid. While methods are known for substituting amino acid residues in polypeptide sequences, it is recognized that serine and threonine has been identified as abundant in transit peptides in comparison to the entire chloroplast targeting protein. Aspartic acid and glutamic acid have been reported as under represented in transit peptides. Such considerations as well as those discussed above may be taken into account when constructing variant transit peptides. However, as detailed below, one of skill in the art can assay whether a variant transit peptide is capable of effecting transport of an operably linked polypeptide for the presence of the operably linked polypeptide in the plastid. For purposes of the invention, a variant of a chloroplast transit peptide sequence of the invention also includes a fragment or fragments of the sequence.

[0021] As used herein, the term “nucleic acid molecule” is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

[0022] By a “crop plant” or “higher plant” is intended any plant that is cultivated for the purpose of producing plant material that is sought after by man for either oral consumption, or for utilization in an industrial, pharmaceutical, or commercial process. The invention may be applied to any of a variety of plants, including, but not limited to maize, wheat, rice, barley, soybean, cotton, sorghum, oats, tobacco, *Miscanthus* grass, Switch grass, trees, beans in general, rape/canola, alfalfa, flax, sunflower, safflower, millet, rye, sugarcane, sugar beet, cocoa, tea, *Brassica*, cotton, coffee, sweet potato, flax, peanut, clover; vegetables such as lettuce, tomato, cucurbits, cassava, potato, carrot, radish, pea, lentils, cabbage, cauliflower, broccoli, Brussels sprouts, peppers, and pineapple; tree fruits such as citrus, apples, pears, peaches, apricots, walnuts, avocado, banana, and coconut; and flowers such as orchids, carnations, roses, and the like.

[0023] As used herein, the term “plant part” or “plant tissue” includes plant cells, plant protoplasts, plant cell tissue cultures from which plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts

of plants such as embryos, pollen, ovules, seeds, leaves, flowers, branches, fruit, kernels, ears, cobs, husks, stalks, roots, root tips, anthers, and the like.

[0024] The article “a” and “an” are used herein to refer to one or more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means one or more element. Throughout the specification the word “comprising,” or variations such as “comprises” or “comprising,” will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

Transit Peptide Compositions

[0025] As indicated, the compositions of the invention include transit peptides capable of transporting operably linked polypeptides into plastids. The term “peptide” broadly refers to an amino acid chain that includes naturally occurring amino acids, synthetic amino acids, genetically encoded amino acids, non-genetically encoded amino acids, and combinations thereof. Peptides can include both L-form and D-form amino acids.

[0026] Representative non-genetically encoded amino acids include but are not limited to 2-aminoadipic acid; 3-aminoadipic acid; β -aminopropionic acid; 2-aminobutyric acid; 4-aminobutyric acid (piperidinic acid); 6-aminocaproic acid; 2-aminoheptanoic acid; 2-aminoisobutyric acid; 3-aminoisobutyric acid; 2-aminopimelic acid; 2,4-diaminobutyric acid; desmosine; 2,2'-diaminopimelic acid; 2,3-diaminopropionic acid; N-ethylglycine; N-ethylasparagine; hydroxyllysine; allo-hydroxyllysine; 3-hydroxyproline; 4-hydroxyproline; isodesmosine; allo-isoleucine; N-methylglycine (sarcosine); N-methylisoleucine; N-methylvaline; norvaline; norleucine; and ornithine.

[0027] Representative derivatized amino acids include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups can be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups can be derivatized to form O-acyl or O-alkyl deriva-

tives. The imidazole nitrogen of histidine can be derivatized to form N-im-benzylhistidine.

[0028] The plastid transit peptide is generally fused N-terminal to the polypeptide to be transported into a plastid. It is recognized that additional amino acid residues may be N-terminal to the plastid transit peptide. The plastid transit peptide is generally cleaved from the polypeptide of interest upon localization to the plastid. The position of cleavage may vary slightly between plant species.

[0029] The transit peptides of the invention include the transit peptide from a *Chlamydomonas* P28, particularly the transit peptide from a *Chlamydomonas reinhardtii* Photosystem I P28, more particularly the amino acid sequence set forth in SEQ ID NO: 2. The transit peptides of the invention include the transit peptide from a *Chlamydomonas* P30, particularly the transit peptide from a *Chlamydomonas reinhardtii* Photosystem I P30, more particularly the amino acid sequence set forth in SEQ ID NO: 4. The transit peptides of the invention include the transit peptide from a *Chlamydomonas* P35, particularly the transit peptide from a *Chlamydomonas reinhardtii* Photosystem I P35, more particularly the amino acid sequence set forth in SEQ ID NO: 6. The transit peptides of the invention include the transit peptide from a *Chlamydomonas* P37, particularly the transit peptide from a *Chlamydomonas reinhardtii* Photosystem I P37, more particularly the amino acid sequence set forth in SEQ ID NO: 8. The transit peptides of the invention include the transit peptide from a *Chlamydomonas* ssRubisco, particularly the transit peptide from a *Chlamydomonas reinhardtii* ssRubisco, more particularly the amino acid sequence set forth in SEQ ID NO: 10. The transit peptides of the invention include the transit peptide from a *Chlamydomonas* ATPase, particularly the transit peptide from a *Chlamydomonas reinhardtii* ATPase, more particularly the amino acid sequence set forth in SEQ ID NO: 12. The transit peptides of the invention include the transit peptide from a cyanobacteria Cytochrome c550, particularly the transit peptide from a *Synechococcus* sp. PCC 7002 Cytochrome c550, more particularly the amino acid sequence set forth in SEQ ID NO: 14. The transit peptides of the invention include the transit peptide from a cyanobacteria Cytochrome c553, particularly the transit peptide from a *Synechocystis* sp. PCC 6803 cytochrome c553, more particularly the amino acid sequence set forth in SEQ ID NO: 16. The transit peptides of the invention include the transit peptide from a *Synechocystis*, particularly the transit peptide from a *Synechocystis* sp. PCC 6803 psaF, more particularly the amino acid sequence set forth in SEQ ID NO: 18. The transit peptides of the invention include the transit peptide from a *Dunaliella*, particularly the transit peptide from a *Dunaliella salina* EPSPS, more particularly the amino acid sequence set forth in SEQ ID NO: 20. Biologically active variants of the peptides of the invention are also encompassed by the present invention. Such variants should retain the ability to transport an operatively linked polypeptide into a cellular plastid. Preferably, the variant has at least the same activity as the native molecule. The ability to transport polypeptides into a plastid can be measured by methods in the art. For example, the nucleotide sequence encoding the transit peptide can be linked to a reporter gene such β -glucuronidase (GUS) or AmCyan and introduced into a plant. Analysis GUS and AmCyan activities in the subcellular fractions of the transformed plant indicate whether the transit peptide is capable of targeting the reporter proteins to the plastids. See, for

example, Silva-Filho et al. (1997) *Journal of Biological Chemistry* 272:15264-15269 and US Patent Application No. 20080168580.

[0030] Suitable biologically active variants can be fragments and derivatives. By "fragment" is intended a peptide consisting of only a part of the intact transit peptide sequence and structure, and can be a C-terminal deletion or N-terminal deletion of amino acids or deletions at both the C- and N-terminal ends. By "derivatives" is intended any suitable modification of a transit peptide or peptide fragment encompassing any change in amino acid residues, so long as the transport activity is retained.

[0031] Peptide variants will generally have at least 70%, preferably at least 80%, more preferably about 90% to 95% or more, about 96%, about 97%, and most preferably about 98%, about 99% or more amino acid sequence identity to the amino acid sequence of the reference peptide molecule. A variant may differ by as few as 5, 4, 3, 2, or even 1 amino acid residue. Methods for determining identity between sequences are well known in the art. See, for example, the ALIGN program (Dayhoff (1978) in *Atlas of Protein Sequence and Structure* 5: Suppl. 3 (National Biomedical Research Foundation, Washington, D.C.) and programs in the Wisconsin Sequence Analysis Package, Version 8 (available from Genetics Computer Group, Madison, Wis.), for example, the GAP program. For purposes of optimal alignment of the two sequences, the contiguous segment of the amino acid sequence of the variant may have additional amino acid residues or deleted amino acid residues with respect to the amino acid sequence of the reference molecule. The contiguous segment used for comparison to the reference amino acid sequence will comprise at least twenty (20) contiguous nucleotides, and may be about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 15, about 20, about 25, about 30, about 40 or more nucleotides. Corrections for increased sequence identity associated with inclusion of gaps in the variant's amino acid sequence can be made by assigning gap penalties. Methods of sequence alignment are well known in the art.

[0032] When considering percentage of amino acid sequence identity, some amino acid residue positions may differ as a result of conservative amino acid substitutions, which do not affect properties of protein function. In these instances, percent sequence identity may be adjusted upwards to account for the similarity in conservatively substituted amino acids. Such adjustments are well known in the art. See, for example, Myers and Miller (1988) *Computer Applications in Biosciences* 4:11-17.

[0033] For example, preferably, conservative amino acid substitutions may be made. A "nonessential" amino acid residue is a residue that can be altered without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side

chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). See, for example, Sambrook J., and Russell, D. W. (2001) *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) and Innis, et al. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, NY).

[0034] The peptides of the invention can be subject to various changes, substitutions, insertions, and deletions where such changes provide for certain advantages in its use. Thus, the term “peptide” encompasses any of a variety of forms of peptide derivatives including, for example, amides, conjugates with proteins, cyclone peptides, polymerized peptides, conservatively substituted variants, analogs, fragments, chemically modified peptides, and peptide mimetics. Any peptide that has desired transport characteristics can be used in the practice of the present invention.

[0035] By “transports,” “targets,” or “transfers” is intended that the transit peptides of the invention are capable of transporting, transferring or carrying polypeptides expressed in the nucleus of the cell into a cellular plastid. In some embodiments, the transit peptides of the invention are capable of transporting 100%, at least 90%, at least 80%, at least 70%, at least 60%, at least 50% of an operably linked polypeptide into a plastid.

[0036] One aspect of the invention pertains to isolated nucleic acid molecules comprising nucleotide sequences encoding transit peptides or biologically active portions thereof. As used herein, the term “nucleic acid molecule” is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

[0037] Nucleic acid molecules that are fragments of these transit peptide encoding nucleotide sequences are also encompassed by the present invention. By “fragment” is intended a portion of the nucleotide sequence encoding a transit peptide. Nucleic acid molecules that are fragments of a transit peptide nucleotide sequence comprise at least about 15, about 20, about 50, about 75, about 100, about 125, about 150, about 175, about 180, about 185, about 190, about 195 contiguous nucleotides. By “contiguous” nucleotides are intended nucleotide residues that are immediately adjacent to one another.

[0038] The skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences of the invention thereby leading to changes in the amino acid sequence of the encoded transit peptides, without altering the transport. Thus, variant isolated nucleic acid molecules can be created by introducing one or more nucleotide substitutions, additions, or deletions into the corresponding nucleotide sequence disclosed herein, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded peptide. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Such variant nucleotide sequences are also encompassed by the present invention.

[0039] The compositions of the invention can be used to identify and isolate corresponding transit peptides from other organisms. In one method, the sequence can be used in hybridization assays to find sequences with substantial homology to the sequences of the invention. As used herein, the term “hybridization” is used in reference to the pairing of complementary (including partially complementary as dis-

cussed above) polynucleotide strands. Hybridization and the strength of hybridization (i.e., the strength of the association between polynucleotide strands) is impacted by many factors well known in the art including the degree of complementarity between the polynucleotides; stringency of the conditions involved that are affected by such conditions as the concentration of salts; the melting temperature (T_m) of the formed hybrid; the presence of other components; the molarity of the hybridizing strands; and, the G:C content of the polynucleotide strands.

[0040] Thus, isolated sequences that are capable of transporting polypeptides into a plastid and which hybridize under stringent conditions to the sequences disclosed herein, or to fragments thereof, are encompassed by the present invention. Such sequences will be at least about 40% to 50% homologous, about 60%, 65%, or 70% homologous, and even at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more homologous with the disclosed sequences. That is, the sequence identity of sequences may range, sharing at least about 40% to 50%, about 60%, 65%, or 70%, and even at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity.

[0041] As used herein, “ T_m ” and “melting temperature” are interchangeable terms which are the temperature at which 50% of a population of double-stranded polynucleotide molecules becomes dissociated into single strands. The equation for calculating the T_m of polynucleotides is well known in the art. For example, the T_m may be calculated by the following equation: $T_m = 69.3 + 0.41 \times (G+C) \% - 650/L$, wherein L is the length of the probe in nucleotides. The T_m of a hybrid polynucleotide may also be estimated using a formula adopted from hybridization assays in 1 M salt, and commonly used for calculating T_m for PCR primers: $[(\text{number of A+T}) \times 2^\circ \text{C.} + (\text{number of G+C}) \times 4^\circ \text{C.}]$, see, for example, Newton et al. (1997) *PCR 2nd Ed.* (Springer-Verlag, New York). Other more sophisticated computations exist in the art, which take structural as well as sequence characteristics into account for the calculation of T_m . A calculated T_m is merely an estimate; the optimum temperature is commonly determined empirically.

[0042] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1× to 2×SSC (20×SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55° C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37° C., and a wash in 0.5× to 1×SSC at 55 to 60° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1×SSC at 60 to 65° C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours. The duration of the wash time will be at least a length of time sufficient to reach equilibrium.

[0043] Corresponding sequences can also be identified by PCR reactions. See, Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.). See also Innis et al., eds. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, eds. (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, eds. (1999) *PCR Methods Manual* (Academic Press, New York). The primers of the present invention can be prepared using techniques known in the art, including, but not limited to, cloning and digestion of the appropriate sequences and direct chemical synthesis.

[0044] Chemical synthesis methods that can be used to make the primers of the present invention, include, but are not limited to, the phosphotriester method described by Narang et al., *Methods in Enzymology*, 68:90 (1979), the phosphodiester method disclosed by Brown et al., *Methods in Enzymology*, 68:109 (1979), the diethylphosphoramidate method disclosed by Beaucage et al., *Tetrahedron Letters*, 22:1859 (1981) and the solid support method described in U.S. Pat. No. 4,458,066. The use of an automated oligonucleotide synthesizer to prepare synthetic oligonucleotide primers of the present invention is also contemplated herein. Additionally, if desired, the primers can be labeled using techniques known in the art and described below.

Plant Expression Cassettes

[0045] As discussed, the plastid targeting peptides of the invention operably linked to a polypeptide of interest transports the linked polypeptide into a plastid. Thus, when assembled into a DNA construct and used to transform a plant, the targeting peptide directs a polypeptide of interest to plastids in the transformed plant cells, plants, and seeds after expression. Thus, the compositions of the invention also comprise nucleic acid sequences for transformation and expression and accumulation of a polypeptide of interest in the plastids of a plant cell of interest. The nucleic acid sequences may be present in DNA constructs or expression cassettes. "Expression cassette" as used herein means a nucleic acid molecule capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operatively linked to the nucleotide sequence of interest (i.e., a nucleotide sequence encoding a polypeptide of interest) which is operatively linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one that is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, i.e., the particular DNA sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter that initiates transcription only when the host cell is exposed to some particular external stimulus. Additionally, the promoter can also be specific to a particular tissue or organ or stage of development.

[0046] The present invention encompasses the transformation of plants with expression cassettes capable of directing expression and accumulation of a polypeptide of interest in the plastids of a plant cell. The expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a polynucleotide encoding a plastid targeting peptide, and a polynucleotide encoding a polypeptide of interest. The expression cassette may optionally comprise a transcriptional and translational termination region (i.e. termination region) functional in plants.

[0047] In addition to the polynucleotide sequence encoding the plastid targeting peptide, the construct may further comprise additional regulatory elements to facilitate transcription, translation, or transport of the polypeptide of interest. The regulatory sequences of the expression construct are operably linked to the polynucleotide of interest. By "operably linked" is intended a functional linkage between a regulatory element and a second sequence wherein the regulatory element initiates and/or mediates transcription, translation, or translocation of the DNA sequence corresponding to the second sequence. Generally, the term "operably linked" means that the nucleotide sequences being linked are contiguous or adjacent to one another. The regulatory elements include promoters, enhancers, and signal sequences useful for targeting cytoplasmically-synthesized proteins to plastids of the plant cell. In one embodiment, the construct comprises, in the 5' to 3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a polynucleotide encoding a plastid targeting peptide, and a polynucleotide encoding a polypeptide of interest.

[0048] Any promoter capable of driving expression in the plant of interest may be used in the practice of the invention. The promoter may be native or analogous or foreign or heterologous to the plant host. The terms "heterologous" and "exogenous" when used herein to refer to a nucleic acid sequence (e.g. a DNA or RNA sequence) or a gene, refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

[0049] A "homologous" nucleic acid (e.g. DNA) sequence is a nucleic acid (e.g. DNA or RNA) sequence naturally associated with a host cell into which it is introduced.

[0050] The choice of promoters to be included depends upon several factors, including, but not limited to, efficiency, selectability, inducibility, desired expression level, and cell- or tissue-preferential expression. It is a routine matter for one of skill in the art to modulate the expression of a sequence by appropriately selecting and positioning promoters and other regulatory regions relative to that sequence.

[0051] Some suitable promoters initiate transcription only, or predominantly, in certain cell types. Thus, as used herein a cell type- or tissue-preferential promoter is one that drives expression preferentially in the target tissue, but may also lead to some expression in other cell types or tissues as well.

Methods for identifying and characterizing promoter regions in plant genomic DNA include, for example, those described in the following references: Jordano, et al., *Plant Cell*, 1:855-866 (1989); Bustos, et al., *Plant Cell*, 1:839-854 (1989); Green, et al., *EMBO Journal* 7, 4035-4044 (1988); Meier, et al., *Plant Cell*, 3, 309-316 (1991); and Zhang, et al., *Plant Physiology* 110: 1069-1079 (1996).

[0052] Promoters active in photosynthetic tissue in order to drive transcription in green tissues such as leaves and stems are of particular interest for the present invention. Most suitable are promoters that drive expression only or predominantly in such tissues. The promoter may confer expression constitutively throughout the plant, or differentially with respect to the green tissues, or differentially with respect to the developmental stage of the green tissue in which expression occurs, or in response to external stimuli.

[0053] Examples of such promoters include the ribulose-1, 5-bisphosphate carboxylase (RbcS) promoters such as the RbcS promoter from eastern larch (*Larix laricina*), the pine cab6 promoter (Yamamoto et al. (1994) *Plant and Cell Physiology* 35:773-778), the Cab-1 gene promoter from wheat (Fejes et al. (1990) *Plant Molecular Biology* 15:921-932), the CAB-1 promoter from spinach (Lubberstedt et al. (1994) *Plant Physiology* 104:997-1006), the cab1R promoter from rice (Luan et al. (1992) *Plant Cell* 4:971-981), the pyruvate orthophosphate dikinase (PPDK) promoter from corn (Matsuoka et al. (1993) *PNAS USA* 90:9586-9590), the tobacco Lhcb1*2 promoter (Cerdan et al. (1997) *Plant Molecular Biology* 33:245-255), the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter (Truernit et al. (1995) *Planta* 196:564-570), and thylakoid membrane protein promoters from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other promoters that drive transcription in stems, leafs and green tissue are described in U.S. Patent Publication No. 2007/0006346, herein incorporated by reference in its entirety.

[0054] A maize gene encoding phosphoenol carboxylase (PEPC) has been described by Hudspeth & Grula (*Plant Molecular Biology* 12: 579-589 (1989)). Using standard molecular biological techniques the promoter for this gene can be used to drive the expression of any gene in a green tissue-specific manner in transgenic plants.

[0055] In some other embodiments of the present invention, inducible promoters may be desired. Inducible promoters drive transcription in response to external stimuli such as chemical agents or environmental stimuli. For example, inducible promoters can confer transcription in response to hormones such as gibberellic acid or ethylene, or in response to light or drought.

[0056] A variety of transcriptional terminators are available for use in expression cassettes. These are responsible for the termination of transcription beyond the transgene and correct mRNA polyadenylation. The termination region may be native with the transcriptional initiation region, may be native with the operably linked DNA sequence of interest, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous to the promoter, the DNA sequence of interest, the plant host, or any combination thereof). Appropriate transcriptional terminators are those that are known to function in plants and include the CAMV 35S terminator, the tml terminator, the nopaline synthase terminator and the pea rbcS E9 terminator. These can be used in both monocotyledons and dicotyledons. In addition, a gene's native transcription terminator may be used.

[0057] In some embodiments, the expression cassette will comprise a selectable marker gene for the selection of transformed cells. Selectable marker genes are utilized for the selection of transformed cells or tissues.

[0058] Numerous sequences have been found to enhance gene expression from within the transcriptional unit and these sequences can be used in conjunction with the genes of this invention to increase their expression in transgenic plants.

[0059] Various intron sequences have been shown to enhance expression, particularly in monocotyledonous cells. For example, the introns of the maize Adhl gene have been found to significantly enhance the expression of the wild-type gene under its cognate promoter when introduced into maize cells. Intron 1 was found to be particularly effective and enhanced expression in fusion constructs with the chloramphenicol acetyltransferase gene (Callis et al., *Genes & Development* 1: 1183-1200 (1987)). In the same experimental system, the intron from the maize bronze 1 gene had a similar effect in enhancing expression. Intron sequences have been routinely incorporated into plant transformation vectors, typically within the non-translated leader.

[0060] A number of non-translated leader sequences derived from viruses are also known to enhance expression, and these are particularly effective in dicotyledonous cells. Specifically, leader sequences from Tobacco Mosaic Virus (TMV, the "W-sequence"), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g. Gallie et al. *Nucleic Acids Research* 15: 8693-8711 (1987); Skuzeski et al. *Plant Molecular Biology* 15: 65-79 (1990)). Other leader sequences known in the art include but are not limited to: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein, O., Fuerst, T. R., and Moss, B. *PNAS USA* 86:6126-6130 (1989)); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al., 1986); MDMV leader (Maize Dwarf Mosaic Virus); *Virology* 154:9-20); human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak, D. G., and Samow, P., *Nature* 353: 90-94 (1991); untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling, S. A., and Gehrke, L., *Nature* 325:622-625 (1987); tobacco mosaic virus leader (TMV), (Gallie, D. R. et al., *Molecular Biology of RNA*, pages 237-256 (1989); and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel, S. A. et al., *Virology* 81:382-385 (1991). See also, Della-Cioppa et al., *Plant Physiology* 84:965-968 (1987).

[0061] As indicated the plastid transit peptide is operably linked to a polypeptide to be transported into the plastid. Polypeptides for traits of interest include agronomic traits that primarily are of benefit to a seed company, a grower, or a grain processor, for example, herbicide resistance, virus resistance, bacterial pathogen resistance, insect resistance, nematode resistance, and fungal resistance. See, e.g., U.S. Pat. Nos. 5,569,823; 5,304,730; 5,495,071; 6,329,504; and 6,337,431. Traits of interest may also be one that increases plant vigor or yield (including traits that allow a plant to grow at different temperatures, soil conditions and levels of sunlight and precipitation), or one that allows identification of a plant exhibiting a trait of interest (e.g., selectable marker gene, seed coat color, etc.). A plethora of genes useful for generating plants with desired secondary traits are available in the art.

[0062] Herbicide resistance genes of interest include those encoding precursors of acetolactase synthetase (ALS), see,

for example, U.S. Pat. No. 5,013,659; mutated acetolactate synthetase; 3-enolpyruvylshikimate-5-phosphate synthetase (EPSP synthetase), see, for example, U.S. Pat. Nos. 4,971,908 and 6,225,114; enzymes that modify a physiological process that occurs in a plastid including photosynthesis, fatty acid, amino acid, oil, arotenoid, terpenoid, and starch; etc. Other genes of interest include but are not limited to those encoding zeaxanthin epoxidase, choline monooxygenase, ferrochelatase, omega-3 fatty acid desaturase, glutamine synthetase, starch modifying enzymes, essential amino acids, provitamin A, hormones, Bt toxin proteins, and the like. Nucleotide sequences for such polypeptides are available in the art.

Plants

[0063] Plants useful in the present invention include plants that are transgenic for at least a polynucleotide encoding a plastid-targeted polypeptide of interest. Such plants will comprise a polynucleotide encoding a targeting peptide operably linked to a polynucleotide encoding a polypeptide of interest. One of skill in the art will recognize that the polypeptide sequences of interest may be associated with or contributing to one or more secondary trait(s) of interest. These polypeptides are cytoplasmically-expressed, and targeted to a plastid.

[0064] The type of plant selected depends on a variety of factors, including for example, the downstream use of the harvested plant material, amenability of the plant species to transformation, and the conditions under which the plants will be grown, harvested, and/or processed. One of skill in the art will further recognize that additional factors for selecting appropriate plant varieties for use in the present invention include high yield potential, good stalk strength, resistance to specific diseases, drought tolerance, rapid dry down and grain quality sufficient to allow storage and shipment to market with minimum loss.

[0065] It is further contemplated that the constructs of the invention may be introduced into plant varieties having improved properties suitable or optimal for a particular downstream use. Plants useful in the present invention include, but are not limited to, monocotyledonous and dicotyledonous plants, particularly crop plants such as maize, soybean, wheat, rice, *Brassica*, and the like. Examples of plant species of interest include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*; *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Coffea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers.

[0066] Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum.

[0067] Plants of interest include cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), and safflower (*Carthamus*, e.g. *tinctorius*); fruits such as apple (*Malus*, e.g. *domesticus*), banana (*Musa*, e.g. *acuminata*), berries (such as the currant, *Ribes*, e.g. *rubrum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), grape (*Vitis*, e.g. *vinifera*), lemon (*Citrus limon*), melon (*Cucumis melo*), nuts (such as the walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogaeae*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyrus*, e.g. *communis*), pepper (*Solanum*, e.g. *capsicum*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata*), tomato (*Lycopersicon*, e.g. *esculentum*); leafy, such as alfalfa (*Medicago*, e.g. *sativa*), sugar cane (*Saccharum*), cabbages (such as *Brassica oleracea*), endive (*Cichorium*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia* e.g. *oleraceae*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*) yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, such as bean (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), wheat (*Triticum*, e.g. *aestivum*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*); grasses, such as *Miscanthus* grass (*Miscanthus*, e.g., *giganteus*) and switchgrass (*Panicum*, e.g. *virgatum*); trees such as poplar (*Populus*, e.g. *tremula*), pine (*Pinus*); shrubs, such as cotton (e.g., *Gossypium hirsutum*); and tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g. *tuberosum*), and the like.

Plant Transformation

[0068] The expression constructs described herein can be introduced into the plant cell in a number of art-recognized ways. The term "introducing" in the context of a polynucleotide, for example, a nucleotide construct of interest, is intended to mean presenting to the plant the polynucleotide in such a manner that the polynucleotide gains access to the interior of a cell of the plant. Where more than one polynucleotide is to be introduced, these polynucleotides can be assembled as part of a single nucleotide construct, or as separate nucleotide constructs, and can be located on the same or different transformation vectors. Accordingly, these polynucleotides can be introduced into the host cell of interest in a single transformation event, in separate transformation events, or, for example, in plants, as part of a breeding protocol. The methods of the invention do not depend on a particular method for introducing one or more polynucleotides into a plant, only that the polynucleotide(s) gains access to the interior of at least one cell of the plant. Methods for introducing polynucleotides into plants are known in the art including,

but not limited to, transient transformation methods, stable transformation methods, and virus-mediated methods.

[0069] “Transient transformation” in the context of a polynucleotide is intended to mean that a polynucleotide is introduced into the plant and does not integrate into the genome of the plant.

[0070] By “stably introducing” or “stably introduced” in the context of a polynucleotide introduced into a plant is intended the introduced polynucleotide is stably incorporated into the plant genome, and thus the plant is stably transformed with the polynucleotide.

[0071] “Stable transformation” or “stably transformed” is intended to mean that a polynucleotide, for example, a nucleotide construct described herein, introduced into a plant integrates into the genome of the plant and is capable of being inherited by the progeny thereof, more particularly, by the progeny of multiple successive generations.

[0072] Numerous transformation vectors available for plant transformation are known to those of ordinary skill in the plant transformation arts, and the genes pertinent to this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation. For certain target species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the nptII gene, which confers resistance to kanamycin and related antibiotics (Messing & Vierra, *Gene* 19: 259-268 (1982); Bevan et al., *Nature* 304:184-187 (1983)), the bar gene, which confers resistance to the herbicide phosphinothricin (White et al., *Nucleic Acids Research* 18: 1062 (1990), Spencer et al. *Theoretical and Applied Genetics* 79: 625-631 (1990)), the hph gene, which confers resistance to the antibiotic hygromycin (Blochinger & Diggelmann, *Molecular and Cellular Biology* 4: 2929-2931), and the dhfr gene, which confers resistance to methotrexate (Bourouis et al., *EMBO Journal* 2(7): 1099-1104 (1983)), the EPSPS gene, which confers resistance to glyphosate (U.S. Pat. Nos. 4,940,935 and 5,188,642), and the mannose-6-phosphate isomerase gene, which provides the ability to metabolize mannose (U.S. Pat. Nos. 5,767,378 and 5,994,629).

[0073] Methods for regeneration of plants are also well known in the art. For example, Ti plasmid vectors have been utilized for the delivery of foreign DNA, as well as direct DNA uptake, liposomes, electroporation, microinjection, and microprojectiles. In addition, bacteria from the genus *Agrobacterium* can be utilized to transform plant cells. Below are descriptions of representative techniques for transforming both dicotyledonous and monocotyledonous plants, as well as a representative plastid transformation technique.

[0074] Many vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, *Nucleic Acids Research* (1984)). For the construction of vectors useful in *Agrobacterium* transformation, see, for example, US Patent Application Publication No. 2006/0260011, herein incorporated by reference.

[0075] Transformation without the use of *Agrobacterium tumefaciens* circumvents the requirement for T-DNA sequences in the chosen transformation vector and consequently vectors lacking these sequences can be utilized in addition to vectors such as the ones described above which contain T-DNA sequences. Transformation techniques that do not rely on *Agrobacterium* include transformation via

particle bombardment, protoplast uptake (e.g. PEG and electroporation) and microinjection. The choice of vector depends largely on the preferred selection for the species being transformed.

[0076] Transformation techniques for dicotyledons are well known in the art and include *Agrobacterium*-based techniques and techniques that do not require *Agrobacterium*. Non-*Agrobacterium* techniques involve the uptake of exogenous genetic material directly by protoplasts or cells. This can be accomplished by PEG or electroporation mediated uptake, particle bombardment-mediated delivery, or microinjection. Examples of these techniques are described by Paszkowski et al., *EMBO Journal* 3: 2717-2722 (1984), Potrykus et al., *Molecular Genetics and Genomics* 199: 169-177 (1985), Reich et al., *Biotechnology* 4: 1001-1004 (1986), and Klein et al., *Nature* 327: 70-73 (1987). In each case the transformed cells are regenerated to whole plants using standard techniques known in the art.

[0077] *Agrobacterium*-mediated transformation is a preferred technique for transformation of dicotyledons because of its high efficiency of transformation and its broad utility with many different species. *Agrobacterium* transformation typically involves the transfer of the binary vector carrying the foreign DNA of interest (e.g. pCIB200 or pCIB2001) to an appropriate *Agrobacterium* strain which may depend of the complement of vir genes carried by the host *Agrobacterium* strain either on a co-resident Ti plasmid or chromosomally (e.g. strain CIB542 for pCIB200 and pCIB2001 (Uknes et al. *Plant Cell* 5: 159-169 (1993))). The transfer of the recombinant binary vector to *Agrobacterium* is accomplished by a triparental mating procedure using *E. coli* carrying the recombinant binary vector, a helper *E. coli* strain which carries a plasmid such as pRK2013 and which is able to mobilize the recombinant binary vector to the target *Agrobacterium* strain. Alternatively, the recombinant binary vector can be transferred to *Agrobacterium* by DNA transformation (Hofgen & Willmitzer, *Nucleic Acids Research* 16: 9877 (1988)).

[0078] Transformation of the target plant species by recombinant *Agrobacterium* usually involves co-cultivation of the *Agrobacterium* with explants from the plant and follows protocols well known in the art. Transformed tissue is regenerated on selectable medium carrying the antibiotic or herbicide resistance marker present between the binary plasmid T-DNA borders.

[0079] Another approach to transforming plant cells with a gene involves propelling inert or biologically active particles at plant tissues and cells. This technique is disclosed in U.S. Pat. Nos. 4,945,050, 5,036,006, and 5,100,792 all to Sanford et al. Generally, this procedure involves propelling inert or biologically active particles at the cells under conditions effective to penetrate the outer surface of the cell and afford incorporation within the interior thereof. When inert particles are utilized, the vector can be introduced into the cell by coating the particles with the vector containing the desired gene. Alternatively, the target cell can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (e.g., dried yeast cells, dried bacterium or a bacteriophage, each containing DNA sought to be introduced) can also be propelled into plant cell tissue.

[0080] Transformation of most monocotyledon species has now also become routine. Preferred techniques include direct gene transfer into protoplasts using PEG or electroporation techniques, and particle bombardment into callus tissue.

Transformations can be undertaken with a single DNA species or multiple DNA species (i.e. co-transformation) and both of these techniques are suitable for use with this invention. Co. transformation may have the advantage of avoiding complete vector construction and of generating transgenic plants with unlinked loci for the gene of interest and the selectable marker, enabling the removal of the selectable marker in subsequent generations, should this be regarded desirable. However, a disadvantage of the use of co-transformation is the less than 100% frequency with which separate DNA species are integrated into the genome (Schocher et al. *Biotechnology* 4: 1093-1096 (1986)).

[0081] Patent Applications EP 0 292 435, EP 0 392 225, and WO 93/07278 describe techniques for the preparation of callus and protoplasts from an elite inbred line of maize, transformation of protoplasts using PEG or electroporation, and the regeneration of maize plants from transformed protoplasts. Gordon-Kamm et al. (*Plant Cell* 2: 603-618 (1990)) and Fromm et al. (*Biotechnology* 8: 833-839 (1990)) have published techniques for transformation of A188-derived maize line using particle bombardment. Furthermore, WO 93/07278 and Kozziel et al. (*Biotechnology* 11: 194-200 (1993)) describe techniques for the transformation of elite inbred lines of maize by particle bombardment. This technique utilizes immature maize embryos of 1.5-2.5 mm length excised from a maize ear 14-15 days after pollination and a PDS-1000He Biolistics device for bombardment.

[0082] Transformation of rice can also be undertaken by direct gene transfer techniques utilizing protoplasts or particle bombardment. Protoplast-mediated transformation has been described for Japonica-types and Indica-types (Zhang et al. *Plant Cell Reports* 7: 379-384 (1988); Shimamoto et al. *Nature* 338: 274-277 (1989); Datta et al. *Biotechnology* 8: 736-740 (1990)). Both types are also routinely transformable using particle bombardment (Christou et al. *Biotechnology* 9: 957-962 (1991)). Furthermore, WO 93/21335 describes techniques for the transformation of rice via electroporation.

[0083] Patent Application EP 0 332 581 describes techniques for the generation, transformation and regeneration of Pooideae protoplasts. These techniques allow the transformation of *Dactylis* and wheat. Furthermore, wheat transformation has been described by Vasil et al. (*Biotechnology* 10: 667-674 (1992)) using particle bombardment into cells of type C long-term regenerable callus, and also by Vasil et al. (*Biotechnology* 11: 1553-1558 (1993)) and Weeks et al. (*Plant Physiology* 102: 1077-1084 (1993)) using particle bombardment of immature embryos and immature embryo-derived callus. A preferred technique for wheat transformation, however, involves the transformation of wheat by particle bombardment of immature embryos and includes either a high sucrose or a high maltose step prior to gene delivery. Prior to bombardment, any number of embryos (0.75-1 mm in length) are plated onto MS medium with 3% sucrose (Murashiga & Skoog, *Physiologia Plantarum* 15: 473-497 (1962)) and 3 mg/L 2,4-D for induction of somatic embryos, which is allowed to proceed in the dark. On the chosen day of bombardment, embryos are removed from the induction medium and placed onto the osmoticum (i.e. induction medium with sucrose or maltose added at the desired concentration, typically 15%). The embryos are allowed to plasmolyze for 2-3 hours and are then bombarded. Twenty embryos per target plate are typical, although not critical. An appropriate gene-carrying plasmid is precipitated onto micrometer size gold particles using standard procedures. Each plate of embryos is

shot with the DuPont BIOLISTICS® helium device using a burst pressure of about 1000 psi using a standard 80 mesh screen. After bombardment, the embryos are placed back into the dark to recover for about 24 hours, still on osmotic media. After 24 hours, the embryos are removed from the osmoticum and placed back onto induction medium where they stay for about a month before regeneration. Approximately one month later the embryo explants with developing embryogenic callus are transferred to regeneration medium (MS+1 mg/L NAA, 5 mg/L GA), further containing the appropriate selection agent. After approximately one month, developed shoots are transferred to larger sterile containers known as "GA7s" which contain half-strength MS, 2% sucrose, and the same concentration of selection agent.

[0084] Transformation of monocotyledons using *Agrobacterium* has also been described. See, WO 94/00977 and U.S. Pat. No. 5,591,616, and, Negrotto et al., *Plant Cell Reports* 19: 798-803 (2000).

[0085] For example, rice (*Oryza sativa*) can be used for generating transgenic plants. Various rice cultivars can be used (Hiei et al., 1994, *Plant Journal* 6:271-282; Dong et al., 1996, *Molecular Breeding* 2:267-276; Hiei et al., 1997, *Plant Molecular Biology*, 35:205-218). Also, the various media constituents described below may be either varied in quantity or substituted. Embryogenic responses are initiated and/or cultures are established from mature embryos by culturing on MS-CIM medium (MS basal salts, 4.3 g/L; B5 vitamins (200x), 5 ml/L; Sucrose, 30 g/L; proline, 500 mg/L; glutamine, 500 mg/L; casein hydrolysate, 300 mg/L; 2,4-D (1 mg/ml), 2 ml/L; adjust pH to 5.8 with 1 N KOH; Phytigel, 3 g/L). Either mature embryos at the initial stages of culture response or established culture lines are inoculated and co-cultivated with the *Agrobacterium tumefaciens* strain LBA4404 (*Agrobacterium*) containing the desired vector construction. *Agrobacterium* is cultured from glycerol stocks on solid YPC medium (100 mg/L spectinomycin and any other appropriate antibiotic) for about 2 days at 28° C. *Agrobacterium* is re-suspended in liquid MS-CIM medium. The *Agrobacterium* culture is diluted to an OD600 of 0.2-0.3 and acetosyringone is added to a final concentration of 200 uM. Acetosyringone is added before mixing the solution with the rice cultures to induce *Agrobacterium* for DNA transfer to the plant cells. For inoculation, the plant cultures are immersed in the bacterial suspension. The liquid bacterial suspension is removed and the inoculated cultures are placed on co-cultivation medium and incubated at 22° C. for two days. The cultures are then transferred to MS-CIM medium with Tetracycline (400 mg/L) to inhibit the growth of *Agrobacterium*. For constructs utilizing the PMI selectable marker gene (Reed et al., *In Vitro Cellular & Developmental Biology-Plant* 37:127-132), cultures are transferred to selection medium containing Mannose as a carbohydrate source (MS with 2% Mannose, 300 mg/L Tetracycline) after 7 days, and cultured for 3-4 weeks in the dark. Resistant colonies are then transferred to regeneration induction medium (MS with no 2,4-D, 0.5 mg/L IAA, 1 mg/L zeatin, 200 mg/L timentin 2% Mannose and 3% Sorbitol) and grown in the dark for 14 days. Proliferating colonies are then transferred to another round of regeneration induction media and moved to the light growth room. Regenerated shoots are transferred to GA7 containers with GA7-1 medium (MS with no hormones and 2% Sorbitol) for 2 weeks and then moved to the greenhouse when they are large enough

and have adequate roots. Plants are transplanted to soil in the greenhouse (T0 generation) grown to maturity, and the T1 seed is harvested.

[0086] The plants obtained via transformation with a nucleic acid sequence of the present invention can be any of a wide variety of plant species, including those of monocots and dicots; however, the plants used in the method of the invention are preferably selected from the list of agronomically important target crops set forth supra. The expression of a gene of the present invention in combination with other characteristics important for production and quality can be incorporated into plant lines through breeding. Breeding approaches and techniques are known in the art. See, for example, Welsh J. R., *Fundamentals of Plant Genetics and Breeding*, John Wiley & Sons, NY (1981); *Crop Breeding*, Wood D. R. (Ed.) American Society of Agronomy Madison, Wis. (1983); Mayo O., *The Theory of Plant Breeding, Second Edition*, Clarendon Press, Oxford (1987); Singh, D. P., *Breeding for Resistance to Diseases and Insect Pests*, Springer-Verlag, NY (1986); and Wricke and Weber, *Quantitative Genetics and Selection Plant Breeding*, Walter de Gruyter and Co., Berlin (1986).

[0087] For the transformation of plastids, seeds of *Nicotiana tabacum* c.v. "Xanthienc" are germinated seven per plate in a 1" circular array on T agar medium and bombarded 12-14 days after sowing with 1 μ m tungsten particles (M10, Biorad, Hercules, Calif.) coated with DNA from plasmids pPH143 and pPH145 essentially as described (Svab, Z. and Maliga, P. (1993) *PNAS USA* 90, 913-917). Bombarded seedlings are incubated on T medium for two days after which leaves are excised and placed abaxial side up in bright light (350-500 μ mol photons/m²/s) on plates of RMOP medium (Svab, Z., Hajdukiewicz, P. and Maliga, P. (1990) *PNAS USA* 87, 8526-8530) containing 500 μ g/ml spectinomycin dihydrochloride (Sigma, St. Louis, Mo.). Resistant shoots appearing underneath the bleached leaves three to eight weeks after bombardment are subcloned onto the same selective medium, allowed to form callus, and secondary shoots isolated and subcloned. Complete segregation of transformed plastid genome copies (homoplasmicity) in independent subclones is assessed by standard techniques of Southern blotting (Sambrook et al., (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor). BamHI/EcoRI-digested total cellular DNA (Mettler, I. J. (1987) *Plant Molecular Biology Reporter* 5, 346349) is separated on 1% Tris-borate (TBE) agarose gels, transferred to nylon membranes (Amersham) and probed with 32P-labeled random primed DNA sequences corresponding to a 0.7 kb BamHI/HindIII DNA fragment from pC8 containing a portion of the plastid targeting sequence. Homoplasmic shoots are rooted aseptically on spectinomycin-containing MS/IBA medium (McBride, K. E. et al. (1994) *PNAS USA* 91, 7301-7305) and transferred to the greenhouse.

[0088] The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction or vegetative growth and can thus be maintained and propagated in progeny plants. Generally, maintenance and propagation make use of known agricultural methods developed to fit specific purposes such as tilling, sowing or harvesting.

[0089] Use of the advantageous genetic properties of the transgenic plants and seeds according to the invention can further be made in plant breeding. Depending on the desired properties, different breeding measures are taken. The rel-

evant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multi-line breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines that, for example, increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow one to dispense with said methods due to their modified genetic properties.

[0090] While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

[0091] The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

[0092] Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by J. Sambrook, E. F. Fritsch and T. Maniatis, *Molecular Cloning: A Laboratory manual*, Cold Spring Harbor laboratory, Cold Spring Harbor, N.Y. (1989) and by T. J. Silhavy, M. L. Berman, and L. W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1984) and by Ausubel, F. M. et al., *Current Protocols in Molecular Biology*, published by Greene Publishing Association and Wiley-Interscience (1987).

Example 1

Biochemically Defined Transit Peptides from *Chlamydomonas reinhardtii* Targeting the Plastid Stroma

[0093] Transit peptides derived from higher plants are not the only molecules capable of directing a foreign protein to the plastid stroma in stably transformed plants. This is based on biological conservation of plastid protein import. The endosymbiotic event that led to plastids occurred long before unicellular and multicellular phototrophs split. During this period endosymbiotic gene transfer from the chloroplast to the nuclear genome led to the acquisition of transit peptides by the transferred genes, and the development of protein import machinery in plastids. It's clear that higher plants possess unique protein import characteristics. However in vitro data show that nuclear encoded plastid proteins from a glaucocystophyte alga like *Cyanophora paradoxa* (Steiner and Luffelhardt, 2005) or the unicellular alga *Chlamydomonas reinhardtii* (Mishkind et al., 1985 and Yu et al., 1988) can be imported by plastids derived from higher plants like spinach and pea.

[0094] The present invention includes transit peptides from lower photosynthetic organisms. The basis for these transit peptides are that they were identified by N-terminal sequencing of proteins purified from plastids. To define the transit peptide according to the invention and map the cleavage site, the N-terminus of the purified protein was compared to the gene sequence. A transit peptide is the 5'-segment of the open reading frame, from the translation start codon to the N-terminus of the plastid purified protein. Several of these have

been identified in *Chlamydomonas reinhardtii* and are summarized in a review by Franzen et al (1990).

[0095] The present invention includes transit peptides derived from the PSI P28, PSI P30, PSI P35, PSI P37, Rubisco SS and ATPase- γ subunit genes from *Chlamydomonas reinhardtii* that function to target a heterologous protein to plastids in transgenic maize. The present invention further includes transit peptides derived from the Cytochrome c550, Cytochrome c553 and psaF subunit genes from cyanobacteria that function to target a heterologous protein to plastids in transgenic maize. Transit peptides derived from the EPSPS gene from *Dunaliella salina* function to target a heterologous protein to plastids in transgenic maize. The transit peptides of the invention are depicted in Table 2.

TABLE 2

Transit peptides derived from <i>Chlamydomonas reinhardtii</i> , cyanobacteria and <i>Dunaliella salina</i> with the corresponding SEQ ID NO.	
SEQ ID NO:	Gene name:
2	PSI P28
4	PSI P30
6	PSI P35
8	PSI P37
10	ssRubisco
12	ATPase gamma
14	Cytochrome c550
16	Cytochrome c553
18	psaF
20	<i>D. salina</i> EPSPS

[0096] Each transit peptide will be back-translated to a maize-optimized using a maize coding sequence table, for example software from Vector NTI. Unless otherwise noted the coding sequence for each transit peptide was assembled by annealing and extending two partially complementary oligonucleotide primers. The chloroplast transit peptides will be linked to the maize optimized AmCyan protein coding sequence, SEQ ID NO: 32. This protein will be used here as a reporter for transit peptide characterization. The transit peptide and trait protein coding sequences will be fused with splicing by overlap extension PCR(SOE-PCR). The PCR product will be digested by the appropriate restriction endonucleases and inserted into an expression cassette. The complete expression cassette, SEQ ID NO: 21, with the addition of the insert will be cloned into an *Agrobacterium tumefaciens* binary vector containing the FMV 34S-CaMV^{35S} dual enhancer complex. Each binary vector will be transformed into maize.

Example 2

Creation of the Transit Peptides Fused to AmCyan

[0097] 2A: Creation of P28, P30, P35, P37, ssRubisco, ATPase, c550, c553 and psaF

[0098] The following primers were ordered from either Sigma or IDT and used as forward PCR primers ("AmCyan rev" was used as a reverse primer for PCR reactions) to fuse the transit peptides to the maize optimized AmCyan, SEQ ID NO: 32. The primer sequences and corresponding SEQ ID NOs are depicted in Table 3. The AmCyan reverse primer, SEQ ID NO: 31, is used as the reverse primer in the PCR fusing the various CTP to the AmCyan sequence.

TABLE 3

Chloroplast transit peptide primer sequences		
SEQ ID NO:	Primer name	Primer sequence 5' - 3'
22	P28	TATATACCATGGCATTGGTCGCCCGACCAAGTTT TATCAGCAAGGGTAGCGGCAAGTCGCCCTCGGG TAGCTGCCCGTAAAGCTGTGAGAGTTAGCGCGG CCCTGAGCAACAAGTTCATCGGCG
23	P30	CAAGCTTTGAGTAGCAGGGTGAATATAGCCGCA AAACCACAGCGAGCGCAACGTTTAGTAGTTAGA GCAGCCCTGAGCAACAAGTTCATCGGCG
24	P35	CAAACCTTTGGCGAGCCGACCATCATTACGTGCT AGTGCCAGGGTCGCCCTAGACGCGCACCAACGG GTTGCAAGTGGTAAACAAAGCTGCCCTGAGCAAC AAGTTCATCGGCG
25	P37	CAAGCATTAGCGACTCGACCTTCAGCTATAAGG CCAACAAAAGCTGCCGTAGAACGAGTGTAGTT GTGCGGGCAGCCCTGAGCAACAAGTTCATCGGC G
26	ssRubisco	TATATACCATGGCCGCGGTATAGCCAAATCAA GCGTTTCCGAGCGGTGGCAAGGCTGTAGAT CTAGCGTGAGGCGGATGGCTGCCCTGAAACCCG CAGTCAAAGCGGCACCTGTGGCAGCTCCAGCAC AAGCGAATCAGGCCCTGAGCAACAAGTTCATCG GCG
27	ATPase	TATATACCATGGCCGCTATGTTAGCAAGTAAAC AAGGCGCGTTTATGGGAAGGAGTAGCTTCGCAC CTGCCCAAAAGGTGTGCTAGCAGAGGGTCAT TGCAGGTGGTAGCGCCCTGAGCAACAAGTTCAT TCGGCG
28	c550	AACAAAATACTGGGATTGATCCACTTAAGAAA CCTATCTTTGGAATAAGTGCAATTCGTATTACTA TTTTGGCAATTGAATGTTGGTGCCGGAATGCT GCCCTGAGCAACAAGTTCATCGGCG
29	c553	TTTAAACTGTTTAAACCAAGCGAGTAGAATATTC TTTGGGATTGCTTTGCCATGTCTTATCTTTTA GGAGGTATATTCAGTTTAGGAAATACAGCCCTA GCAGCCCTGAGCAACAAGTTCATCGGCG
30	psaF	AAACATTTACTTGCGTTGTCTGCTAGCCTTTACA TTATGGTTCAATTTTGCTCCAAGTGCAAGTGCA GCCCTGAGCAACAAGTTCATCGGCG
31	AmCyan rev	TATATAGAGCTCTCAGAACG

The primers were used in the following PCR mixture:

[0099] 0.5 μ l pDNA template (AmCyan-individual chloroplast transit peptide: additional detail are provided below), 1.0 μ l forward primer (20 μ M), 1.0 μ l reverse primer (20 μ M), 5.0 μ l Extensor green buffer, 2.0 μ l Quik Solution™, 1.0 μ l dNTPs (10 mM) 0.5 μ l PFU Turbo polymerase, 0.5 μ l Extensor polymerase blend, 38.5 μ l d₂H₂O.

The following thermocycler program was used:

[0100] 95° C. for 5 minutes (denaturing), 10 cycles of 95° C. for 1 minutes, 30° C. for 30 seconds, 68° C. for 4 minutes followed by 20 cycles of 95° C. for 30 seconds, 45° C. for 1 minutes, and 68° C. for 4 minutes with a 68° C. final extension for 15 minutes.

Products were gel purified and cut with Sad or NcoI/SacI and ligated into an appropriately cut backbone vector pSYN15460, SEQ ID NO: 21, as described below.

pSYN15460, SEQ ID NO: 21, was cut with NcoI/SacI to prepare for insertion of the following: p28-AmCyan, ssRUBISCO-AmCyan and ATPase-AmCyan. pSYN15460, SEQ ID NO: 21, was cut with NcoI, filled in using T4 DNA polymerase and then cut with Sad to create a blunt/SacI fragment for insertion of the following: c550-AmCyan, c553-AmCyan, psaF-AmCyan, p30-AmCyan, p35-AmCyan, and p37-AmCyan.

[0101] 2B: Creation of *D. salina* EPSPS

[0102] The following primers were ordered from IDT and used as forward and reverse PCR primers to fuse the transit peptides to the maize optimized AmCyan, SEQ ID NO: 32. Backbone vector pSYN15460, SEQ ID NO: 21, was cut with NcoI, filled in using T4 DNA polymerase and then cut with Sad to create a blunt/SacI fragment for insertion of the *D. salina* EPSPS-AmCyan reporter gene. An EPSPS overlap sequence was added to AmCyan via PCR using the primers, SEQ ID NO: 31 and 34. The primer sequences and corresponding SEQ ID NOs are depicted in Table 4.

TABLE 4

Chloroplast transit peptide primer sequences		
SEQ ID NO:	Primer name	Primer sequence 5' - 3'
31	AmCyan rev	TATATAGAGCTCTCAGAACG
33	EPSPS CTP forward	CTGGCCAGGCAGGGCGGCAGCCTGAGGGCCAGCCA GTGCAACGCCGCGCTGGCCAGGAGGGTGGAGGTGG GCGCCCTGGTGGTGCCGAGGCCGATCAGCGTGAAC GACGTGGTGCCGCACGTGTACAGCGCCCGCTGAG CG
34	EPSPS CTP reverse	TGCTCAGGGCCGGGGCGCTGTGGGCGGCCAGGGTG GCGCTGCACACGGTGGTCTGCAGCCTCCTGGTGT CCTGATGTGCTCTTGCTGCAGCTCCTCTGGCCA CGCTCAGCGGGGCGCTGTACACGTGCGGCACCAACG TCGTT
35	AmCyan w/EPSPS forward	CAGCGCCCCGGCCCTGAGCA

The primers were used in the following mixture:

[0103] 1.0 μ l pDNA template (AmCyan-EPSPS), 1.0 μ l forward primer (20 μ M), 1.0 μ l reverse primer (20 μ M), 2.5 μ l Pfu buffer, 1.0 μ l dNTPs (25 mM), 1.0 μ l Pfu Turbo polymerase, 17.5 μ l d_2H_2O .

The following thermocycler program was used:

[0104] 95° C. for 2 minutes (denaturing), 30 cycles of 95° C. for 1 minutes, 45° C. for 1 minute and 68° C. for 4 minutes with a 68° C. final extension for 15 minutes.

The PCR product was gel purified and combined with the *D. salina* EPSPS transit peptide sequence in equimolar concentration. The following primers, SEQ ID NO: 31 and 34, were used the PCR mixture according to the following conditions. The primers were used in the following mixture:

[0105] 1.0 μ l pDNA template (AmCyan w/EPSPS overlap), 1.0 μ l dsDNA template (EPSPS transit peptide) 1.0 μ l forward primer (20 μ M), 1.0 μ l reverse primer (20 μ M), 2.5 μ l Pfu buffer, 1.0 μ l dNTPs (25 mM), 1.0 μ l Pfu Turbo polymerase, 16.5 μ l d_2H_2O .

The following thermocycler program was used:

[0106] 95° C. for 2 minutes (denaturing), 30 cycles of 95° C. for 1 minutes, 45° C. for 1 minute and 68° C. for 4 minutes with a 68° C. final extension for 15 minutes.

The PCR product was gel purified, cut with SacI, ligated to the pSYN15460 backbone, SEQ ID NO: 21.

[0107] Completed vectors comprising the insertion, Examples 2A and 2B, were transformed into DH5 α competent cells. Then, the transformed DH5 α cells are used to make a glycerol stock suitable for long term storage. These cells are used to inoculate and grow liquid cultures suitable for DNA extraction. The extracted DNA derived from this glycerol stock is the basis for subsequent cloning into the *Agrobacterium tumefaciens* binary vector.

Example 3

Chloroplast Isolation

[0108] Maize chloroplasts were isolated from maize plants that were at the V2-V3 stage. Isolation was adapted from Asakura et al. (*Plant Cell* 16(1): 201-214 2004). Plants were grown in soil in a greenhouse until isolation, they were then placed in a dark chamber for a period of 3-5 hours to decrease photosynthesis to eliminate starch in the preparations. Leaves were removed and midveins were removed from the leaves. All subsequent steps were done on ice. The leaves were cut into smaller pieces, typically in a total of 15 g amounts. The cut plant pieces were placed in an ice cold grind buffer containing 50 mM HEPES, pH 7.6, 0.33M sorbitol, 1 mM $MgCl_2$, 2 mM EDTA, and 1% (w:v) BSA at a 1:4 (w:v) ratio. Plants were homogenized to a fine mince in cold buffer lightly to release the chloroplasts either via a blender or via hand with a sharp razor blade on ice in a polypropylene tube to try and reduce crushing of the chloroplasts. After homogenization, the homogenate was filtered through two layers of Miracloth into a beaker on ice. This filtrate was then filtered once more through 4 layers of Miracloth. This filtrate was placed in a 50 mL polycarbonate tube and centrifuged at 4,000 $\times$ g, 4° C., for 8 minutes and the supernatant was discarded. The pellet was resuspended in 1-2 mL resuspension (RB) buffer (50 mM HEPES, pH 7.6, 0.33M sorbitol, 1 mM DTT) and layered onto a 12.5 mL 30% (v:v) percoll gradient containing 50 mM HEPES, pH 7.6, 0.33M sorbitol, and 5 mM DTT. The gradient was then centrifuged in a 50 mL polycarbonate tube in a clinical centrifuge, swinging bucket attachment, at 1350 $\times$ g, 4° C. for 12 minutes. The pellet contained the chloroplasts and the supernatant, which contained broken chloroplast material, was discarded; the pellet was resuspended in 0.5 mL RB. Protein quantitation was performed of the resuspended pellet via the Bradford (*Analytical Biochemistry* 72: 248-254 1976) method. A small aliquot of the resuspended pellet was also visualized on a Leica DMLB light microscope at 40 and 100 $\times$ to examine chloroplasts for intactness.

[0109] Tobacco isolations were based upon protocols by Spencer and Wildman (*Biochemistry*. 3(7): 954-959 1964). Tobacco was isolated from young plants grown in soil that had 4-5 small leaves. Typically plants were isolated in 4-5 g batches. Leaves were cut into smaller pieces and then placed in an ice cold grind buffer containing 50 mM HEPES, pH 7.6, 0.33M sorbitol, 1 mM $MgCl_2$, 2 mM EDTA, and 1% (w:v) BSA at a 1:4 (w:v) ratio. Plants were homogenized to a fine mince either via a blender or via hand with a sharp razor blade on ice in a polypropylene tube to try and reduce crushing of the chloroplasts. The homogenate was then filtered through 2 layers of Miracloth into a beaker on ice. This filtrate was again filtered once more through 4 layers of Miracloth. The filtrate was placed in a 50 mL polycarbonate tube and centrifuged at 1000 $\times$ g, 4° C., for 15 minutes. The supernatant was discarded

and the pellet, which contained chloroplasts was resuspended in 0.5 mL RB. Protein quantitation was performed of the resuspended pellet via the Bradford (*Analytical Biochemistry* 72: 248-254 1976) method. A small aliquot of the resuspended pellet was also visualized on a Leica DMLB light microscope at 40 and 100× to visualize chloroplasts for intactness.

Example 4

Tobacco Transient Assays

[0110] To determine if heterologous proteins encoded by peptide constructs could be incorporated into chloroplasts in a transient system, the peptide constructs were transformed into *Agrobacterium* (LBA4404 strain). The *Agrobacterium* harboring the peptide construct of interest was grown in YP media overnight, 28° C., and then centrifuged 5000 rpm for ten minutes. The pellet was resuspended in MS inducing media (0.44% (w:v) MS basal salt mixture, 2% sucrose (w:v) and allowed to induce for 2 hours at room temperature. Young tobacco plants (having only 3-4 leaves) that were grown in soil were then infiltrated with the induced *Agrobacterium* by injecting the underside of leaves with a blunt ended syringe. Infiltration could be seen by eye as the liquid traveled into the leaf. Plants that were infiltrated were allowed to grow under normal greenhouse conditions for 3-4 days after infiltration before tissue was harvested for chloroplast isolations.

[0111] Reactions from in vitro recombinant peptide-AmCyan importation studies with maize chloroplasts were treated with thermolysin as stated above and then resuspended in RB. Small aliquots of the reactions (10 µL) were put under a Zeiss confocal microscope with filters applied at 486 and 594 to visualize AmCyan and autofluorescence of chloroplasts respectively. Overlays were done to determine if the protein was imported into the chloroplast.

[0112] The peptides, P28, P35, P37, ATPase and SSRubisco, were derived from *Chlamydomonas reinhardtii* sequences and were shown according to the invention to enable heterologous protein import into chloroplasts. Of these peptides fused to AmCyan, all five of them allow transport of AmCyan into the chloroplast in in vitro chloroplast importation assays. The remaining examples are in progress experimentally. Thus, the following peptides, P30, cytochrome *c*₅₅₀, cytochrome *c*₅₅₃, psaF and *D. salina* EPSPS receive a place holder of N/A, meaning not applicable. These results are depicted in Table 5.

TABLE 5

Transient assay results	
Transit Peptide	AmCyan
P28	Positive
P30	N/A
P35	Positive
P37	Positive
ssRubisco	Positive
ATPase	Positive
cytochrome <i>c</i> ₅₅₀	N/A
cytochrome <i>c</i> ₅₅₃	N/A
psaF	N/A
<i>D. salina</i> EPSPS	N/A

TABLE 6

Includes data for P28, P35, P37, SSR, ATPase transit peptides, confirming positive chloroplast targeting as shown in Table 5, and further includes data for remaining transit peptides C553, C550, P30, PSAF, EPSPS, PSAF.

Transit Peptide	Maize			Tobacco		
	Low	Medium	High	Low	Medium	High
P28			x			x
C553	X				x	
C550	X			x		
ATPase		x				x
P30		x			x	
P35			x		x	
SSR			x			x
P37			x		x	
PSAF	X				x	
EPSPS	X			x		

All tobacco constructs were analyzed at T0 stage. All maize constructs were analyzed at T1, with the exception of SSR and EPSPS, which were analyzed at T0 stage. All targeting capacity estimations were based on confocal microscopy of chloroplast fractions, where visualization of the AmCyan reporter protein expression was performed.

Example 5

Methods for Determining Chloroplast Targeting in Transgenic Plants

[0113] 5.A. Maize Transformation:

[0114] Transformation of immature maize embryos will be performed essentially as described in Negrotto et al., *Plant Cell Reports* 19:798-803 (2000). Various media constituents described therein can be substituted.

[0115] *Agrobacterium* strain LBA4404 (Invitrogen) containing the plant transformation plasmid is grown on YEP (yeast extract (5 g/L), peptone (10 g/L), NaCl (5 g/L), 15 g/L agar, pH 6.8) solid medium for 2 to 4 days at 28° C. Approximately 0.8×10^9 *Agrobacteria* are suspended in LS-inf media supplemented with 100 µM acetosyringone (As) (LSAs medium) (Negrotto et al., *Plant Cell Reports* 19:798-803 (2000)). Bacteria are pre-induced in this medium for 30-60 minutes.

[0116] Immature embryos from maize line, A188, or other suitable maize genotypes are excised from 8-12 day old ears into liquid LS-inf+100 µM As (LSAs). Embryos are vortexed for five (5) seconds and rinsed once with fresh infection medium. Infection media is removed and *Agrobacterium* solution is then added and embryos are vortexed for 30 seconds and allowed to settle with the bacteria for 5 minutes. The embryos are then transferred scutellum side up to LSAs medium and cultured in the dark for two to three days. Subsequently, between 20 and 25 embryos per petri plate are transferred to LSDc medium supplemented with cefotaxime (250 mg/L) and silver nitrate (1.6 mg/L) (Negrotto et al., *Plant Cell Reports* 19:798-803 (2000)) and cultured in the dark for 28° C. for 10 days.

[0117] Immature embryos producing embryogenic callus are transferred to LSD1M0.5S medium (LSDc with 0.5 mg/L 2,4-D instead of Dicamba, 10 g/L mannose, 5 g/L sucrose and no silver nitrate). The cultures are selected on this medium for 6 weeks with a subculture step at 3 weeks. Surviving calli are transferred either to LSD1M0.5S medium to

be bulked-up or to Reg1 medium (as described in Negrotto et al., *Plant Cell Reports* 19:798-803 (2000)). Following culturing in the light (16 hour light/8 hour dark regiment), green tissues are then transferred to Reg2 medium without growth regulators (as described in Negrotto et al., *Plant Cell Reports* 19:798-803 (2000)) and incubated for 1-2 weeks. Plantlets are transferred to Magenta GA-7 boxes (Magenta Corp, Chicago Ill.) containing Reg3 medium, as described in Negrotto et al. 2000, and grown in the light. Plants that are PCR positive for any component of the expression cassette are transferred to soil and grown in the greenhouse. The presence of any component of the expression cassette is determined by +/-PCR assay or by a Taqman copy number assay.

[0118] One skilled in the art will recognize maize transformation as an example of a monocot crop species. The results of this experimentation serve as an example extendible to other monocot species, such as rice, wheat, barley and sugarcane.

[0119] 5.B. Tobacco Transformation:

[0120] *Agrobacterium tumefaciens* strain LBA4404 containing a transformation vector containing an expression cassette will be used to infect leaf explants of *Nicotiana tabacum* c.v. Petit Havana (SR1). Initially, the tobacco leaves are cut

into 1-2 mm wide slices, exposed to the *Agrobacterium* for 5 minutes, and are placed on sterile paper to blot away excess liquid and then placed on co-cultivation medium for 3 days. The leaf slices are moved to selection/regeneration medium containing the appropriate selection agent. Selection agent resistant shoots are transplanted to soil. The plants are selfed or outcrossed with pollens from nontransgenic SR1 plants to produce seeds. The presence of any component of the expression cassette is determined by +/-PCR assay or by a Taqman copy number assay.

[0121] One skilled in the art will recognize tobacco transformation as an example of a dicot crop species. The results of this experimentation serve as an example extendible to other dicot species, such as soybean, sugarbeet, tomato and sunflower.

[0122] All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 32

<210> SEQ ID NO 1

<211> LENGTH: 90

<212> TYPE: DNA

<213> ORGANISM: *Chlamydomonas reinhardtii*

<400> SEQUENCE: 1

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gctgcccgtta aagctgtgag agtttagcgcg                                     90
```

<210> SEQ ID NO 2

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: *Chlamydomonas reinhardtii*

<400> SEQUENCE: 2

```
Met Ala Leu Val Ala Arg Pro Val Leu Ser Ala Arg Val Ala Ala Ser
1           5           10          15
Arg Pro Arg Val Ala Ala Arg Lys Ala Val Arg Val Ser Ala
                20          25          30
```

<210> SEQ ID NO 3

<211> LENGTH: 72

<212> TYPE: DNA

<213> ORGANISM: *Chlamydomonas reinhardtii*

<400> SEQUENCE: 3

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atgcaagctt tgagtagcag ggtgaatata gccgcaaaac cacagcgagc gcaacgttta      60
gtagttagag ca                                     72
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<210> SEQ ID NO 4

<211> LENGTH: 24

<212> TYPE: PRT

-continued

<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 4

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Met Gln Ala Leu Ser Ser Arg Val Asn Ile Ala Ala Lys Pro Gln Arg
1           5           10           15
Ala Gln Arg Leu Val Val Arg Ala
                20

```

<210> SEQ ID NO 5

<211> LENGTH: 90

<212> TYPE: DNA

<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 5

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atgcaaaactt tggcgagccg accatcatta cgtgctagtgc ccagggtcgc gcctagacgc      60
gcaccacggg ttgcagtggg aacaaaagct                                     90

```

<210> SEQ ID NO 6

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 6

```

Met Gln Thr Leu Ala Ser Arg Pro Ser Leu Arg Ala Ser Ala Arg Val
1           5           10           15
Ala Pro Arg Arg Ala Pro Arg Val Ala Val Val Thr Lys Ala
                20           25           30

```

<210> SEQ ID NO 7

<211> LENGTH: 78

<212> TYPE: DNA

<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 7

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atgcaagcat tagcgactcg accttcagct ataaggccaa caaaagctgc ccgtagaagc      60
agtgtagtgtg tgccgggca                                     78

```

<210> SEQ ID NO 8

<211> LENGTH: 26

<212> TYPE: PRT

<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 8

```

Met Gln Ala Leu Ala Thr Arg Pro Ser Ala Ile Arg Pro Thr Lys Ala
1           5           10           15
Ala Arg Arg Ser Ser Val Val Val Arg Ala
                20           25

```

<210> SEQ ID NO 9

<211> LENGTH: 135

<212> TYPE: DNA

<213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 9

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atggccgagg tcatagccaa atcaagcggt tccgcagccg tggcaaggcc tgctagatct      60
agcgtgaggc cgatggctgc cttgaaaccc gcagtcaaag cggcacctgt ggcagctcca    120
gcacaagcga atcag                                           135

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-continued

<210> SEQ ID NO 10
 <211> LENGTH: 45
 <212> TYPE: PRT
 <213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 10

Met Ala Ala Val Ile Ala Lys Ser Ser Val Ser Ala Ala Val Ala Arg
 1 5 10 15

Pro Ala Arg Ser Ser Val Arg Pro Met Ala Ala Leu Lys Pro Ala Val
 20 25 30

Lys Ala Ala Pro Val Ala Ala Pro Ala Gln Ala Asn Gln
 35 40 45

<210> SEQ ID NO 11
 <211> LENGTH: 105
 <212> TYPE: DNA
 <213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 11

atggcgccta tgtagcaag taaacaaggc gcgtttatgg gaaggagtag cttcgcacct 60

gccccaaaag gtgttgctag cagaggggtca ttgcaggtgg tagcgc 105

<210> SEQ ID NO 12
 <211> LENGTH: 35
 <212> TYPE: PRT
 <213> ORGANISM: Chlamydomonas reinhardtii

<400> SEQUENCE: 12

Met Ala Ala Met Leu Ala Ser Lys Gln Gly Ala Phe Met Gly Arg Ser
 1 5 10 15

Ser Phe Ala Pro Ala Pro Lys Gly Val Ala Ser Arg Gly Ser Leu Gln
 20 25 30

Val Val Ala
 35

<210> SEQ ID NO 13
 <211> LENGTH: 102
 <212> TYPE: DNA
 <213> ORGANISM: Synechococcus sp. PCC 7002

<400> SEQUENCE: 13

atgaacaaaa tactggggat tgatccactt aagaaaccta tctttggaat aagtgcattc 60

gtattactat ttggcaatt gaatgttggt gccgcgaatg ct 102

<210> SEQ ID NO 14
 <211> LENGTH: 34
 <212> TYPE: PRT
 <213> ORGANISM: Synechococcus sp. PCC 7002

<400> SEQUENCE: 14

Met Asn Lys Ile Leu Gly Ile Asp Pro Leu Lys Lys Pro Ile Phe Gly
 1 5 10 15

Ile Ser Ala Phe Val Leu Leu Phe Trp Gln Leu Asn Val Gly Ala Ala
 20 25 30

Asn Ala

<210> SEQ ID NO 15

-continued

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<211> LENGTH: 105
<212> TYPE: DNA
<213> ORGANISM: Synechocystis sp. PCC 6803

<400> SEQUENCE: 15
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atcttttttag gaggtatatt cagtttagga aatacagccc tagca                        105

<210> SEQ ID NO 16
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Synechocystis sp. PCC 6803

<400> SEQUENCE: 16
Met Phe Lys Leu Phe Asn Gln Ala Ser Arg Ile Phe Phe Gly Ile Ala
 1             5             10             15
Leu Pro Cys Leu Ile Phe Leu Gly Gly Ile Phe Ser Leu Gly Asn Thr
      20             25             30
Ala Leu Ala
      35

<210> SEQ ID NO 17
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Synechocystis sp. PCC 6803

<400> SEQUENCE: 17
atgaaacatt tacttgcggt gctgctagcc tttacattat ggttcaattt tgetccaagt      60
gcaagtgca                                     69

<210> SEQ ID NO 18
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Synechococcus sp. PCC 7002

<400> SEQUENCE: 18
Met Lys His Leu Leu Ala Leu Leu Leu Ala Phe Thr Leu Trp Phe Asn
 1             5             10             15
Phe Ala Pro Ser Ala Ser Ala
      20

<210> SEQ ID NO 19
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Dunaliella salina

<400> SEQUENCE: 19
atgctggcga ggcagggtgg ctctctcagg gcctcgcagt gtaatgcagg gctggctagg      60
agggtcgagg tgggcgccct ggttgtgcc cgtcccatct cggtaaatga cgtggtcctt      120
catgtgtaca gcgccccct ttcggtggcg aggagaagtt gcagcaagag cagcatcagg      180
agcacgaggc gcctgcagac gacagtttgc tctgtaett tggcggetca cagcgcc        237

<210> SEQ ID NO 20
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Dunaliella salina

<400> SEQUENCE: 20

```

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Met Leu Ala Arg Gln Gly Gly Ser Leu Arg Ala Ser Gln Cys Asn Ala
 1 5 10 15
 Gly Leu Ala Arg Arg Val Glu Val Gly Ala Leu Val Val Pro Arg Pro
 20 25 30
 Ile Ser Val Asn Asp Val Val Pro His Val Tyr Ser Ala Pro Leu Ser
 35 40 45
 Val Ala Arg Arg Ser Cys Ser Lys Ser Ser Ile Arg Ser Thr Arg Arg
 50 55 60
 Leu Gln Thr Thr Val Cys Ser Ala Thr Leu Ala His Ser Ala
 65 70 75

<210> SEQ ID NO 21

<211> LENGTH: 4145

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Cloning Vector Sequence

<400> SEQUENCE: 21

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ccacctaaat tgtaagcgtt aatattttgt taaaattcgc gttaaatttt tgttaaatca    60
gctcattttt taaccaatag gccgaaatcg gcaaaatccc ttataaatca aaagaataga    120
ccgagatagg gttgagtgtt gttccagttt ggaacaagag tccactatta aagaacgtgg    180
actccaacgt caaagggcga aaaaccgtct atcagggcga tggcccacta cgtgaaccat    240
caccctaate aagttttttg gggtcgaggt gccgtaaagc actaaatcgg aaccctaaag    300
ggagcccccg atttagagct tgacggggaa agccggcgaa cgtggcgaga aaggaaggga    360
agaaagcgaa aggagcgggc gctagggcgc tggcaagtgt agcggtcacg ctgcgcgtaa    420
ccaccacacc cgccgcgctt aatgcgcgcg tacagggcgc gtcccattcg ccattcaggc    480
tgcgcaactg ttgggaaggg cgatcggtgc gggcctcttc gctattacgc cagctggcga    540
aaggggggatg tgctgaagg cgattaagtt gggtaacgcc agggttttcc cagtcaacgac    600
gttgtaaaac gacggccagt gagcgcgcgt aatacgactc actatagggc gaattgggta    660
cggggaccca agctttggca gacaaagtgg cagacatact gtcccacaaa tgaagatgga    720
atctgtaaaa gaaaacgcgt gaaataatgc gtctgacaaa ggtaggtcg gctgccttta    780
atcaatacca aagtggctcc taccacgatg gaaaaactgt gcagtcgggt tggctttttc    840
tgacgaacaa ataagattcg tggccgacag gtgggggtcc accatgtgaa ggcattctca    900
gactccaata atggagcaat gacgtaaggg cttacgaaat aagtaagggt agtttgggaa    960
atgtccactc acccgtcagt ctataaatac ttagcccttc cctcattgtt aaggggagcaa   1020
aatctcagag agatagtcct agagagagaa agagagcaag tagcctagaa gtggatcccc   1080
accatggcgc ccaccgtgat gatggcctcg tcggccaccg ccgtcgctcc gttccagggg   1140
ctcaagtcca ccgccagcct ccccgtcgcc cgccgctcct ccagaagcct cggcaacgtc   1200
agcaacggcg gaaggatccg ctgcatgagc tcttcataatg acgatcgttc aaacatttgg   1260
caataaagtt tcttaagatt gaatcctgtt gccggtcttg cgatgattat catataattt   1320
ctgttgtaatt acgttaagca tgtaataatt aacatgtaat gcatgacgtt atttatgaga   1380
tgggttttta tgattagagt cccgcaatta tacatttaat acgcgataga aaacaaaata   1440
tagcgcgcaa actaggataa attatcgcgc gcggtgtcat ctatgttact agatcgcgga   1500

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cggaagcata	aagtgtaaag	cctgggggtgc	ctaagtgatg	agctaactca	cattaattgc	1680
gttgcgctca	ctgcccgctt	tccagtcggg	aaacctgtcg	tgccagctgc	attaatgaat	1740
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tgactcgctg	cgctcggtcg	ttcggtcgcg	gcgagcggtg	tcagctcact	caaaggcggt	1860
aatacgggta	tccacagaat	caggggataa	cgcaggaaag	aacatgtgag	caaaaggcca	1920
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ccctgacgag	catcacaaaa	atcgacgctc	aagtcagagg	tggcgaaacc	cgacaggact	2040
ataaagatac	caggcgcttc	cccctggaag	ctccctcggt	cgctctctcg	ttccgaccct	2100
gccgcttacc	ggatacctgt	ccgcctttct	cccttcggga	agcgtggcgc	tttctcatag	2160
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tgacgctcag	tggaaacgaa	actcacgtta	agggattttg	gtcatgagat	tatcaaaaag	2640
gatcttcacc	tagatccttt	tcgacccaat	aaatacctgt	gacggaagat	cacttcgcag	2700
aataaataaa	tctgtgtgct	cctgttgata	cggggaagcc	ctgggccaac	ttttggcgaa	2760
aatgagacgt	tgatcggtgc	gtaagagggt	ccaactttca	ccataatgaa	ataagatcac	2820
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aaaaaatcac	tggatatacc	accgttgata	tatcccaatg	gcacgtaaa	gaacattttg	2940
aggeatttca	gtcagttgct	caatgtacct	ataaccagac	cgttcagctg	gatattacgg	3000
cctttttaaa	gaccgtaaag	aaaaataagc	acaagtttta	tccggccttt	attcacattc	3060
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gaatgcttaa	tgaattacaa	cagtactgcg	atgagtggca	gggcggggcg	taattttttt	3540
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ggatgaatgg	cagaaattcg	aaagcaaat	cgacccggtc	gtcgggttcag	ggcagggtcg	3660
ttaaatagcc	gcttatgtct	attgtcgtgt	taccggttta	ttgactaccg	gaagcagtgt	3720
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aattgacgat atgatccttt tttctgacg aaaaagtgc catcattgga aaacgttctt	3840
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gtgcacccaa ctgatcttca gcattcttta ctttcaccag cgtttctggg tgagcaaaaa	3960
caggaaggca aaatgccga aaaaaggga taaggcgac acggaatgt tgaatactca	4020
tactcttctt ttttcaatat tattgaagca tttatcaggg ttattgtctc atgagcggat	4080
acatatTTga atgtatttag aaaaataaac aaataggggt tccgcgcaca tttccccgaa	4140
aagtg	4145

<210> SEQ ID NO 22
 <211> LENGTH: 123
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Photosystem I P28 including primer

<400> SEQUENCE: 22

tataaccat gccattggtc gcccgaccag ttttatcagc aagggtagcg gcaagtcgcc	60
ctcgggtagc tgcccgtaaa gctgtgagag ttagcgcggc cctgagcaac aagttcatcg	120
gcg	123

<210> SEQ ID NO 23
 <211> LENGTH: 94
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Photosystem I P30 including primer

<400> SEQUENCE: 23

caagctttga gtagcagggt gaatatagcc gcaaaaccac agcgagcgca acgttttagta	60
gttagagcag ccctgagcaa caagttcatc ggcg	94

<210> SEQ ID NO 24
 <211> LENGTH: 112
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Photosystem I P35 including primer

<400> SEQUENCE: 24

caaaacttgg cgagccgacc atcattacgt gctagtgccg gggtcgcgcc tagacgcgca	60
ccacgggttg cagtggtaac aaaagctgcc ctgagcaaca agttcatcgg cg	112

<210> SEQ ID NO 25
 <211> LENGTH: 100
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Photosystem I P37 including primer

<400> SEQUENCE: 25

caagcattag cgactcgacc ttcagctata aggccaaaca aagctgccc tagaagcagt	60
gtagttgtgc gggcagccct gagcaacaag ttcacggcg	100

<210> SEQ ID NO 26
 <211> LENGTH: 168
 <212> TYPE: DNA

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<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: SSRubisco including primer

<400> SEQUENCE: 26
tatataccat ggccgcggtc atagccaaat caagcgtttc cgcagccgtg gcaaggcctg      60
ctagatctag cgtgaggccg atggctgcct tgaaaccgcg agtcaaagcg gcacctgtgg      120
cagctccagc acaagcgaat caggccctga gcaacaagtt catcggcg      168

<210> SEQ ID NO 27
<211> LENGTH: 138
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: ATPase including primer

<400> SEQUENCE: 27
tatataccat ggccgctatg ttagcaagta aacaaggcgc gtttatggga aggagtagct      60
tcgcacctgc cccaaaaggt gttgctagca gagggtcatt gcagggtgga gcggccctga      120
gcaacaagtt catcggcg      138

<210> SEQ ID NO 28
<211> LENGTH: 124
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Cytochrome c550 including primer

<400> SEQUENCE: 28
aacaaaatac tggggattga tccacttaag aaacctatct ttggaataag tgcattcgta      60
ttactatttt ggcaattgaa tgttggtgcc gcgaatgctg ccctgagcaa caagttcatc      120
ggcg      124

<210> SEQ ID NO 29
<211> LENGTH: 127
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Cytochrome c553 including primer

<400> SEQUENCE: 29
tttaaactgt ttaaccaagc gagtagaata ttctttggga ttgctttgcc atgtcttata      60
tttttaggag gtatattcag tttaggaaat acagccctag cagccctgag caacaagtgc      120
atcggcg      127

<210> SEQ ID NO 30
<211> LENGTH: 91
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: psaF including primer

<400> SEQUENCE: 30
aaacatttac ttgcgttgct gctagccttt acattatggt tcaattttgc tccaagtgca      60
agtgcagccc tgagcaacaa gttcatcggc g      91

<210> SEQ ID NO 31

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: AmCyan reverse primer

<400> SEQUENCE: 31

tatatagagc tctcagaacg                               20

<210> SEQ ID NO 32
<211> LENGTH: 154
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Maize optimized AmCyan

<400> SEQUENCE: 32

gccctgagca acaagttcat cggcgacgac atgaagatga cctaccacat ggacggctgc      60
gtgaacggcc actacttcac cgtgaagggc gagggcagcg gcaagccata cgaggggcacc     120
cagaccagca ccttcaaggt gacgatggcc aacg                                     154

```

What is claimed:

1. A plant having stably incorporated into its genome a DNA construct, said construct comprising a nucleotide sequence encoding a plastid targeting peptide wherein said nucleotide sequence is operably linked to a nucleotide sequence encoding a polypeptide of interest, wherein said nucleotide sequence encoding a plastid targeting peptide is selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19;
- b) a nucleotide sequence having at least 90% sequence identity to SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19, wherein said nucleotide sequence encodes a peptide capable of transporting an operably linked polypeptide to a plastid;
- c) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20; and,
- d) a nucleotide sequence encoding an amino acid sequence having at least 90% sequence identity to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 wherein said amino acid sequence is capable of transporting an operably linked polypeptide to a plastid.

2. The plant of claim 1, wherein said plant is a monocotyledonous plant.

3. The plant of claim 2, wherein said monocotyledonous plant is a maize, rice or sugarcane plant.

4. The plant of claim 1, wherein said plant is a dicotyledonous plant.

5. The plant of claim 4, wherein said dicotyledonous plant is a soybean plant.

6. A method of expressing a polypeptide of interest in a plant, said method comprising introducing into said plant a DNA construct comprising a nucleotide sequence encoding a plastid targeting peptide, wherein said nucleotide sequence encoding a plastid targeting peptide is operably linked to a nucleotide sequence encoding said polypeptide of interest, said nucleotide sequence encoding a plastid targeting peptide is selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19;
 - b) a nucleotide sequence having at least 90% sequence identity to SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19, wherein said nucleotide sequence encodes a peptide capable of transporting an operably linked polypeptide to a plastid;
 - c) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20; and,
 - d) a nucleotide sequence encoding an amino acid sequence having at least 90% sequence identity to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 wherein said amino acid sequence is capable of transporting an operably linked polypeptide to a plastid.
7. The method of 6, wherein said plant is a monocotyledonous plant.
8. The method of 6, wherein said plant is a dicotyledonous plant.
9. The method of 6, wherein said polypeptide sequence of interest is a bioprocessing enzyme.
10. The method of 6, wherein said nucleotide sequence encoding said polypeptide of interest is a herbicide tolerant gene.

11. A substantially purified peptide capable of transporting a polypeptide into a cellular plastid wherein said peptide comprises an amino acid sequence set forth in the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19 and variants thereof, wherein said variant retains the ability to transport a polypeptide.

12. The peptide of claim 11, wherein said peptide is operably linked to a polypeptide of interest.

13. A nucleotide sequence that encodes one of the peptides of any one of claims 11-12.

14. A nucleotide sequence having 90% sequence identity to a nucleotide sequence of claim 13.

15. A DNA construct comprising the nucleotide sequence of claim 13 or 14.

16. A plant cell having stably incorporated into its genome a DNA construct, said construct comprising a nucleotide sequence encoding a plastid targeting peptide wherein said nucleotide sequence is operably linked to a nucleotide sequence encoding a polypeptide of interest, wherein said nucleotide sequence encoding a plastid targeting peptide is selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20;
- b) a nucleotide sequence having at least 90% sequence identity to SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19, wherein said nucleotide sequence encodes a peptide capable of transporting an operably linked polypeptide to a plastid;

c) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20; and,

d) a nucleotide sequence encoding an amino acid sequence having at least 90% sequence identity to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 wherein said amino acid sequence is capable of transporting an operably linked polypeptide to a plastid.

17. The plant cell of claim **16**, wherein said plant cell is from a dicotyledonous plant.

18. The plant cell of claim **16**, wherein said plant cell is from a monocotyledonous plant.

19. A plant comprising the plant cell of claim **18**.

20. Stably transformed seed of the plant of claim **19**.

* * * * *