progressive and severe neurological impairment. PKU is estimated to affect approximately 15,000 people in the U.S. and there are no treatments available that address the genetic defect in PKU.

[0014] Despite the tremendous advances in understanding the biochemistry, molecular biology, and genetics of PKU, little progress has been made in developing new treatments for the disorder. There is large unmet need for disease-modifying therapies in PKU. First, current therapies are not disease modifying and are only effective in a subset of patients, and still require strict dietary restrictions, and non-compliance can lead to neuronal damage. Second, there are no approved gene therapies for PKU, and AAV based therapies cannot be used by 25% to 40% of patients due to pre-existing antibodies. AAV can only be administered once, and the resulting PAH levels might not be high enough to be efficacious, or may be supranormal, dose levels cannot be titrated.

[0015] Accordingly, there is need in the field for a technology that permits expression of a therapeutic PAH protein in a cell, tissue or subject for the treatment of PKU.

SUMMARY

[0015a] In one aspect, the present disclosure refers to a closed-ended DNA (ceDNA) vector comprising: at least one nucleotide sequence positioned between flanking inverted terminal repeats (ITRs), wherein the at least one nucleotide sequence encodes at least one phenylalanine hydroxylase (PAH) protein, wherein the at least one nucleotide sequence comprises a sequence having at least 95% identity to SEQ ID NO: 382.

[0015b] In another aspect, the present disclosure refers to the use of the ceDNA vector as disclosed herein in the manufacture of a medicament for expressing an PAH protein in a cell *in vivo*.

[0015c] In another aspect, the present disclosure refers to an *in vitro* method of expressing a PAH protein in a cell, the method comprising contacting the cell with the ceDNA vector as disclosed herein.

[0015d] In another aspect, the present disclosure refers to the use of the ceDNA vector as disclosed herein in the manufacture of a medicament for treating a subject with phenylketonuria (PKU).

[0015e] In another aspect, the present disclosure refers to a pharmaceutical composition comprising the ceDNA vector as disclosed herein.

[0015f] In another aspect, the present disclosure refers to a cell comprising the ceDNA vector as disclosed herein.

[0015g] In another aspect, the present disclosure refers to a composition comprising the ceDNA vector as disclosed herein and a lipid.

[0015h] In yet another aspect, the present disclosure refers to a kit comprising the ceDNA vector as disclosed herein, the pharmaceutical composition as disclosed herein, the cell as disclosed herein, or the composition as disclosed herein.

CLAIMS

1. A closed-ended DNA (ceDNA) vector comprising:

at least one nucleotide sequence positioned between flanking inverted terminal repeats (ITRs), wherein the at least one nucleotide sequence encodes at least one phenylalanine hydroxylase (PAH) protein, wherein the at least one nucleotide sequence comprises a sequence having at least 95% identity to SEQ ID NO: 382.

2. The ceDNA vector of claim 1, wherein the ceDNA vector comprises a promoter linked to the at least one nucleotide sequence that encodes at least one PAH protein.

3. The ceDNA vector of claim 2, wherein the promoter comprises a nucleic acid sequence having at least 85% identity to SEQ ID NO: 191.

4. The ceDNA vector of any of claims 1 to 3, wherein the ceDNA vector comprises:

an enhancer;

a 5' UTR and/or intron sequence;

a 3' UTR;

at least one poly A sequence; and/or

at least one promoter operably linked to the at least one nucleotide sequence.

5. The ceDNA vector of any one of claims 1-4, wherein the at least one nucleotide sequence is a cDNA.

6. The ceDNA vector of any one of claims 1-5, wherein

at least one of the flanking ITRs comprises a functional terminal resolution site (TRS) and a Rep binding site:

one or both of the flanking ITRs are derived from a virus selected from the group consisting of: a parvovirus, a dependovirus, and an adeno-associated virus (AAV);

the flanking ITRs are symmetric or asymmetric; optionally wherein

the flanking ITRs are symmetric or substantially symmetric; or

the flanking ITRs are asymmetric;

one of the flanking ITRs is a wild-type ITR, or wherein both of the ITRs are wild-type ITRs;

the flanking ITRs are derived from different viral serotypes;

the flanking ITRs are derived from a pair of viral serotypes set forth in Table 2;

one or both of the flanking ITRs comprise a sequence selected from the group consisting of: the sequences set forth in Table 3, Table 5A, Table 5B, and Table 6;

at least one of the flanking ITRs is altered from a wild-type AAV ITR sequence by a deletion, an addition, and/or a substitution that affects the overall three-dimensional conformation of the ITR;

one or both of the flanking ITRs are derived from an AAV serotype selected from the

group consisting of: AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, and AAV12;

and/or

one of the flanking ITRs is not a wild-type ITR, or wherein both of the flanking ITRs are not wild-type ITRs.

7. The ceDNA vector of any one of claims 1-6, wherein one or both of the flanking ITRs are synthetic.

8. The ceDNA vector of any one of claims 1-7, wherein one or both of the flanking ITRs is modified by a deletion, an insertion, and/or a substitution in at least one of the ITR regions selected from the group consisting of: the A, A', B, B', C, C', D, and D' regions: optionally wherein:

one or both of the flanking ITRs is modified by a deletion, an insertion, and/or a substitution in at least one of the ITR regions selected from A, A', B, B', C, C', D, and D', wherein the deletion, the insertion, and/or the substitution results in the deletion of all or part of a stem-loop structure formed by the A, A', B, B' C, or C' regions; or

one or both of the flanking ITRs are modified by a deletion, an insertion, and/or a substitution that results in the deletion of all or part of a stem-loop structure formed by the B and B' regions; or

one or both of the flanking ITRs are modified by a deletion, an insertion, and/or a substitution that results in the deletion of all or part of a stem-loop structure formed by the C and C' regions; or

one or both of the flanking ITRs are modified by a deletion, an insertion, and/or a substitution that results in the deletion of all or part of a stem-loop structure formed by the B and B' regions and/or part of a stem-loop structure formed by the C and C' regions; further optionally wherein:

one or both of the flanking ITRs comprise a single stem-loop structure in the region that, in a wild-type ITR, would comprise a first stem-loop structure formed by the B and B' regions and a second stem-loop structure formed by the C and C' regions;

one or both of the flanking ITRs comprise a single stem and two loops in the region that comprises a first stem-loop structure formed by the B and B' regions and a second stem-loop structure formed by the C and C' regions; further optionally wherein:

one or both of the flanking ITRs comprise a single stem and a single loop in the region that, in a wild-type ITR, would comprise a first stem-loop structure formed by the B and B' regions and a second stem-loop structure formed by the C and C' regions; further optionally wherein:

both flanking ITRs are altered in a manner that results in an overall three-dimensional symmetry when the flanking ITRs are inverted relative to each other.

9. The ceDNA vector of any one of claims 1-8, wherein the at least one nucleotide sequence

comprises a sequence having at least 96% identity to SEQ ID NO:382.

10. The ceDNA vector of any one of claims 1-9, wherein the ceDNA vector comprises a nucleic acid sequence that is at least 90% identical to SEQ ID NO: 192.

11. The ceDNA vector of any one of claims 1-10, wherein the ceDNA vector comprises at least one regulatory switch.

12. Use of the ceDNA vector of any one of claims 1-11 in the manufacture of a medicament for expressing an PAH protein in a cell *in vivo*.

13. The use of claim 12, wherein the cell is a hepatic cell.

14. An *in vitro* method of expressing a PAH protein in a cell, the method comprising contacting the cell with the ceDNA vector of any one of claims 1-11.

15. The use of any one of claims 12 or 13 or the method of claim 14, wherein the at least one nucleotide sequence is codon optimized for expression in the cell.

16. Use of the ceDNA vector of any one of claims 1-11 in the manufacture of a medicament for treating a subject with phenylketonuria (PKU).

17. The use of claim 16, wherein the ceDNA vector is delivered to a hepatic cell.

18. The use of any of claims 16-17, wherein the ceDNA vector expresses the PAH protein in a hepatic cell.

19. The use of any of claims 16-18, wherein the ceDNA vector is to be administered via any one or more routes selected from the group consisting of: intravenous injection, intramuscular injection, and infusion.

20. The use of any one of claims 16-19, wherein the subject exhibits at least about a 50% decrease in level of serum phenylalanine as compared to a level of serum phenylalanine in the subject prior to treatment.

21. The use of any one of claims 16-20, wherein the subject has a serum phenylalanine level of less than about 1500 μM after treatment.

22. The use of any one of claims 16-21, wherein the subject exhibits at least about a 10% increase in PAH activity after treatment as compared to a level of PAH activity prior to treatment.

23. A pharmaceutical composition comprising the ceDNA vector of any one of claims 1-11.

24. A cell comprising the ceDNA vector of any of claims 1-11.

25. The cell of claim 24, wherein the cell is a hepatic cell.

26. A composition comprising the ceDNA vector of any of claims 1-11 and a lipid.

27. The composition of claim 26, wherein the lipid is a lipid nanoparticle (LNP).

28. A kit comprising the ceDNA vector of any one of claims 1-11, the pharmaceutical composition of claim 23, the cell of claim 24 or claim 25, or the composition of claim 26 or 27.