Vectors comprising novel regulatory elements

BACKGROUND

The invention relates to the field of recombinant DNA technology and, in particular, the development of vectors for the expression of recombinant proteins. Expression of heterologous genes in eukaryotic cells is a fundamental aspect of biotechnology with many academic and commercial applications. Expression of such genes requires transcription by RNA polymerase II (Pol II), which is driven by *cis*-acting genetic elements known as promoters and enhancers.

In simple terms, promoters are directional elements that act to initiate transcription of sequences situated less than 100 (and usually less than 50) nucleotide base pairs (bp) downstream. They contain a number of short consensus nucleotide sequences that act as binding sites for various proteins that participate in the initiation of transcription and the assembly of a multi-subunit complex known as the pre-initiation complex (McKnight and Tjian, 1987, Cell 46: 795–805). In most genes, this occurs at a very widely conserved sequence known as the TATA box (TATAAA) to which the TATA box-binding protein (TBP, a subunit of the general transcription factor TFIID) binds. There follows an ordered assembly of more than ten further transcription factors to finally form the Pol II holoenzyme complex. RNA transcription actually starts at an initiator site about 25–30 bases downstream (Breathnach and Chambon, 1981, Annu Rev Biochem 50: 349–393) to which TBP also binds.

Most functional promoters contain further upstream promoter elements (UPEs), of which the most highly conserved are the CAAT box (CCAAT, the binding site for the transcription factors CBF, C/EBP and NF-1), about 70–200bp upstream, and the GC box (GGGCGG, binding site for the general transcription factor Sp-1) a similar distance upstream. Although basal levels of transcription occur from the TATA box alone, for most promoters at least the CAAT and GC boxes are required for optimal levels of transcription.

Enhancers are sequences that act non-directionally to increase transcription from promoters situated locally but not necessarily immediately adjacent (up to several kilobases away (Kadonaga (2004) Cell 116: 247–257). Enhancers contain short (8–12bp) consensus sequences representing the binding sites for a wide range of transcriptional activator proteins (Ondek *et al*, 1988, Science 236: 1237–1244) including

some, such as NF-1 and SP-1 that are also associated with promoter elements. These sequences are often duplicated in tandem or inverted repeats.

In some natural transcription units, including the very active immediate/early gene transcription units of many DNA viruses such as cytomegalovirus, enhancer and promoter elements may be functionally combined into what is effectively one extended upstream element.

Promoters may be regulated, being responsive to cell type, temperature, metal ions or other factors; or constitutive, giving transcription that is unresponsive to such factors. For many purposes a strong, constitutive promoter giving consistent, high, levels of transcription in many, if not all, cell types is highly advantageous. For many years the enhancer/promoter element driving immediate/early gene expression in human cytomegalovirus has been very widely used for driving such expression of heterologous genes in eukaryotic expression vectors (Foecking & Hoffstetter, 1986, Gene 45: 101–105).

Human cytomegalovirus (CMV) is a member of the betaherpesvirus family and is responsible for gastrointestinal and respiratory infections, hepatitis, and retinitis. As with other herpesviruses, CMV can persist in latent infections and can be reactivated in immunocompromised individuals. In cell culture, human CMV replicates productively in terminally differentiated cells such as fibroblast, epithelial, and endothelial cells and in monocyte-derived macrophages (Isomura and Stinski, 2003, J Virol 77: 3602–3614 and references therein).

During productive infection, there is an ordered expression of sets of CMV genes, designated immediate-early (IE), early, or late. The human CMV IE genes are thought to play a critical role in the efficiency of replication (reviewed in Castillo and Kowalik, 2002, Gene 290: 19–34).

The region upstream of the human CMV IE promoter is divided into three regions, the modulator, the unique region, and the enhancer. The enhancer is also divided into a distal and a proximal enhancer. The distal enhancer is necessary for efficient IE gene expression and viral replication at a low MOI. Human CMVs have very strong enhancers for the expression of IE genes. The human CMV enhancer has four 18-bp repeat elements containing an NF-κB or rel binding site, five 19-bp repeat elements containing

a CREB or ATF binding site, two AP-1 binding sites, and multiple SP-1 sites (Thomsen *et al*, 1984, Proc Natl Acad Sci USA 81: 659–663; Meier and Stinski, 1996, Intervirology 39: 331–342). The murine CMV enhancer contains six NF-□B or *rel* binding sites, one CREB or ATF binding site, and at least seven AP-1 binding sites (Dorsch-Hasler *et al*, 1985, Proc Natl Acad Sci USA 82: 8325–8329). The different *cis*-acting elements act individually and synergistically to stabilize the RNA polymerase II transcription initiation complex on the promoter.

A number of cytomegaloviruses predominantly infecting other host species are known, although, in many cases, the exact taxonomy and degree of cross-species relatedness is provisional. Cytomegalovirus-like viruses infecting a number of primate species (including African green monkey, Rhesus monkey and bonobo) and rodents including mouse, rat and guinea pig are recognised. Of these, only the murine and rat promoter-enhancers have been subject to detailed functional analysis. Comparison of these species with human CMV shows that the functions of the IE promoter-enhancers are not directly comparable, probably because of the presence of unrecognised *cis*-acting elements contributing to downstream transcription in cells of different species (Isomura and Stinski, 2003, J Virol 77: 3602–3614).

However, both human and murine CMV IE promoter-enhancers produce high levels of constitutive expression of heterologous genes in eukaryotic expression vectors and are widely used in biotechnology. Such use of the human CMV promoter was disclosed in US 5,168, 062 (Stinski / University of Iowa). Use of the promoter, enhancer and functionally complete 5' (upstream) untranslated region including the first intron of the human cytomegalovirus major immediate-early gene, wherein this is not directly linked to its natural DNA coding sequence is claimed by US 5,591,639 (Bebbington /Celltech). Use of the murine CMV IE enhancer is disclosed by US 4,968,615 (Koszinowski *et al*)

Guinea pig CMV (GPCMV) produces a disease of guinea pigs with many similarities to the pathology of human CMV infections. Attempts to characterise the genome (Isom *et al*, 1984, J Virology 49: 426–436; Gao and Isom, 1984, J Virology 52: 436–447) suggested that the structural organisation of the genome was unique amongst herpesviruses. Although of a similar size to human and murine CMV, the GPCMV genome was far simpler than that of human CMV and most closely resembled that of murine CMV. However, the GPCMV genome had several unusual features, particularly in the structure of the terminal regions. Later studies of IE gene expression identified an

IE region by sequence comparison with human CMV (Yin *et al*, 1990, J Virol 64: 1537–1548) and the expression and processing of IE transcripts was analysed. However, there was no analysis of the usefulness of the IE promoter-enhancer for the expression of heterologous genes.

The sequence of the 'HRv' (*Hin*d III–*Eco*RV) immediate-early upstream fragment of the GPCMV genome, containing the 5' end of IE1 coding sequence and the upstream promoter/enhancer regions was sequenced (Yin, 1991, *Guinea pig cytomegalovirus immediate-early gene expression*, PhD thesis, Pennsylvania State University, USA) and shown to contain a region of repetitive sequences, typical of a CMV IE regulatory region. Three short repeats, GP-1, GP-2 and GP-3 were identified. GP-1 is an 18-bp repeat occurring 9 times (73–100% similarity to a GGCCCGGGACTTTCCA consensus) containing an NF-κB binding site and corresponding to the HCMV 18-bp repeat. GP-2 is a 17-bp repeat occurring 10 times (86–100% similarity to a TGTCCTTTTTGGCAAA consensus) and containing a core sequence similar to the consensus SRE (serum response element). GP-3 is repeated 4 times in the proximal upstream region and contains GTGACTTT, a sequence identified as a binding site for c-*jun* or GCN4 (Hill *et al*, 1984, Science 234: 451–457).

Although this work suggested that the GPCMV IE upstream region contained a strong promoter, due to the way the reporter constructs were made certain artefacts could not be excluded. Firstly, the HRv fragment also appears to include the first exon and part of the first intron of the IE1 gene. This intron contains three copies of a putative NF-1 binding site, which may have artificially boosted the apparent strength of the promoter. Secondly, the reporter constructs used to test the GPCMV fragments contained an SV40 promoter (itself a strong viral promoter), so that reporter expression resulted from the effect of a double GPCMV / SV40 promoter. As a result it is not possible to make comparisons of the GPCMV enhancer/promoter alone with other strong promoters generally, or even with other CMV IE enhancer/promoters.

The applicant's co-pending patent application PCT/GB99/02357 (WO 00/05393), incorporated by reference herein, describes elements that are responsible, in their natural chromosomal context, for establishing an open chromatin structure across a locus that consists exclusively of ubiquitously expressed, housekeeping genes. These elements are not derived from a Locus Control Region (LCR) and comprise extended

methylation-free CpG islands. The term Ubiquitous Chromatin Opening Element (UCOE) has been used to describe such elements.

In mammalian DNA, the dinucleotide CpG is recognised by a DNA methyltransferase enzyme that methylates cytosine to 5-methylcytosine. However, 5-methylcytosine is unstable and is converted to thymine. As a result, CpG dinucleotides occur far less frequently than one would expect by chance. Some sections of genomic DNA nevertheless do have a frequency of CpG that is closer to that expected, and these sequences are known as "CpG islands". As used herein a "CpG island" is defined as a sequence of DNA, of at least 200bp, that has a GC content of at least 50% and an observed / expected CpG content ratio of at least 0.6 (i.e. a CpG dinucleotide content of at least 60% of that which would be expected by chance) (Gardiner-Green M and Frommer M. *J Mol Biol* 196, 261–282 (1987); Rice P, Longden I and Bleasby A *Trends Genet* 16, 276–277 (2000).

Methylation-free CpG islands are well-known in the art (Bird *et al* (1985) Cell 40: 91-99, Tazi and Bird (1990) Cell 60: 909-920) and may be defined as CpG islands where a substantial proportion of the cytosine residues are not methylated and which usually extend over the 5' ends of two closely spaced (0.1-3 kb) divergently transcribed genes. These regions of DNA are reported to remain hypomethylated in all tissues throughout development (Wise and Pravtcheva (1999) Genomics 60: 258-271). They are often associated with the 5' ends of ubiquitously expressed genes, as well as an estimated 40% of genes showing a tissue-restricted expression profile (Antequera, F. & Bird, A. *Proc. Natl. Acad. Sci. USA* 90, 1195-11999 (1993); Cross, S.H. & Bird, A.P. *Curr. Opin, Genet. Dev. 5,* 309-314 (1995) and are known to be localised regions of active chromatin (Tazi, J. & Bird, A. *Cell* 60, 909-920 (1990).

An 'extended' methylation-free CpG island is a methylation-free CpG island that extends across a region encompassing more than one transcriptional start site and/or extends for more than 300bp and preferably more than 500bp. The borders of the extended methylation-free CpG island are functionally defined through the use of PCR over the region in combination with restriction endonuclease enzymes whose ability to digest (cut) DNA at their recognition sequence is sensitive to the methylation status of any CpG residues that are present. One such enzyme is *Hpa*II, which recognises and digests at the site CCGG, which is commonly found within CpG islands, but only if the central CG residues are *not* methylated. Therefore, PCR conducted with *Hpa*II-digested DNA and

over a region harbouring *Hpa*II sites, does *not* give an amplification product due to *Hpa*II digestion if the DNA is *unmethylated*. The PCR will *only* give an amplified product if the DNA is *methylated*. Therefore, beyond the methylation-free region *Hpa*II will not digest the DNA a PCR amplified product will be observed thereby defining the boundaries of the "extended methylation-free CpG island".

International application WO 00/05393 demonstrates that regions spanning methylation-free CpG islands encompassing dual, divergently transcribed promoters from the human TATA binding protein (*TBP*)/proteosome component-B1 (*PSMBI*) and heterogeneous nuclear ribonucleoprotein A2/B1 (*hnRNPA2*)/heterochromatin protein 1Hsγ (*HP1* $^{Hs\gamma}$) gene loci impart enhanced levels of gene expression to operably linked genes. Methylation-free CpG islands associated with actively transcribing promoters possess the ability to remodel chromatin and are thus thought to be a prime determinant in establishing and maintaining an open domain at housekeeping gene loci.

UCOEs confer an increased proportion of productive gene integration events with improvements in the level and stability of transgene expression. This has important research and biotechnological applications including the generation of transgenic animals and recombinant protein products in cultured cells.

WO 00/05393 discloses functional UCOE fragments of approximately 4.0kb, in particular, the '5.5 RNP' fragment defined by nucleotides 4102 to 8286 of Figure 21 (as disclosed on p11, lines 6 and 7). The same application discloses a '1.5kb RNP' fragment (Figs 22 and 29, derivation described on p51, lines 1 to 5). However, this fragment is actually a 2165bp *Bam*HI–*Tth*111I fragment of the '5.5 RNP' fragment described above, consisting of nucleotides 4102 to 6267 of Figure 21 of that application.

A further application , WO 02/24930, discloses artificially-constructed UCOEs composed of fragments of naturally-occurring CpG islands. A third application, WO 04/067701 describes polynucleotides comprising small functional fragments of UCOEs. Such polynucleotides comprise methylation-free CpG islands of no more than approximately 2kb, or fragments of larger such islands, of not more than approximately 2kb.

Given the importance of recombinant protein expression in biotechnology, there remains a need for improved expression vectors comprising novel promoter / enhancer combinations.

SUMMARY OF THE INVENTION

Throughout the description and claims of this specification, the words "comprise" and "contain" and variations of the words, for example "comprising" and "comprises", means "including but not limited to", and is not intended to (and does not) exclude other moieties, additives, components, integers or steps.

Throughout the description and claims of this specification, the singular encompasses the plural unless the context otherwise requires. In particular, where the indefinite article is used, the specification is to be understood as contemplating plurality as well as singularity, unless the context requires otherwise.

Features, integers, characteristics, compounds, chemical moieties or groups described in conjunction with a particular aspect, embodiment or example of the invention are to be understood to be applicable to any other aspect, embodiment or example described herein unless incompatible therewith.

As used herein, the term "operably linked" refers to a relationship of operability between elements in the polynucleotides of the invention. "Operably linked" is a term, well known to those of skill in the art, that describes a functional relationship between *cis*-acting DNA sequences. The exact structural relationship may or may not be relevant and differs for different types of elements. For a promoter, it implies an essentially adjacent (usually within less than 100bp) position 5' to the open reading frame that it drives. In the case of extended methylation-free CpG islands, it appears that a regional effect on chromatin structure is responsible for increasing the level and consistency of gene expression. By way of example, the element comprising an extended methylation-free CpG-island may be positioned 5' of the enhancer / promoter controlling transcription of the expressible gene. However, "operably-linked" embraces the possibility of its being positioned elsewhere, as long as a clear functional effect can be demonstrated.

By 'functional homologue' is meant a polynucleotide sequence capable of hybridising, under stringent conditions, to the disclosed sequence, and which has similar properties of conferring increased expression of operably-linked expressible open reading frames in two or more tissues. Stringent hybridisation/washing conditions are well known in the art. For example, nucleic acid hybrids that are stable after washing in 0.1 x SSC ,0.1%

SDS at 60°C. It is well known in the art that optimal hybridisation conditions can be calculated if the sequence of the nucleic acid is known. For example, hybridisation conditions can be determined by the GC content of the nucleic acid subject to hybridisation. See Sambrook *et al* (1989), Molecular Cloning; A Laboratory Approach. A common formula for calculating the stringency conditions required to achieve hybridisation between nucleic acid molecules of a specified homology is:

$T_m = 81.5^0$ C + 16.6 Log $[Na^+]$ + 0.41[% G + C] –0.63 (%formamide)

An object of the invention is to provide novel DNA molecules and vectors containing transcriptional enhancers providing very high levels of expression of operably-linked expressible nucleic acid sequences in eukaryotic cells. Advantageously the enhancers may be used in combination with their naturally-associated promoters and / or other genetic elements that increase transcription.

The invention relates to the guinea pig cytomegalovirus early-immediate promoter / enhancer and its use in expression vectors, particularly for obtaining high levels of expression of recombinant proteins. The invention provides eukaryotic expression vectors that are capable of providing increased levels of expression in many cell types over that obtainable from human or murine CMV IE enhancer /promoter elements

The guinea pig cytomegalovirus early-immediate upstream regulatory region consists of the approximately 1500bp upstream of the IE1 gene and more especially the sequence disclosed by Figure 1 and SEQ ID NO:1. It comprises both promoter and enhancer elements. By 'promoter' is meant at least the transcriptional start site, TATA box and CAAT box, being a fragment comprising nucleotides 779 to 880 of Figure 1 (SEQ ID NO: 1) or a functional homologue thereof.

Accordingly, the invention provides an isolated polynucleotide comprising at least 100, preferably 200, and more preferably at least 500, contiguous polynucleotides of the guinea pig CMV immediate/early regulatory region as depicted in Figure 1 and SEQ ID NO:1 and an expressible polynucleotide sequence, transcription of said expressible polynucleotide sequence being driven by a promoter situated between enhancer and gene or other expressible sequence, which may be the endogenous guinea pig CMV immediate/early promoter or some other, heterologous, promoter not naturally associated with the enhancer. The expressible polynucleotide sequence is not a guinea

pig CMV immediate /early gene and is not naturally operably linked with the promoter. It will be understood, by one of skill in the art, that in the case of a circular isolated polynucleotide (as in a plasmid vector) by 'between' is meant upstream of the directly operably linked expressible polynucleotide sequence (5' with respect to the sense strand), and downstream (3') of the operably linked enhancer. It is understood that such an isolated polynucleotide may comprise other promoters, not associated with expression of the inserted expressible sequence of interest (such as those required for expression of selectable markers or those associated with other elements).

Hence the isolated polynucleotide comprises

a) an element comprising at least 200, and preferably at least 500, contiguous nucleotides of SEQ ID NO:1 and

b) an element comprising an expressible polynucleotide sequence;

characterised in that said isolated polynucleotide comprises, in a 5' to 3' direction with respect to the sense strand of the expressible polynucleotide sequence, an enhancer, a single promoter, and said expressible polynucleotide sequence, and wherein said enhancer is operably linked to said promoter, which is directly operably linked to said expressible polynucleotide sequence and wherein said promoter is not naturally operably linked to said expressible polynucleotide sequence..

Preferably the isolated polynucleotide contains a 5' fragment of the immediate/early regulatory region comprising nucleotides 50 to 550 or, alternatively, a 3' fragment comprising nucleotides 275 to 775. Such fragments contain functional enhancer fragments, without the endogenous promoter.

In one embodiment, therefore, the isolated polynucleotide of the invention comprises at least the promoter from the immediate/early regulatory region of guinea pig CMV directly operably linked to an expressible nucleic acid sequence to which it is not naturally operably linked, said promoter preferably comprising nucleotides 779 to 880 of SEQ ID NO: 1. By 'directly operably linked' is meant that transcription of the gene or other expressible nucleic acid is driven directly from the promoter.

Preferably, said isolated polynucleotide further comprises the enhancer from the major immediate/early regulatory region of guinea pig CMV, more preferably comprising nucleotides 1 to 887 of SEQ ID NO:1

In one preferred embodiment, said isolated polynucleotide further comprises an extended, methylation-free CpG island operably linked to said expressible nucleic acid sequence. More preferably, said extended, methylation-free CpG island comprises one or more further promoters, particularly dual or bi-directional promoters that transcribe divergently. Hence the invention provides an isolated polynucleotide comprising at least 200 contiguous nucleotides of Figure 1 (SEQ ID NO:1), operably linked to an expressible polynucleotide sequence, and further comprising an extended, methylation-free CpG island operably linked to said expressible polynucleotide sequence. Such an extended, methylation-free CpG island may be conveniently situated adjacent to, and upstream of, the enhancer sequence. Preferably such an isolated polynucleotide comprises at least 500 contiguous polynucleotides of Figure 1 (SEQ ID NO:1), more preferably a 5' fragment of the immediate/early regulatory region comprising nucleotides 50 to 550 or, alternatively, a 3' fragment comprising nucleotides 275 to 775. Most more preferably it comprises nucleotides 1 to 887 of SEQ ID NO:1

In one embodiment, said extended, methylation-free CpG island comprises a 44kb DNA fragment spanning the human TATA binding protein gene and 12kb each of the 5' and 3' flanking sequence, or functional fragment thereof. Preferably, the functional fragment comprises a 25kb DNA fragment spanning the human TATA binding protein gene with 1kb 5' and 5kb 3' flanking sequence or a functional fragment thereof. More preferably, the functional fragment of the TATA binding protein gene-associated extended, methylation-free CpG island is of not more than 2kb, further preferably of no more than approximately 1 kb, most preferably comprising a 987bp *Bsp*E1 – *Esp*3I restriction fragment.

In a second embodiment, said extended, methylation-free CpG island comprises a 60 kb DNA fragment spanning the human hnRNP A2 gene with 30 kb 5' and 20 kb 3' flanking sequence, or a functional fragment thereof. Preferably, said functional fragment comprises a 16kb DNA fragment spanning the human hnRNP A2 gene with 5kb 5' and 1.5kb 3' flanking sequence, more preferably a fragment of the human hnRNP A2 gene of no more than 2kb, more preferably no more than 1.6kb, comprising a 1546bp *Esp*3I restriction fragment. Preferably, said fragment is orientated in forward orientation.

In a third embodiment, the isolated polynucleotide of the present invention comprises a fragment of the β-actin CpG island/ promoter region, preferably of human origin, more

preferably a DNA fragment within the range of 100bp to 2kb spanning the human β-actin CpG island/ promoter region.

In a fourth embodiment, the isolated polynucleotide of the present invention comprises a fragment of the PDCD2 CpG island/ promoter region, preferably of human origin, more preferably a DNA fragment within the range from 100bp to 2 kb spanning the human PDCD2 CpG island/ promoter region.

In a final alternative embodiment, said extended, CpG-rich unmethylated CpG island is an artificial sequence, not occurring in nature, comprising a DNA fragment within the range from 100bp to 1.9kb spanning the human β-actin CpG island/ promoter region and a DNA fragment within the range from 100bp to 2kb spanning the human PDCD2 CpG island/ promoter region. Preferably said fragments are directly adjacent with their promoters oriented divergently.

In a further aspect the invention provides a vector comprising the isolated polynucleotide as described above. The vector may be any vector capable of transferring DNA to a cell. Preferably the vector is a eukaryotic expression vector. Such vectors comprise elements such as promoters and enhancers capable of directing and enhancing transcription in eukaryotic cells. They also preferably contain other features to facilitate and optimise their function. Such features include origins of replication selected to allow replication in the appropriate eukaryotic host cell and also in prokaryotic cells used to manufacture the vectors themselves, one or more selectable markers (often conferring resistance to antibiotics or toxins) allow selection of cells containing the vector in either cell type, elements allowing amplification of the vector or integrated fragments of it, and polylinkers or multicloning sites conveniently situated downstream of the main enhancer/ promoter to allow easy insertion of an expressible polynucleotide sequence (commonly referred to as an 'insert') encoding a desired polypeptide product. Such refinements are well-known in the art.

Preferably, the vector is an integrating vector or an episomal vector.

Preferred integrating vectors include recombinant retroviral vectors. A recombinant retroviral vector will include DNA of at least a portion of a retroviral genome which portion is capable of infecting the target cells. The term "infection" is used to mean the process by which a virus transfers genetic material to its host or target cell. Preferably,

the retrovirus used in the construction of a vector of the invention is also rendered replication-defective to remove the effect of viral replication of the target cells. In such cases, the replication-defective viral genome can be packaged by a helper virus in accordance with conventional techniques. Generally, any retrovirus meeting the above criteria of infectiousness and capability of functional gene transfer can be employed in the practice of the invention.

Suitable retroviral vectors include but are not limited to pLJ, pZip, pWe and pEM, well known to those of skill in the art. Suitable packaging virus lines for replication-defective retroviruses include, for example, ΨCrip, ΨCre, Ψ2 and ΨAm.

Other vectors useful in the present invention include adenovirus, adeno-associated virus, SV40 virus, vaccinia virus, HSV and poxvirus vectors. A preferred vector is the adenovirus. Adenovirus vectors are well known to those skilled in the art and have been used to deliver genes to numerous cell types, including airway epithelium, skeletal muscle, liver, brain and skin (Hitt *et al*, 1997; Anderson, 1998).

A further preferred vector is the adeno-associated (AAV) vector. AAV vectors are well known to those skilled in the art and have been used to stably transduce human T-lymphocytes, fibroblasts, nasal polyp, skeletal muscle, brain, erythroid and haematopoietic stem cells for gene therapy applications. International Patent Application WO 91/18088 describes specific AAV based vectors.

Preferred episomal vectors include transient non-replicating episomal vectors and self-replicating episomal vectors with functions derived from viral origins of replication such as those from EBV, human papovavirus (BK) and BPV-1. Such integrating and episomal vectors are well known to those skilled in the art and are fully described in the body of literature well known to those skilled in the art. In particular, suitable episomal vectors are described in WO98/07876.

Mammalian artificial chromosomes can also be used as vectors in the present invention. The use of mammalian artificial chromosomes is discussed by Calos (1996).

In a preferred embodiment, the vector of the present invention is a plasmid. The plasmid may be a non-replicating, non-integrating plasmid.

The term "plasmid" as used herein refers to any nucleic acid encoding an expressible gene and includes linear or circular nucleic acids and double or single stranded nucleic acids. The nucleic acid can be DNA or RNA and may comprise modified nucleotides or ribonucleotides, and may be chemically modified by such means as methylation or the inclusion of protecting groups or cap- or tail structures.

A non-replicating, non-integrating plasmid is a nucleic acid which when transfected into a host cell does not replicate and does not specifically integrate into the host cell's genome (i.e. does not integrate at high frequencies and does not integrate at specific sites).

Highly preferred embodiments of vectors of the invention comprise nucleotides 1 to 1003 and 1747 to 5749 of SEQ ID NO: 2; nucleotides 1 to 9328 and 10072 to 14119 of SEQ ID NO: 3; or nucleotides 1 to 2592 and 3336 to 7383 of SEQ ID NO: 4, being expression vectors suitable for insertion of an expressible sequence in place of the exemplary enhanced green fluorescent protein reporter encoded by the full sequences.

The present invention also provides a host cell transfected with the vector of the present invention. The host cell may be any eukaryotic cell. Preferably it is a mammalian cell, more preferably a human or rodent cell.

Numerous techniques are known and are useful according to the invention for delivering the vectors described herein to cells, including the use of nucleic acid condensing agents, electroporation, complexing with asbestos, polybrene, DEAE cellulose, Dextran, liposomes, cationic liposomes, lipopolyamines, polyornithine, particle bombardment and direct microinjection .

A vector of the invention may be delivered to a host cell non-specifically or specifically (i.e. to a designated subset of host cells) via a viral or non-viral means of delivery. Preferred delivery methods of viral origin include viral particle-producing packaging cell lines as transfection recipients for the vector of the present invention into which viral packaging signals have been engineered, such as those of adenovirus, herpes viruses and papovaviruses. Preferred non-viral based gene delivery means and methods may also be used in the invention and include direct naked nucleic acid injection, nucleic acid condensing peptides and non-peptides, cationic liposomes and encapsulation in liposomes.

Delivery of a vector according to the invention is contemplated using nucleic acid condensing peptides. Nucleic acid condensing peptides, which are particularly useful for condensing the vector and delivering the vector to a cell, are described in International Patent Application WO 96/41606. Functional groups may be bound to peptides useful for delivery of a vector according to the invention, as described in WO 96/41606. These functional groups may include a ligand that targets a specific cell-type such as a monoclonal antibody, insulin, transferrin, asialoglycoprotein, or a sugar. The ligand thus may target cells in a non-specific manner or in a specific manner that is restricted with respect to cell type.

The functional groups also may comprise a lipid, such as palmitoyl, oleyl, or stearoyl; a neutral hydrophilic polymer such as polyethylene glycol (PEG), or polyvinylpyrrolidine (PVP); a fusogenic peptide such as the HA peptide of influenza virus; or a recombinase or an integrase. The functional group also may comprise an intracellular trafficking protein such as a nuclear localisation sequence (NLS), an endosome escape signal such as a membrane disruptive peptide, or a signal directing a protein directly to the cytoplasm.

The invention further provides a host cell comprising an isolated polynucleotide or vector as herein described. Preferably said cell is a eukaryotic cell, more preferably a mammalian cell, further preferably a human or rodent cell.

In a further aspect, the invention provides a method of expressing an expressible polynucleotide, preferably encoding a polypeptide, comprising inserting an isolated polynucleotide according to the invention into a suitable expression vector as described herein and further inserting said vector into a suitable host cell as described herein and culturing said host cell in suitable conditions to allow expression.

Preferably, said polypeptide is a therapeutically useful polypeptide, preferably selected from the list consisting of an immunoglobulin or a functional epitope-binding fragment of an immunoglobulin, a growth factor, a receptor or soluble fragment thereof and a blood clotting factor.

Also provided is a pharmaceutical preparation comprising a polynucleotide, vector or host cell according to the invention and a pharmaceutically acceptable carrier, excipient, buffer or medium.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide sequence of the GPCMV IE enhancer/promoter (SEQ ID NO:1). Potential binding sites for the transcription factors AP-1, NF-κB, SRF and GCN4 are shown, together with CAAT and TATA boxes, the CRS initiator site and transcriptional start (arrow).

Figure 2 shows expression levels obtained with a number of EGFP reporter constructs in CHO-K1 cells, expressed as median fluorescence as measured by FACS. The results compare human and guinea pig CMV IE enhancer/promoters, with and without a 1.5kb hnRNP UCOE element.

Figure 3 shows a map of reporter plasmid CET 1005 GPCMV-EGFP comprising the GPCMV IE enhancer/promoter (GPCMV) driving expression of an enhanced green fluorescence protein reporter gene (EGFP). The eukaryotic selectable marker is a puromycin resistance gene expressed from a mouse phosphoglycerate kinase promoter. The prokaryotic selectable marker is ampicillin resistance.

Figure 4 shows a map of reporter plasmid CET1015 8kb-GPCMV-EGFP. This is similar to CET 1005 GPCMV-EGFP with the addition of the 8kb hnRNP UCOE element upstream of the GPCMV IE enhancer/promoter.

Figure 5 shows a map of reporter plasmid CET1015 1.5kb-GPCMV-EGFP. This is similar to CET 1015 8kb-GPCMV-EGFP with the replacement of the 8kb hnRNP UCOE with a 1.5kb hnRNP UCOE element.

Figure 6 compares EGFP expression driven by human and guinea pig CMV IE enhancer/ promoter elements in HEK293 cells (human embryonic kidney cells transformed with sheared adenovirus type 5 DNA)

Figure 7 shows a similar comparison using luciferase-based reporter constructs.

DETAILED DESCRIPTION

Example 1

Generation of stably transfected CHO-K1 cells using vectors containing either the hCMV promoter or the gpCMV promoter

The plasmids constructs were generated as follows. The ampicillin resistance gene was isolated from pBluescript® (Stratagene) by PCR incorporating *Nru*I sites within each end of the primer (5'-TGTCGCGAGTCTGACAGTTACCAAT GCTTAATC 3' (SEQ ID NO:5),

5'- CATCGCGAGCACTTTTCGGGGAAATGTGTGCGC-3' (SEQ ID NO:6). The PCR product was inserted into the *Pvu*II site of p*Mae*II (Nucleic Acids Research 2001 29:E26) to generate pCA1. The following oligonucleotides

1. 5'- TCGAAGTTTAAACATTTAAATCTAGAAGCTTAT-3' (SEQ ID NO:7)
2. 5'-CCGGTATCGATAAGCTTCTAGATTTAAATGTTTAAACT-3' (SEQ ID NO:8)
3. 5'-CGATACCGGTGGCGCGCCAATTGTTAATTAAGATCTGG-3' (SEQ ID NO:9)
4. 5'-CCCATTGGGCCAGATCTTAATTAACAATTGGCGCGCCA-3' (SEQ ID NO:10)
5. 5'-CCCAATGGGCCGTACGAATTCCTTAGGCTCGAG-3' (SEQ ID NO:11)
6. 5'-GGCCCTCGAGCCTAAGGAATTCGTACGG-3' (SEQ ID NO:12)

were annealed (1 with 2; 3 with 4; 5 with 6; and then the three dimers were annealed together) and used to replace the multicloning site of pCA1 between the *Xho*I and *Not*I sites destroying these sites during the construction. This generated pCA1MCS. The *Age*I site was deleted from the PGK promoter within pPGK-Puro-bgh pA by *Age*I restriction digestion followed by blunting with T4 DNA polymerise and re-ligation. The PGK-Puromycin pA cassette was removed from this vector as an *Eco*RI-*Xho*I fragment and ligated into pCA1MCS that had similarly been digested with *Eco*RI and *Xho*I. This vector was designated pCIA-Puro (CET 1000). The bghpA in pCIA-Puro was then replaced with the HSV TkpA. The HSV-Tk polyA was removed from pEGFP-N1 as a *Bst*BI-*Eco*109I fragment, blunted with T4 DNA polymerase, and ligated into pCIA-Puro that had been digested with *Sac*I and blunted with T4 DNA polymerase. This vector was designated CET 1005.

To construct pCET1005 1.5kb-GPCMV-EGFP, the 1.5kb hnRNP UCOE fragment was excised from pCET20 (described previously) using *Bsm*BI, blunt-ended using T4 polymerase and then cloned into the blunted *Xho*I site of pEGFP-N1 (Clontech, Palo Alto, CA, USA) generating pEGFP-N1 1.5kb-EGFP. The 2.4kb "hnRNP-EGFP" cassette was then excised from this plasmid using *Nhe*I (blunt-ended)/*Not*I and subcloned into the backbone of pCET1005-EGFP that had been digested with *Swa*I/*Not*I to give pCET1005 1.5kb-EGFP. The GPCMV promoter was then excised from pPCRScript GPCMV (synthesized by Geneart, Regensburg, Germany) with *Nhe*I and *Eco*RI, blunt-ended and subcloned into the blunted *Bam*HI of this plasmid to yield pCET1005 1.5kb-GPCMV-EGFP. Excising the 1.5kb hnRNP UCOE using *Pme*I/*Sac*I, blunt-ending and religating the backbone generated the plasmid pCET1005 GPCMV-EGFP.

To construct pCET1015 8kb-GPCMV-EGFP, the 5.3kb *Sac*I (blunt)/*Pac*I fragment of pCET1005 1.5kb-GPCMV-EGFP was subcloned into the *Asc*I (blunt)/*Pac*I-digested backbone of pCET1015. The plasmid pCET1005 1.5kb-HCMV-EGFP was constructed by subcloning the blunted 1.5kb hnRNP *Bsm*BI fragment from pCET20 into the blunted *Cla*I site of pCET1005-EGFP.

CHO-K1 cells were maintained in F12 (HAM) nutrient mixture (Gibco, UK) supplemented with 10% Foetal Calf Serum (Invitrogen, UK) and 5 U/ml Penicillin and Streptomycin mix (Sigma, UK). For stable transfection of CHO-K1, plasmids were linearised with *Pci*I, extracted in phenol: chloroform: isoamyl alcohol and chloroform, precipitated in ethanol and resuspended at a concentration of 0.25μg/μl in sterile water. In a sterile electroporation cuvette, equivalent molar quantities of linearised plasmids were diluted to 25μl in sterile water (1.39μg pCET1005-EGFP, 1.78μg pCET1005 1.5kb-HCMV-EGFP, 1.45μg pCET1005 GPCMV-EGFP or 1.85μg pCET1005 1.5kb-GPCMV-EGFP) and mixed with $5x10^6$ CHO-K1 cells in 250μl growth medium. After incubation on ice for 15 minutes, the cells were electroporated at 250V/975μF (BioRad Gene Pulser II™) and incubated at room temperature for a further 10 minutes. Cells were then transferred into 10ml of growth media, harvested by centrifugation and transferred into a 225cm^2 tissue culture flask in a total of 50ml of growth medium. Cells were incubated for 24 hours at 37°C in a 5% CO_2 incubator before addition of Puromycin (Sigma, UK) to a concentration of 12.5μg/ml. Cells were cultured for 8 days (replacing selective media after 4 days) before the stable transfectants were harvested, subcultured in 6-well tissue culture dishes (maintaining selection) and analysed by Fluorescence Activated Cell Sorting using the FL1 channel to view EGFP. Figure 2 clearly shows that the two gpCMV containing constructs pCET1005-GPCMV-EGFP (Figure 3) and pCET1005-1.5kb-GPCMV-EGFP (Figure 5) generate pools which express the transgene to a higher level than the corresponding constructs which use the hCMV promoter, pCET1005-EGFP and pCET1005-1.5kb-HCMV-EGFP respectively.

Example 2

HEK293 cells were maintained in Dulbecco's Modified Eagle Medium (DMEM; Sigma, UK) supplemented with 10% Foetal Calf Serum and 5 U/ml Penicillin and Streptomycin mix. For stable transfection, HEK293 cells were seeded into 6-well dishes at a density of $1x10^6$ cells/well and cultured for 24 hours at 37°C in a 5% CO_2 incubator. Cells were then transfected with 4μg of the indicated plasmid (pCET1005-EGFP or pCET1005-gpCMV-EGFP)(linearised with *Pci*I) using 10μl Lipofectamine 2000 (Invitrogen, UK).

The DNA and Lipofectamine 2000 were diluted separately in 250μl OptiMEM I (Gibco, UK) and, after incubation at room temperature for 5 minutes, mixed together and incubated for a further 20 minutes. Growth media on the cells was replaced with 1ml of OptiMEM I supplemented with 15% FCS and the DNA/Lipofectamine 2000 mixture was then added. Cells were incubated at 37°C in a 5% CO_2 incubator for 5 hours before 3.5ml of OptiMEM I supplemented with 10% FCS was added. Cells were then incubated at 37°C in a 5% CO_2 incubator for 24 hours before being harvested and transferred to a 225cm^2 tissue culture flask in a total of 50ml of DMEM growth medium, supplemented with 0.5μg/ml Puromycin. Cells were grown for approximately 14 days (replacing the selective media every 3-4 days) before the stable transfectants were harvested by centrifugation, subcultured in 6-well tissue culture dishes (maintaining selection) and analysed by Fluorescence Activated Cell Sorting using the FL1 channel to view EGFP. Figure 6 shows that the pools generated with the gpCMV construct give EGFP expression levels three to four fold higher than those generated with the hCMV construct.

Example 3

CHO-K1 cells were cultured as described for Example 1. 1.5x10^5 CHO-K1 cells were seeded 24 hrs before transfection into 12-wells. 24 hrs later, cells were transfected with 1 ug Luciferase reporter plasmid (phCMV-Luc or pgpCMV-Luc) using 1.5 ul FUGENE (Roche, UK). For this, FUGENE and DNA were both diluted separately in Opti-MEM I (Invitrogen), mixed together and incubated for 30 min at RT before added to the cells. Luciferase expression was analysed 24 hrs later using a Berthold luminometer (Berthold, Wildbad, Germany). Generally, cell lysis and luciferase reporter assay were performed as described earlier (Lipinski *et al.,* Gene Therapy, 2001 (8): 274-281). Transfections were done in triplicate and the mean and standard deviation of one representative experiment are shown (Figure 7). Clearly the gpCMV vector was at least two-fold more active luciferase than the hCMV plasmid.

The plasmid hCMV-Luc has been described earlier (Lipinski *et al.,* Gene Therapy (2001) 8: 274-281). The plasmid gpCMV-Luc was generated by preparing a *Nde*I/*Eco*RI fragment from pCRScript/gpCMV (customer gene synthesis company: Geneart, Regensburg, Germany) and cloning this gpCMV promoter fragment into the blunted *Xho*I site of pGL3basic (Promega).

CLAIMS

1. An isolated polynucleotide comprising
   a. an element comprising at least 200 contiguous nucleotides of SEQ ID NO:1 and
   b. an element comprising an expressible polynucleotide sequence;

   characterised in that said isolated polynucleotide comprises, in a 5' to 3' direction with respect to the sense strand of the expressible polynucleotide sequence, an enhancer, a single promoter, and said expressible polynucleotide sequence, and wherein said enhancer is operably linked to said promoter, which is directly operably linked to said expressible polynucleotide sequence and wherein said promoter is not naturally operably linked to said expressible polynucleotide sequence.

2. An isolated polynucleotide according to claim 1, comprising at least 500 contiguous nucleotides of SEQ ID NO:1

3. An isolated polynucleotide according to either of claim 1 or 2, comprising nucleotides 50 to 550 of SEQ ID NO:1

4. An isolated polynucleotide according to either of claim 1 or 2, comprising nucleotides 275 to 775 of SEQ ID NO:1

5. An isolated polynucleotide according to either of claim 1 or 2, comprising the promoter from the immediate/early regulatory region of guinea pig CMV directly operably linked to an expressible nucleic acid sequence to which it is not naturally operably linked.

6. An isolated polynucleotide according to claim 5, comprising nucleotides 679 to 880 of SEQ ID NO: 1.

7. An isolated polynucleotide according to any preceding claim , comprising nucleotides 1 to 887 of SEQ ID NO:1

8. An isolated polynucleotide according to any preceding claim, further comprising an extended, methylation-free CpG island operably linked to said expressible nucleic acid sequence.

9. A vector comprising the polynucleotide of any preceding claim.

10. A eukaryotic expression vector according to claim 9.

11. A vector according to either claim 9 or claim 10, comprising the polynucleotide sequence of nucleotides 1 to 1003 and 1747 to 5749 of SEQ ID NO: 2.

12. A vector according to either claim 9 or claim 10, comprising nucleotides 1 to 9328 and 10072 to 14119 of SEQ ID NO: 3.

13. A vector according to either claim 9 or claim 10, comprising nucleotides 1 to 2592 and 3336 to 7383 of SEQ ID NO: 4.

14. A host cell comprising an isolated polynucleotide according to any of claims 1 to 5, or the vector of any of claims 11 to 13.

15. A method of expressing a polypeptide comprising inserting an expressible nucleic acid sequence encoding said polypeptide into an expression vector according to any of claims 11 to 13 into an appropriate host cell and culturing said host cell in suitable conditions to allow expression.

16. Method according to claim 15, wherein said polypeptide is a therapeutically useful polypeptide.

17. Method according to claim 16, wherein said polypeptide is selected from the list consisting of: an immunoglobulin, a functional epitope-binding fragment of an immunoglobulin, a growth factor, soluble receptor and blood clotting factor.

18. A pharmaceutical preparation comprising a polynucleotide according to any of claims 1 to 8, a vector according to any of claims 11 to 13, or a host cell according to claim 14 and a pharmaceutically acceptable carrier, excipient, buffer or medium.