

# Torus Black-Hole Inspired by Mitochondrial-DNA in (1 + 3)-Dimensions

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**How to cite this paper:** Nieto-Marín, N. and Nieto, J.A. (2025) Torus Black-Hole Inspired by Mitochondrial-DNA in (1 + 3)-Dimensions. *Journal of Applied Mathematics and Physics*, **13**, 2902-2912.  
<https://doi.org/10.4236/jamp.2025.139166>

**Received:** August 9, 2025

**Accepted:** September 12, 2025

**Published:** September 15, 2025

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## Abstract

In this work, we investigate a possible conceptual link between torus-shaped black hole solutions of the vacuum gravitational field equations in (1 + 3)-dimensional general relativity and mitochondrial DNA (mtDNA). We propose that this analogy could serve as a framework for transferring insights and methodologies between the study of mtDNA and toroidal black hole geometries. By establishing this connection, we aim to provide novel perspectives that could contribute to advancements in both theoretical physics and molecular biology, offering new tools for understanding complex structures in these disciplines.

## Keywords

Torus Black-Hole, (1 + 3)-Dimensional General Relativity, Mitochondrial-DNA, Genetic Code

## 1. Introduction

In [1], the necessary computations were established for considering black-hole solutions for any compact, simply connected manifolds with genus  $g$  [2]. Of course, the traditional black-hole is associated with a 2-dimensional sphere  $S^2$  of genus  $g = 0$ . Since there is no mathematical reason to specifically choose  $g = 0$ , rather than  $g \neq 0$ , as an example a solution of a black-hole of genus  $g = 1$ , corresponding to a donut or torus, was established.

Previously, torus-like black-holes were considered in [3]. Several studies on the thermodynamics of torus-like black-holes have been conducted, including fluctuations, statistical entropy [4], the quantum effect on Hawking radiation [5], thermal fluctuations and quasi-normal modes [6], thermodynamic instability [7], Gibbs

free energy [8], variation of the chaos bound in two regions [9], and weak cosmic censorship conjecture [10]. Additionally, there has been significant interest in topological aspects of torus-like black holes: dimensional black holes with toroidal or higher genus horizons [11], Born-Infeld-dilaton black-holes [12] and topological black holes in anti-de Sitter space [13]. Notably, there are also studies of 3-dimensional black-holes associated with  $S^3$  event horizon (see [14] and references therein).

In order to establish a kind of link between mitochondrial-DNA and the torus black hole, we shall use the progress in the developments from [1]. Topologically, the torus can be described by the structure  $S^1 \times S^1$ . So if we make a distinction of these two circles, let's say  $S^1_{(b)} \times S^1_{(a)}$ , with  $a$  is the radius of a helix and  $b$  is the distance from the axis to the center of the torus or the radius of the ring, we can consider a rotation of two opposite points on  $S^1_{(a)}$  in such a way that they describe a double helix structure around  $S^1_{(b)}$ . This idea can be understood as analogous to the structure of mitochondrial-DNA structure. The central aim of this work is to explore these observations in greater detail.

Now, DNA consists of two strands in the form of a double right-handed helix of repeating units called nucleotides, each of which consists of a 4-base, Adenine (A), Thymine (T), Cytosine (C) and Guanine (G) which form the stair rungs. The 4-nucleotides are joined together by covalent bonds between the phosphate group of one nucleotide and the sugar molecule of the next, forming a phosphate-sugar backbone from which the nitrogenous bases protrude. The two strands are held together by hydrogen bonds between the bases. Importantly, the four bases have specific pairing properties: adenine can only pair with thymine, and cytosine can only pair with guanine [15]. Schematically, we can consider these 4 options in the form

$$\begin{aligned} A - T, \\ T - A, \\ C - G, \\ G - C. \end{aligned} \tag{1}$$

The genetic code can be constructed by considering the so-called codons, which are a triplet of the 4-nucleotide. In turn, the triality of nucleotides means that there are  $64 = 4 \times 4 \times 4$  possible combinations or codons. Indeed, 61 codons specify 20 amino acids, one as a starting (initiation) codon which establishes the beginning of synthesis and simultaneously encodes the amino acid methionine; on the other hand, 3 are used as stop signals (see [16]). So, the first problem is how to distribute the  $41 = 61 - 20$  codons into 20 amino acids. This is achieved by allowing some amino acids to be specified by more than one codon.

It turns out that (1) can be simplified by making the identifications

$$\begin{aligned} T &\leftrightarrow 1, \\ C &\leftrightarrow 2, \\ A &\leftrightarrow 3, \\ G &\leftrightarrow 4. \end{aligned} \tag{2}$$

and then writing (1) in the form

$$\begin{aligned}
 1 &\leftrightarrow 1^*, \\
 2 &\leftrightarrow 2^*, \\
 1^* &\leftrightarrow 1, \\
 2^* &\leftrightarrow 2.
 \end{aligned}
 \tag{3}$$

By defining

$$\begin{aligned}
 a &= (1, 2), \\
 a^* &= (1^*, 2^*).
 \end{aligned}
 \tag{4}$$

we see that the relations  $1 \leftrightarrow 1^*$  and  $2 \leftrightarrow 2^*$ , established the duality relation

$$a \leftrightarrow a^*.
 \tag{5}$$

An even clearer prescription of previous duality symmetry is achieved by considering the sets  $\{\uparrow, \downarrow\}$  and  $\{\rightarrow, \leftarrow\}$ . The key idea is first to write 1 as  $\uparrow$ ,  $1^*$  as  $\downarrow$ , while 2 as  $\rightarrow$  and  $2^*$  as  $\leftarrow$ . We call  $\uparrow$  up,  $\downarrow$  down, while we call  $\rightarrow$  right and  $\leftarrow$  left. It is evident that up/down are dual concepts, while right/left are also dual concepts. This means that all the genetic code are written in terms of two dual concepts: up/down and right/left (see [17]).

The two options  $\{\uparrow, \downarrow\}$  and  $\{\rightarrow, \leftarrow\}$  can be associated with the quantity  $C_{ijkl}$ , which if it satisfies the symmetries

$$C_{ijkl} = -C_{ijlk} = -C_{jikl},
 \tag{6}$$

and

$$C_{k[lj]} = 0
 \tag{7}$$

(as the Riemann tensor in general relativity theory (see page 326 of [18])), we obtained that the several possible codons for  $C_{ijkl}$  is 20, the same number of amino acids. So, we wonder whether an analogue exists of this duality symmetry in the case of a torus black-hole. We shall propose that if we associate two points on the rotating circle  $S_{(a)}^1$  with opposite dual particles, say in the spinning system  $\{\uparrow, \downarrow\}$ , and simultaneously associate the other dual spinning particles  $\{\rightarrow, \leftarrow\}$  with two opposite points in  $S_{(a)}^1$  we might obtain a double helix structure analogous to that observed on the torus surface of a black hole [17].

Mitochondrial DNA (mtDNA) is a small circular (torus-shaped) chromosome found within mitochondria. It consists of a double-stranded molecule inherited maternally and encodes 13 essential proteins involved in oxidative phosphorylation, as well as rRNA and tRNA necessary for mitochondrial protein synthesis. With its bacterial-like genome structure, mtDNA serves as a remnant of the evolutionary origins of mitochondria as endosymbionts. Since our formalism explores the possibility of mtDNA torus black holes beyond the traditional 2-dimensional spherical event horizon, this circular structure and its central role in energy production provide a compelling analogy to dynamic systems. Additionally, mtDNA's replication dynamics, susceptibility to mutations, and involvement in metabolic diseases highlight the potential for further exploration in this context.

A few areas of research that could be improved are:

1) Although the previous paragraphs provide a general idea of the work's objectives, it remains to explain the progression of ideas considered in our formalism. In fact, there are attempts to connect the small with the large scales in our universe. Certainly the mtDNA exists at the microscopic level of the cell, while black-holes are most of the time thought of as large structures. So, this contrast makes it particularly intriguing to explore a potential connection between these dual small/large-scale scenarios.

2) Perhaps, our work may offer valuable insights into both scenarios, mtDNA and black-holes; ideas in the rein of mtDNA can be useful in the black-hole scenario and *vice versa*.

A double helix wrapped around the torus can be described by the equations

$$\begin{aligned} x(t) &= (b + a \cos(n\varpi t + \lambda\pi)) \cos \omega t, \\ y(t) &= (b + a \cos(n\varpi t + \lambda\pi)) \sin \omega t, \\ z(t) &= a \sin(n\varpi t + \lambda\pi). \end{aligned} \tag{8}$$

Further,  $\varpi = \frac{2\pi}{\tilde{\tau}}$ ,  $\omega = \frac{2\pi}{\tau}$ ,  $\lambda = \{0,1\}$  and  $n$  are natural numbers measuring the number of windings per helix. Moreover,  $\tau$  and  $\tilde{\tau}$  are the periods around the torus and around the moving circle of the helix.

If we rename the quantities in (1) as follows:

$$\theta \equiv n\varpi t + \lambda\pi \tag{9}$$

and

$$\phi \equiv \omega t \tag{10}$$

then we find that (1) can be written as

$$\begin{aligned} x &= (b + r \cos \theta) \cos \phi, \\ y(t) &= (b + r \cos \theta) \sin \phi, \\ z(t) &= r \sin \theta, \end{aligned} \tag{11}$$

with  $r \equiv a$ , and therefore the flat space-time line element

$$ds^2 = -c^2 dt^2 + dx^2 + dy^2 + dz^2 \tag{12}$$

becomes

$$ds^2 = -c^2 dt^2 + dr^2 + r^2 d\theta^2 + (r + r \cos \theta)^2 d\phi^2. \tag{13}$$

The key goal of this work is to generalize (13) in the form

$$ds^2 = -e^{f(r,\theta)} dt^2 + e^{h(r,\theta)} dr^2 + e^{g(r,\theta)} d\theta^2 + e^{p(r,\theta)} d\phi^2, \tag{14}$$

and in this way to compute the relativistic gravitational field equations. It turns out that such a solution corresponds to a torus black-hole solution. This means that a double helix described by (1) can be associated with such a torus black-hole. Hence, we argue that a kind of mitDNA can also be associated with the torus black-hole.

## 2. Proposed Metric Tensor

Here, we shall briefly review Ref. [1]. The proposed metric tensor, or ansatz, associated with (14) is given by the matrix;

$$g_{\mu\nu} = \begin{pmatrix} -e^{f(r,\theta)} & 0 & 0 & 0 \\ 0 & e^{h(r,\theta)} & 0 & 0 \\ 0 & 0 & e^{q(r,\theta)} & 0 \\ 0 & 0 & 0 & e^{p(r,\theta)} \end{pmatrix}, \tag{15}$$

Thus, the non-vanishing Christoffel symbols [18]

$$\Gamma^{\mu}_{\alpha\beta} = \frac{1}{2} g^{\mu\nu} \left\{ \frac{\partial g_{\nu\alpha}}{\partial x^{\beta}} + \frac{\partial g_{\nu\beta}}{\partial x^{\alpha}} - \frac{\partial g_{\alpha\beta}}{\partial x^{\nu}} \right\} = \Gamma^{\mu}_{\beta\alpha} \tag{16}$$

associated with (15) are

$$\begin{aligned} \Gamma^1_{12} &= \frac{f'}{2}, & \Gamma^2_{22} &= \frac{h'}{2}, & \Gamma^2_{11} &= \frac{e^{f-h} f'}{2}, \\ \Gamma^2_{33} &= -\frac{e^{q-h} q'}{2}, & \Gamma^2_{44} &= -\frac{e^{p-h} p'}{2}, & \Gamma^3_{32} &= \frac{q'}{2}, \\ \Gamma^4_{42} &= \frac{p'}{2}, \end{aligned} \tag{V(17)}$$

and also

$$\begin{aligned} \Gamma^1_{13} &= \frac{\dot{f}}{2}, & \Gamma^2_{23} &= \frac{\dot{h}}{2}, & \Gamma^3_{11} &= \frac{e^{f-q} \dot{f}}{2}, \\ \Gamma^3_{22} &= -\frac{e^{h-q} \dot{h}}{2}, & \Gamma^3_{44} &= -\frac{e^{p-h} \dot{p}}{2}, & \Gamma^3_{33} &= \frac{\dot{q}}{2}, \\ \Gamma^4_{43} &= \frac{\dot{p}}{2}. \end{aligned} \tag{18}$$

Here, we used the notations  $F' \equiv \frac{\partial F}{\partial r}$  and  $\dot{H} \equiv \frac{\partial F}{\partial \theta}$ , for arbitrary functions  $F = F(r, \theta)$  and  $H = H(r, \theta)$ . From these Christoffel symbols we may obtain the non-vanishing Riemann tensor

$$R^{\mu}_{\nu\alpha\beta} = \frac{\partial \Gamma^{\mu}_{\nu\beta}}{\partial x^{\alpha}} - \frac{\partial \Gamma^{\mu}_{\nu\alpha}}{\partial x^{\beta}} + \Gamma^{\mu}_{\sigma\alpha} \Gamma^{\sigma}_{\nu\beta} - \Gamma^{\mu}_{\sigma\beta} \Gamma^{\sigma}_{\nu\alpha}. \tag{19}$$

and the Ricci tensor

$$R_{\mu\nu} = R^{\alpha}_{\mu\alpha\nu} \tag{20}$$

And in this way, the vacuum gravitational field equations

$$R_{\mu\nu} = 0, \tag{21}$$

leads

$$\begin{aligned} R_{11} &= \frac{1}{2} e^{f-h} \left( f'' + \frac{1}{2} f'^2 - \frac{1}{2} f' h' + \frac{1}{2} f' q' + \frac{1}{2} f' p' \right) \\ &+ \frac{1}{2} e^{f-q} \left( \dot{f} + \frac{1}{2} \dot{f}^2 - \frac{1}{2} \dot{f} \dot{q} + \frac{1}{2} \dot{f} \dot{h} + \frac{1}{2} \dot{f} \dot{p} \right) = 0, \end{aligned} \tag{22}$$

$$\begin{aligned}
 R_{22} = & -\frac{1}{2}\left(f'' + \frac{1}{2}f'^2 - \frac{1}{2}f'h'\right) \\
 & -\frac{1}{2}\left(p'' + \frac{1}{2}p'^2 - \frac{1}{2}p'h' + q'' + \frac{1}{2}q'^2 - \frac{1}{2}q'h'\right) \\
 & -\frac{1}{2}e^{h-q}\left(\ddot{h} + \frac{1}{2}\dot{h}^2 - \frac{1}{2}\dot{h}\dot{q} + \frac{1}{2}\dot{h}\dot{f} + \frac{1}{2}\dot{h}\dot{p}\right) = 0,
 \end{aligned} \tag{23}$$

$$\begin{aligned}
 R_{33} = & -\frac{1}{2}e^{q-h}\left(q'' + \frac{1}{2}q'^2 - \frac{1}{2}q'h' + \frac{1}{2}q'f' + \frac{1}{2}q'p'\right) \\
 & -\frac{1}{2}\left(\ddot{f} + \frac{1}{2}\dot{f}^2 - \frac{1}{2}\dot{f}\dot{q} + \ddot{h} + \frac{1}{2}\dot{h}^2 - \frac{1}{2}\dot{h}\dot{q} + \ddot{p} + \frac{1}{2}\dot{p}^2 - \frac{1}{2}\dot{p}\dot{q}\right) = 0,
 \end{aligned} \tag{24}$$

$$\begin{aligned}
 R_{44} = & -\frac{1}{2}e^{p-h}\left(p'' + \frac{1}{2}p'^2 - \frac{1}{2}p'h' + \frac{1}{2}p'f' + \frac{1}{2}p'q'\right) \\
 & -\frac{1}{2}e^{p-q}\left(\ddot{p} + \frac{1}{2}\dot{p}^2 - \frac{1}{2}\dot{p}\dot{q} + \frac{1}{2}\dot{p}\dot{h} + \frac{1}{2}\dot{p}\dot{f}\right) = 0.
 \end{aligned} \tag{25}$$

Our main goal now is to solve (22) - (25) for the torus and try to relate such a solution to an mtDNA torus.

### 3. Towards the Mitochondrial-DNA Torus Black-Hole

Assuming that

$$q'' + \frac{1}{2}q'^2 = 0 \tag{26}$$

and

$$p'' + \frac{1}{2}p'^2 = 0. \tag{27}$$

we find the general solution is of the form

$$e^{\frac{\xi}{2}} = rA_\xi(\theta) + B_\xi(\theta) \tag{28}$$

for  $\xi = q$  or  $\xi = p$ . For the 2-sphere case, we have  $e^{\frac{q}{2}} = r$  and  $e^{\frac{p}{2}} = r \sin \theta$ . The choice  $e^{\frac{q}{2}} = r$  implies that  $A_q = 1$  and  $B_q = 0$ , while choosing  $e^{\frac{p}{2}} = r \sin \theta$  means that  $A_p = \sin \theta$  and  $B_p = 0$ . For the torus we have again  $e^{\frac{q}{2}} = r$ , but  $e^{\frac{p}{2}} = r \sin \theta + a$  which means that  $A_p = \sin \theta$  and  $B_p = a$ . Thus, considering (19) and (20) we get that (16), (17) and (18) simplify in the form

$$\begin{aligned}
 R_{22} = & -\frac{1}{2}\left(f'' + \frac{1}{2}f'^2 - \frac{1}{2}f'h'\right) + \frac{1}{4}h'(p' + q') \\
 & -\frac{1}{2}e^{h-q}\left(\ddot{h} + \frac{1}{2}\dot{h}^2 + \frac{1}{2}\dot{h}\dot{f} + \frac{1}{2}\dot{h}\dot{p}\right) = 0,
 \end{aligned} \tag{29}$$

$$\begin{aligned}
 R_{33} = & -\frac{1}{4}e^{q-h}\left(-q'h' + q'f' + q'p'\right) \\
 & -\frac{1}{2}\left(\ddot{f} + \frac{1}{2}\dot{f}^2 + \ddot{h} + \frac{1}{2}\dot{h}^2 + \ddot{p} + \frac{1}{2}\dot{p}^2 - \frac{1}{2}\dot{p}\dot{q}\right) = 0,
 \end{aligned} \tag{30}$$

and

$$R_{44} = -\frac{1}{4}e^{p-h}(-p'h' + p'f' + p'q') - \frac{1}{2}e^{p-q}\left(\ddot{p} + \frac{1}{2}\dot{p}^2 + \frac{1}{2}\dot{p}\dot{h} + \frac{1}{2}\dot{p}\dot{f}\right) = 0, \tag{31}$$

where we also set  $\dot{q} = 0$  because our choice  $e^{\frac{q}{2}} = r$ . The expression (15) becomes

$$R_{11} = \frac{1}{2}e^{f-h}\left(f'' + \frac{1}{2}f'^2 - \frac{1}{2}f'h' + \frac{1}{2}f'(q' + p')\right) + \frac{1}{2}e^{f-q}\left(\ddot{f} + \frac{1}{2}\dot{f}^2 + \frac{1}{2}\dot{f}\dot{h} + \frac{1}{2}\dot{f}\dot{p}\right) = 0, \tag{32}$$

Assuming

$$f' + h' = 0 \tag{33}$$

and

$$\dot{f} + \dot{h} = 0. \tag{34}$$

We also find

$$\ddot{p} + \frac{1}{2}\dot{p}^2 = -rp'. \tag{35}$$

Thus, (24) becomes

$$r(e^{-h})' + e^{-h} - 1 = 0. \tag{36}$$

Multiply (29) for  $\sin \theta$  we get

$$r \sin \theta (e^{-h})' + \sin \theta e^{-h} - \sin \theta = 0. \tag{37}$$

and making some computations we find that (29) admits the solution

$$e^{-h} = \left(1 - \frac{\mathcal{A}(\theta)}{b + r \sin \theta}\right), \tag{38}$$

with  $\mathcal{A}(\theta)$  an arbitrary function of  $\theta$ . The proof that (32) is, in fact, a solution to (29) is straightforward. Now it remains to determine  $\mathcal{A}(\theta)$ . We apply the well-known procedure to derive the event horizon by setting

$$\left(1 - \frac{\mathcal{A}(\theta)}{b + r_s \sin \theta}\right) = 0, \tag{39}$$

with  $r_s = const$ , a fixed torus radius. Therefore (32) becomes

$$e^{-h} = \left(1 - \frac{b + r_s \sin \theta}{b + r \sin \theta}\right), \tag{40}$$

and since  $e^f = e^{-h}$  we find that the line element can be written as

$$ds^2 = -\left(1 - \frac{b + r_s \sin \theta}{b + r \sin \theta}\right)c^2 dt^2 + \frac{dr^2}{\left(1 - \frac{b + r_s \sin \theta}{b + r \sin \theta}\right)} + r^2 d\theta^2 + (b + r \sin \theta)^2 d\phi^2. \tag{41}$$

This line element is reduced to the usual one when  $b = 0$ . In fact, when  $b = 0$  we get

$$ds^2 = -\left(1 - \frac{r_s}{r}\right) c^2 dt^2 + \frac{dr^2}{\left(1 - \frac{r_s}{r}\right)} + r^2 d\theta^2 + r^2 \sin^2 \theta d\phi^2, \tag{42}$$

as expected.

According to the usual literature, mitochondrial DNA (mtDNA) is described as “closed circular DNA,” consisting of approximately 16,569 nucleotides that encode some of the mitochondrial proteins essential for cellular energy production. Unlike nuclear DNA, mtDNA is inherited maternally and is located in the mitochondria, the powerhouses of the cell. These organelles are responsible for generating most of the cell’s supply of adenosine triphosphate (ATP), which is used as a source of chemical energy.

However, this simplified definition of mtDNA erroneously introduces the concept of “closed circular DNA,” which marks a significant difference from the DNA found in the cell nucleus. Unlike the chromosomal DNA in the nucleus, which is linear and complex, mtDNA is circular and relatively compact. Despite this, in both cases, as mentioned in the introduction, both mtDNA and nuclear DNA are double-stranded helices with a right-handed orientation, composed of repeating units called nucleotides. Each nucleotide consists of 4 bases: adenine (A), thymine (T), cytosine (C), and guanine (G), which form the “rungs” of the helical ladder.

In humans, mtDNA encodes for 37 genes, 13 of which are involved in the Electron Transport Chain (ETC) and oxidative phosphorylation, processes critical for ATP production. The remaining genes encode transfer RNA (tRNA) and ribosomal RNA (rRNA), which are involved in protein synthesis within the mitochondrion. Because mtDNA does not have the same repair mechanisms as nuclear DNA, it is more prone to mutations, which can lead to mitochondrial diseases.

Given this, it must be evident that the simplified term “closed circular DNA” is not entirely accurate. Instead, mtDNA should be visualized as a double helix on a toroidal geometry. Additionally, since it is sometimes useful to connect different scenarios, we wonder if the mtDNA structure could also manifest in the context of toroidal black holes. To explore this, we propose substituting Equations (2) and (3) into Equation (35), yielding

$$ds^2 = -\left(1 - \frac{b + r_s \sin(n\omega t + \lambda\pi)}{b + r \sin(n\omega t + \lambda\pi)}\right) c^2 dt^2 + \frac{dr^2}{\left(1 - \frac{b + r_s \sin(n\omega t + \lambda\pi)}{b + r \sin(n\omega t + \lambda\pi)}\right)} + r^2 d\theta^2 + (b + r \sin(n\omega t + \lambda\pi))^2 d\phi^2. \tag{43}$$

Since  $\lambda = \{0, 1\}$  (37) can be broken into two line elements, namely

$$ds_0^2 = -\left(1 - \frac{b + r_s \sin(n\omega t)}{b + r \sin(n\omega t)}\right) c^2 dt^2 + \frac{dr^2}{\left(1 - \frac{b + r_s \sin(n\omega t)}{b + r \sin(n\omega t)}\right)} + r^2 d\theta^2 + (b + r \sin(n\omega t))^2 d\phi^2. \tag{44}$$

and

$$ds_{\pi}^2 = -\left(1 - \frac{b+r_s \sin(n\omega t + \pi)}{b+r \sin(n\omega t + \pi)}\right) c^2 dt^2 + \frac{dr^2}{\left(1 - \frac{b+r_s \sin(n\omega t + \pi)}{b+r \sin(n\omega t + \pi)}\right)} + r^2 d\theta^2 + (b+r \sin(n\omega t + \pi))^2 d\phi^2. \tag{45}$$

It is important to observe that because the distance between the dual particles on the torus remains the same, the orthogonal line element  $dl^2 = ds_0^2 - ds_{\pi}^2$  must be zero, that is

$$ds_0^2 - ds_{\pi}^2 = 0 \tag{46}$$

All these refer to two dual particles. However, the mtDNA is a two-stranded molecule in the form of a double right-handed helix of repeating units called nucleotides. So we need to extend the previous observation to the level of the double helix along the torus combining different opposite particles. Since these opposite particles are of the type  $\{\uparrow, \downarrow\}$  and  $\{\rightarrow, \leftarrow\}$  we expect to obtain a kind of Ising model.

#### 4. Final Remarks

There are two interesting subjects that can be explored in further research. First, the present algorithm can also be used to find a kind of spiral black-hole solution. In particular, we may also choose  $A_q(\theta) = A_p(\theta) = 1$  and  $B_q(\theta) = \alpha\theta$  and  $B_p(\theta) = \alpha\theta \sin \theta$ . This means that the last terms of (39)

$$dl^2 \equiv r^2 (d\theta^2 + \sin^2 \theta d\phi^2) \tag{47}$$

can be written in the alternative form

$$dl^2 = (r + \alpha\theta)^2 (d\theta^2 + \sin^2 \theta d\phi^2). \tag{48}$$

When  $r = 0$  the radius becomes

$$\rho \equiv \alpha\theta, \tag{49}$$

which correspond to the typical radius of a spiral curve. We are tempted to propose that (42) may be useful for describing galaxy dynamics, with a black-hole as a source system. The question emerges what does this mean in the case of mtDNA black-hole.

Second we may explore the significance of the singularity at  $r \neq 0$ , for  $g \neq 1$ , as opposed to  $r = 0$  for  $g = 0$ . In addition, this result may provide an alternative solution to the long-standing problem of singularity in black-hole physics. In any case, we wonder what such a concept of singularities means in the case of mtDNA.

Finally, we would like to make additional comments. First of all, this duality symmetry is not merely a formal relabeling, but rather reflects fundamental biochemical properties of the genetic code. The pairing of T-A and C-G corresponds to purine-pyrimidine complementarity, which ensures the structural stability of

the double helix and the high fidelity of the replication and transcription process. In mitochondrial DNA, this complementarity is essential to preserve functional integrity despite higher mutation rates. Thus, the abstract duality introduced here has a direct counterpart in the known biochemical and functional organization of the genetic system (see [19]).

Secondly, in order to emphasize the key development of this work, we avoid presenting the solution of the gravitational field equations in sufficient detail. However, the reader can verify that the computations are straightforward (see [1]).

Third, at first sight, we may be intrigued by the apparent enormous difference in physical scales between mtDNA and black-holes. However, we may assume the fact that we may also consider “small” black-holes, which may be created just after the big-bang. In any case, since quantum gravity is still an open problem, we wonder whether new ideas, such as the one presented in this work, may establish that “small” scales, such as mtDNA may describe the right route for a successful quantum gravity.

## Acknowledgements

We would like to thank an anonymous reviewer for valuable comments. This work was partially supported by PROFAPI/UAS.

## Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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