

## THE CODES OVER A FAMILY OF FINITE RINGS AND SOME APPLICATIONS

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**ABSTRACT.** Some types of codes have received much attention due to their applications in DNA computing. One of them is the skew cyclic codes. The other is the linear codes with special generator matrices. In this paper, by using two types of codes, the DNA codes are obtained. Firstly, the skew cyclic codes over a family of the finite rings  $M_e = Z_4[u_1, \dots, u_e]/\langle u_i^3 - 1, u_i u_j - u_j u_i \rangle$  are introduced, where  $i, j = 1, 2, \dots, e, i \neq j$ . We define a non trivial automorphism  $\theta_e$  over  $M_e$  and a generalized Gray map over  $M_e$  which preserves DNA reversibility. The DNA  $3^i$ -mers are matched with the elements of the finite rings  $M_i$ , where  $i = 1, \dots, e$ . The reversibility problem for DNA codes over a family of the finite rings  $M_e$  is solved, by using the skew cyclic codes over  $M_e$ . Secondly, in [4], a novel design strategy has been given to obtain DNA codes. We generalized it to the codes over a family of the finite rings  $M_e$ .

2010 *Mathematics Subject Classification*: 94B05, 94B60.

*Keywords*: DNA codes, skew cyclic codes.

### 1. INTRODUCTION

One type of biological computing is DNA computing. It computes faster with a lower energy consumption. It uses DNA as a data storage device to solve complex problems. As DNA (Deoxyribonucleic Acid) is a good platform to store more data effectively, designing DNA codes that satisfy some constraints has been a topic of popular research, recently. There are lots of methods to obtain them. The two methods are used in this paper to create them.

A DNA code  $C$  of length  $n$  is a subset of  $S_{D_4}^n$ , where  $S_{D_4} = \{A, T, C, G\}$  is DNA alphabet.

The reversibility problem is very important in DNA computing. Let  $(\alpha_1, \alpha_2) \in M_1^2$  be a codeword corresponds to *ATTGCC*. The reverse of the  $(\alpha_1, \alpha_2)$  is  $(\alpha_2, \alpha_1)$ .

The vector  $(\alpha_2, \alpha_1)$  corresponding to  $GCCATT$ . It is not the reverse of  $ATTGCC$ . The reverse of  $ATTGCC$  is  $CCGTTA$ .

Some authors used different approaches to solve this problem [1, 2, 6, 7, 8].

In [3], by defining a nontrivial automorphism, the skew cyclic codes over the finite ring  $R_2 = F_4 + uF_4 + vF_4 + uvF_4, u^2 = u, v^2 = v, uv = vu$  were introduced. DNA 4-bases were matched with the elements 256 of the finite ring  $R_2$ . The reversible DNA codes were obtained from them.

In [5], the reversibility problem for DNA  $2^a$ -bases was studied by using the skew cyclic codes over the finite ring  $R_a$ .

In the first part of this paper, motivated by these works, we study the reversibility problem for DNA  $3^e$ -bases. Thanks to them, reversible DNA codes are obtained.

In [4], a new method was given to obtain DNA codes. In the second part of this paper, we generalize it to codes over a family of the finite rings  $M_e$ .

The rest of the paper is organized as follows. In Section II, preliminaries are presented. In Section III, a non-trivial automorphism on  $M_e$  is given to define the skew cyclic codes over  $M_e$ . In Section IV, a distance conserving map from  $M_i$  to  $S_{D_4}^{3^i}$  is defined. By using a method in [4], we derive some conditions on the generator matrix of a linear code over  $M_i$ , for  $i = 1, 2, 3, \dots, e$ . We get the DNA codes that satisfy some constraints. In Section V, by using Reed-Muller types codes over  $M_i$ , the constructions of DNA codes are presented, where  $i = 2, \dots, e$ . The parameters of the DNA codes obtained by this method are given. Some examples are obtained.

## 2. PRELIMINARIES

A family of the finite rings  $M_e = Z_4[u_1, \dots, u_e] / \langle u_i^3 - 1, u_i u_j - u_j u_i \rangle$ , where  $i, j = 1, 2, \dots, e, i \neq j$  contains the commutative the finite rings with characteristic 4 and cardinality  $4^{3^e}$ . The finite rings of the family are written as recursively

$$M_j = M_{j-1} + u_j M_{j-1} + u_j^2 M_{j-1}$$

where  $j = 1, 2, \dots, e$  and  $u_j^3 = 1$ .

Moreover  $M_1 = Z_4 + u_1 Z_4 + u_1^2 Z_4, u_1^3 = 1$ , where  $M_0 = Z_4 = \{0, 1, 2, 3\}$ .

We defined the Gray map as follows,

$$\begin{aligned} \phi_i & : M_i \longrightarrow M_{i-1}^3 \\ x_{i-1} + u_i y_{i-1} + u_i^2 z_{i-1} & \longmapsto (y_{i-1}, x_{i-1}, z_{i-1}) \end{aligned}$$

where  $i = 2, \dots, e$  and

$$\begin{aligned} \phi_1 & : M_1 \longrightarrow M_0^3 \\ x_0 + u_1 y_0 + u_1^2 z_0 & \longmapsto (y_0, x_0, z_0) \end{aligned}$$

Moreover

$$\begin{aligned} \phi & : M_i \longrightarrow M_0^{3^i} \\ \alpha_i = x_{i-1} + u_i y_{i-1} + u_i^2 z_{i-1} & \longmapsto (\phi_1(\phi_2(\dots(\phi_i(\alpha_i)))))) \end{aligned}$$

where  $i = 1, 2, \dots, e$ .

**Example 1.** Let  $e = 2$ . Then the Gray map is  $\phi(x_1 + u_2 y_1 + u_2^2 z_1) = \phi_1(\phi_2((x_1 + u_2 y_1 + u_2^2 z_1))) = \phi_1(y_1, x_1, z_1) = (\phi_1(y_1), \phi_1(x_1), \phi_1(z_1)) \in M_0^9$ .

By defining the matching the elements of  $M_0$  and  $S_{D_4} = \{A, T, C, G\}$  which is given as  $\xi_0(0) = A, \xi_0(3) = T, \xi_0(1) = C, \xi_0(2) = G$  and by using the Gray map from  $M_1 = Z_4 + u_1 Z_4 + u_1^2 Z_4$  to  $Z_4^3$ , we define a  $\xi_1$  correspondence between the elements of the finite ring  $M_1 = Z_4 + u_1 Z_4 + u_1^2 Z_4$  and DNA 3-mers as follows

$$\begin{aligned} \xi_1 & : M_1 \longrightarrow S_{D_4}^3 \\ \alpha_1 = x_0 + u_1 y_0 + u_1^2 z_0 & \longmapsto (\xi_0(y_0), \xi_0(x_0), \xi_0(z_0)) = \xi_1(\alpha_1) \end{aligned}$$

and give the following table,

elements $\alpha_1$	DNA 3-mers $\xi_1(\alpha_1)$
0	AAA
1	ACA
2	AGA
3	ATA
$u_1$	CAA
$1 + u_1$	CCA
$2 + u_1$	CGA
$3 + u_1$	CTA
$2u_1$	GAA
$1 + 2u_1$	GCA
$2 + 2u_1$	GGA
$3 + 2u_1$	GTA
$3u_1$	TAA
$1 + 3u_1$	TCA
$2 + 3u_1$	TGA
$3 + 3u_1$	TTA
$u_1^2$	AAC
$1 + u_1^2$	ACC
$2 + u_1^2$	AGC
$3 + u_1^2$	ATC
$u_1 + u_1^2$	CAC
$1 + u_1 + u_1^2$	CCC

elements $\alpha_1$	DNA 3-mers $\xi_1(\alpha_1)$
$2 + u_1 + u_1^2$	<i>CGC</i>
$3 + u_1 + u_1^2$	<i>CTC</i>
$2u_1 + u_1^2$	<i>GAC</i>
$1 + 2u_1 + u_1^2$	<i>GCC</i>
$2 + 2u_1 + u_1^2$	<i>GGC</i>
$3 + 2u_1 + u_1^2$	<i>GTC</i>
$3u_1 + u_1^2$	<i>TAC</i>
$1 + 3u_1 + u_1^2$	<i>TCC</i>
$2 + 3u_1 + u_1^2$	<i>TGC</i>
$3 + 3u_1 + u_1^2$	<i>TTC</i>
$2u_1^2$	<i>AAG</i>
$1 + 2u_1^2$	<i>ACG</i>
$2 + 2u_1^2$	<i>AGG</i>
$3 + 2u_1^2$	<i>ATG</i>
$u_1 + 2u_1^2$	<i>CAG</i>
$1 + u_1 + 2u_1^2$	<i>CCG</i>
$2 + u_1 + 2u_1^2$	<i>CGG</i>
$3 + u_1 + 2u_1^2$	<i>CTG</i>
$2u_1 + 2u_1^2$	<i>GAG</i>
$1 + 2u_1 + 2u_1^2$	<i>GCG</i>
$2 + 2u_1 + 2u_1^2$	<i>GGG</i>
$3 + 2u_1 + 2u_1^2$	<i>GTG</i>
$3u_1 + 2u_1^2$	<i>TAG</i>
$1 + 3u_1 + 2u_1^2$	<i>TCG</i>
$2 + 3u_1 + 2u_1^2$	<i>TGG</i>
$3 + 3u_1 + 2u_1^2$	<i>TTG</i>
$3u_1^2$	<i>AAT</i>
$1 + 3u_1^2$	<i>ACT</i>
$2 + 3u_1^2$	<i>AGT</i>
$3 + 3u_1^2$	<i>ATT</i>
$u_1 + 3u_1^2$	<i>CAT</i>
$1 + u_1 + 3u_1^2$	<i>CCT</i>
$2 + u_1 + 3u_1^2$	<i>CGT</i>
$3 + u_1 + 3u_1^2$	<i>CTT</i>
$2u_1 + 3u_1^2$	<i>GAT</i>
$1 + 2u_1 + 3u_1^2$	<i>GCT</i>
$2 + 2u_1 + 3u_1^2$	<i>GGT</i>
$3 + 2u_1 + 3u_1^2$	<i>GTT</i>
$3u_1 + 3u_1^2$	<i>TAT</i>
$1 + 3u_1 + 3u_1^2$	<i>TCT</i>
$2 + 3u_1 + 3u_1^2$	<del><i>TGT</i></del>
$3 + 3u_1 + 3u_1^2$	<i>TTT</i>

For  $\alpha_1 \in M_1$ , we have that the complement of  $\xi_1(\alpha_1)$  is equal to  $[\xi_1(\alpha_1^c)]$  where  $\alpha_1^c = 3 + 3u_1 + 3u_1^2 - \alpha_1$ .

**Example 2.** Let  $\alpha_1 = 3 + u_1 + 2u_1^2 \in M_1$ . Then  $\xi_1(\alpha_1) = CTG$ . On the other hand, we get  $\xi_1(\alpha_1^c) = GAC$ , since  $\alpha_1^c = 2u_1 + u_1^2$ .

Similarly, we define a  $\xi_2$  correspondence between elements of the ring  $M_2 = (Z_4 + u_1Z_4 + u_1^2Z_4) + u_2(Z_4 + u_1Z_4 + u_1^2Z_4) + u_2^2(Z_4 + u_1Z_4 + u_1^2Z_4)$  and DNA 9-mers as follows:

$$\begin{aligned} \xi_2 & : M_2 \longrightarrow S_{D_4}^9 \\ \alpha_2 = x_1 + u_2y_1 + u_2^2z_1 & \longmapsto (\xi_1(y_1), \xi_1(x_1), \xi_1(z_1)) \end{aligned}$$

and give the following table,

elements $\alpha_2$	DNA 9-mers $\xi_2(\alpha_2)$
0	AAAAAAAAAA
1	AAAACAAAA
2	AAAAGAAAA
3	AAAATAAAA
...	
...	

For  $\alpha_2 \in M_2$ , we have that the complement of  $\xi_2(\alpha_2)$  is equal to  $\xi_2(\alpha_2^c)$  where  $\alpha_2^c = \mathbf{3} + \mathbf{3u} + \mathbf{3u}^2 - \alpha_2$ , where  $\mathbf{3} + \mathbf{3u} + \mathbf{3u}^2 \in M_2$  where its all coefficients are  $3 + 3u_1 + 3u_1^2$ .

**Example 3.** Let  $\alpha_2 = 1 + 2u_1 + u_2 + 2u_2^2 \in M_2$ . Then  $\xi_2(\alpha_2) = \xi_2((1 + 2u_1) + u_2 + 2u_2^2) = (\xi_1(1), \xi_1(1 + 2u_1), \xi_1(2)) = ACAGCAAGA$ . On the other hand,  $\xi_2(\alpha_2^c) = \xi_2((3 + 3u_1 + 3u_1^2) - (1 + 2u_1) + u_2((3 + 3u_1 + 3u_1^2) - 1) + u_2^2((3 + 3u_1 + 3u_1^2) - 2)) = (\xi_1(2 + 3u_1 + 3u_1^2), \xi_1(2 + 3u_1 + 3u_1^2), \xi_1(1 + 3u_1 + 3u_1^2)) = TGTCGTTCT$ , where  $\alpha_2^c = (2 + u_1 + 3u_1^2) + u_2(2 + 3u_1 + 3u_1^2) + u_2^2(1 + 3u_1 + 3u_1^2)$ .

Similarly, we can define  $\xi_i$  for  $i = 3, \dots, e$ . Moreover for every  $\alpha_i \in M_i$ , we have that the complement of  $\xi_i(\alpha_i)$  is equal to  $[\xi_i(\alpha_i^c)]$  where  $\alpha_i^c = \mathbf{3} + \mathbf{3u} + \mathbf{3u}^2 - \alpha_i$ , where  $\mathbf{3} + \mathbf{3u} + \mathbf{3u}^2 \in M_i$  where its all coefficients are  $3 + 3u_1 + 3u_1^2$ , where  $i = 3, \dots, e$ .

### 3. SKEW CYCLIC CODES OVER $M_e$

**Definition 1.** Let  $B$  be a finite ring and  $\theta$  be a non-trivial automorphism on  $B$ . A subset  $C$  of  $B^n$  is called a skew cyclic code of length  $n$  if  $C$  satisfies the following conditions,

1.  $C$  is a submodule of  $B^n$
2. If  $c = (c_0, c_1, \dots, c_{n-1}) \in C$ , then  $\sigma_\theta(c) = (\theta(c_{n-1}), \theta(c_0), \dots, \theta(c_{n-2})) \in C$ , where  $\sigma_\theta$  is the skew cyclic shift operator.

By defining a non-trivial automorphism on  $M_e$  as follows, we can define the skew cyclic codes over  $M_e$ .

$$\begin{aligned} \theta_i & : M_i \longrightarrow M_i \\ x_{i-1} + u_i y_{i-1} + u_i^2 z_{i-1} & \longmapsto \theta_{i-1}(x_{i-1}) + u_i \theta_{i-1}(z_{i-1}) + u_i^2 \theta_{i-1}(y_{i-1}) \end{aligned}$$

and

$$\begin{aligned} \theta_1 & : M_1 \longrightarrow M_1 \\ x_0 + u_1 y_0 + u_1^2 z_0 & \longmapsto x_0 + u_1 z_0 + u_1^2 y_0 \end{aligned}$$

where  $i = 2, 3, \dots, e$ . The order of  $\theta_i$  is 2, where  $i = 1, 2, \dots, e$ .

The rings

$$M_i[x, \theta_i] = \{b_0^i + b_1^i x + \dots + b_{n-1}^i x^{n-1} : b_j^i \in M_i, n \in \mathbb{N}, i = 1, \dots, a, j = 0, \dots, n-1\}$$

are called skew polynomial rings with the usual polynomial addition and multiplication as follows

$$(\varrho x^s)(\eta x^t) = \varrho \theta_i^s(\eta) x^{s+t}$$

where  $i = 1, \dots, e$ . They are non-commutative rings.

In polynomial representation, a skew cyclic code of length  $n$  over  $M_i$  is defined as a left ideal of the quotient ring  $M_{\theta_i, n} = M_i[x, \theta_i] / \langle x^n - 1 \rangle$ , if the order of  $\theta_i$  divides  $n$ , that is  $n$  is even. If the order of  $\theta_i$  does not divide  $n$ , a skew cyclic code of length  $n$  over  $M_i$  is defined as a left  $M_i[x, \theta_i]$ -submodule of  $M_{\theta_i, n}$ , since the set  $M_{\theta_i, n} = M_i[x, \theta_i] / \langle x^n - 1 \rangle = \{f_i(x) + \langle x^n - 1 \rangle : f_i(x) \in M_i[x, \theta_i]\}$  is a left  $M_i[x, \theta_i]$ -module with the multiplication from left defined by

$$r_i(x)(f_i(x) + \langle x^n - 1 \rangle) = r_i(x)f_i(x) + \langle x^n - 1 \rangle$$

where for any  $r_i(x) \in M_i[x, \theta_i]$ , for  $i = 1, \dots, e$ .

In both cases, the following is held.

**Theorem 1.** *Let  $C_i$  be a skew cyclic code over  $M_i$  and let  $f_i(x)$  be a polynomial in  $C_i$  of minimal degree,  $i = 1, \dots, e$ . If the leading coefficient of  $f_i(x)$  is a unit in  $M_i$ , then  $C_i = \langle f_i(x) \rangle$ , where  $f_i(x)$  is a right divisor of  $x^n - 1$ .*

**Definition 2.** For  $\mathbf{x} = (x_0^i, x_1^i, \dots, x_{n-1}^i) \in M_i^n$ , the vector  $(x_{n-1}^i, x_{n-2}^i, \dots, x_1^i, x_0^i)$  is called the reverse of  $\mathbf{x}$  and is denoted by  $\mathbf{x}^r$ . A linear code  $C_i$  of length  $n$  over  $M_i$  is called reversible if  $\mathbf{x}^r \in C_i$  for every  $\mathbf{x} \in C_i$ , where  $i = 1, \dots, e$ .

We can express the matching the elements  $M_1$  and  $S_{D_4}^3 = S_{D_{64}} = \{AAA, TTT, \dots, GGG\}$  by means of the automorphism  $\theta_1$  as follows.

Each element  $\alpha_1 = x_0 + u_1 y_0 + u_1^2 z_0 \in M_1$  and  $\theta_1(\alpha_1)$  are mapped to DNA 3-mers which are reverse of each other. Let  $\xi_1$  be a correspondence between the elements of the finite ring  $M_1$  and DNA 3-mers. For example

$$\xi_1(u_1) = CAA, \text{ while } \xi_1(\theta_1(u_1)) = AAC$$

This can be extended to a map  $\gamma_i$  from  $M_{i-1}^3$  to  $3^i$ -mers as follows,

$$\gamma_i(s_{i-1}, t_{i-1}, r_{i-1}) = (\xi_{i-1}(s_{i-1}), \xi_{i-1}(t_{i-1}), \xi_{i-1}(r_{i-1}))$$

where  $s_{i-1}, t_{i-1}, r_{i-1} \in M_{i-1}$ , for  $i = 1, \dots, e$ .

By using a map  $\xi_i = \gamma_i \circ \phi_i$ , we can explain the relationship between skew cyclic codes and DNA codes.  $\xi_i(r_i)$  and  $\xi_i(\theta_i(r_i))$  are DNA reverse of each other, where  $m_i = a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1}$  and  $a_{i-1}, b_{i-1}, c_{i-1} \in M_{i-1}$ , where  $i = 1, \dots, e$ .

For  $m_i = a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1} \in M_i$ , we have

$$\begin{aligned} \xi_i(m_i) &= \gamma_i(\phi_i(a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1})) = \gamma_i(b_{i-1}, a_{i-1}, c_{i-1}) \\ &= (\xi_{i-1}(b_{i-1}), \xi_{i-1}(a_{i-1}), \xi_{i-1}(c_{i-1})) \end{aligned}$$

On the other hand,

$$\begin{aligned} \xi_i(\theta_i(m_i)) &= \xi_i(\theta_{i-1}(a_{i-1}) + u_i \theta_{i-1}(c_{i-1}) + u_i^2 \theta_{i-1}(b_{i-1})) \\ &= \gamma_i(\phi_i(\theta_{i-1}(a_{i-1}) + u_i \theta_{i-1}(c_{i-1}) + u_i^2 \theta_{i-1}(b_{i-1}))) \\ &= \gamma_i(\theta_{i-1}(c_{i-1}), \theta_{i-1}(a_{i-1}), \theta_{i-1}(b_{i-1})) \\ &= (\xi_{i-1}(\theta_{i-1}(c_{i-1})), \xi_{i-1}(\theta_{i-1}(a_{i-1})), \xi_{i-1}(\theta_{i-1}(b_{i-1}))) \end{aligned}$$

where  $i = 1, \dots, e$ .

This map can be extended as follows. For any  $m_i = (m_0^i, \dots, m_{n-1}^i) \in M_i^n$ , where  $i = 1, 2, \dots, e$ .

$$(\xi_i(m_0^i), \xi_i(m_1^i), \dots, \xi_i(m_{n-1}^i))^r = (\xi_i(\theta_i(m_{n-1}^i)), \dots, \xi_i(\theta_i(m_1^i)), \xi_i(\theta_i(m_0^i)))$$

**Example 4.** If  $m_2 = u_1 + u_2(1 + 2u_1) + u_2^2 \in M_2$ , then we have

$$\begin{aligned} \xi_2(m_2) &= \gamma_2(\phi_2(m_2)) = \gamma_2(1 + 2u_1, u_1, 1) \\ &= (\xi_1(1 + 2u_1), \xi_1(u_1), \xi_1(1)) = GCACAAACA \end{aligned}$$

On the other hand,

$$\begin{aligned}
 \xi_2(\theta_2(m_2)) &= \xi_2(\theta_1(u_1) + u_2\theta_1(1) + u_2^2\theta_1(1 + 2u_1)) \\
 &= \gamma_2(\theta_1(1), \theta_1(u_1), \theta_1(1 + 2u_1)) \\
 &= (\xi_1(\theta_1(1)), \xi_1(\theta_1(u_1)), \xi_1(\theta_1(1 + 2u_1))) \\
 &= ACAAACACG
 \end{aligned}$$

**Definition 3.** Let  $C_i$  be a code of length  $n$  over  $M_i$ , for  $i = 1, \dots, e$ . If  $\xi_i(\mathbf{c})^r \in \xi_i(C_i)$  for all  $\mathbf{c} \in C_i$ , then  $C_i$  or equivalently  $\xi_i(C_i)$  is called a reversible DNA code.

**Definition 4.** Let  $g_i(x) = b_0^i + b_1^i x + b_2^i x^2 + \dots + b_s^i x^s$  be a polynomial of degree  $s$  over  $M_i$ , for  $i = 1, \dots, e$ .  $g_i(x)$  is called a palindromic polynomial if  $b_j^i = b_{s-j}^i$  for all  $j \in \{0, 1, \dots, s\}$ .  $g_i(x)$  is called a  $\theta_i$ -palindromic polynomial if  $b_j^i = \theta_i(b_{s-j}^i)$  for all  $j \in \{0, 1, \dots, s\}$ , for  $i = 1, \dots, e$ .

As the order of  $\theta_i$  is 2, a skew cyclic code of odd length  $n$  over  $M_i$  with respect to  $\theta_i$  is an ordinary cyclic code. So we will take the length  $n$  to be even, where  $i = 1, 2, \dots, e$ .

**Theorem 2.** Let  $C_i = \langle f_i(x) \rangle$  be a skew cyclic code of length  $n$  over  $M_i$ , for  $i = 1, \dots, e$ , where  $f_i(x)$  is a right divisor of  $x^n - 1$  and  $\deg(f_i(x))$  is odd. If  $f_i(x)$  is a  $\theta_i$ -palindromic polynomial then  $\xi_i(C_i)$  is a reversible DNA code.

*Proof.* Let  $f_i(x)$  be a  $\theta_i$ -palindromic polynomial and  $f_i(x) = a_0^i + a_1^i x + \dots + a_{2s-1}^i x^{2s-1}$ . So  $a_d^i = \theta_i(a_{2s-1-d}^i)$ , for all  $d = 0, 1, \dots, s-1$ . Let  $h_i(x) = h_0^i + h_1^i x + \dots + h_{2k-1}^i x^{2k-1}$ . Let  $b_l^i$  be the coefficient of  $x^l$  in  $h_i(x)f_i(x)$  where  $l = 1, \dots, n-1$ . For any  $t < n/2$ , the coefficient of  $x^t$  in  $h_i(x)f_i(x)$  is

$$b_t^i = \sum_{j=0}^t h_j^i \theta_i^j(a_{t-j}^i)$$

and the coefficient of  $x^{n-t}$  is  $b_{n-t}^i = \sum_{j=0}^t h_{2k-1-j}^i \theta_i^{2k-1-j}(a_{2s-1-(t-j)}^i)$ .

The polynomial  $h_i(x)f_i(x) = \sum_{p=0}^{2k-1} h_p^i x^p f_i(x)$  corresponds a vector  $b = (b_0^i, b_1^i, \dots, b_{n-1}^i) \in C_i$ , for  $i = 1, \dots, a$ .

The vector  $\xi_i(b)^r = ((\xi_i(b_0^i), \xi_i(b_1^i), \dots, \xi_i(b_{n-1}^i)))^r$  is equal to the vector  $\xi_i(z)$ , where the vector  $z$  corresponds to polynomial  $\sum_{p=0}^{2k-1} \theta_i(h_p^i) x^{2k-1-p} f_i(x)$ , for  $i = 1, \dots, a$ .

Since  $z = (z_1^i, \dots, z_n^i) \in C_i$ , then  $\xi_i(C_i)$  is a reversible DNA code, for  $i = 1, \dots, a$ .

**Theorem 3.** Let  $C_i = \langle f_i(x) \rangle$  be a skew cyclic code of length  $n$  over  $M_i$ , for  $i = 1, \dots, e$ , where  $f_i(x)$  is a right divisor of  $x^n - 1$  and  $\deg(f_i(x))$  is even. If  $f_i(x)$  is a palindromic polynomial then  $\xi_i(C_i)$  is a reversible DNA code.



*Proof.* Let  $f_i(x)$  be a palindromic polynomial with an even degree.  $f_i(x) = a_0^i + a_1^i x + \dots + a_{2s}^i x^{2s}$  and  $a_d^i = a_{2s-d}^i$ , for all  $d = 0, 1, \dots, s$ . Let  $h_i(x) = h_0^i + h_1^i x + \dots + h_{2k}^i x^{2k}$ . Let  $b_l^i$  be the coefficient of  $x^l$  in  $h_i(x)f_i(x)$  where  $l = 1, \dots, n-1$ . For any  $t < n/2$ , the coefficient of  $x^t$  in  $h_i(x)f_i(x)$  is

$$b_t^i = \sum_{j=0}^t h_j^i \theta_i^j(a_{t-j}^i)$$

and the coefficient of  $x^{n-t}$  is  $b_{n-t}^i = \sum_{j=0}^t h_{2k-j}^i \theta_i^{2k-j}(a_{2s-(t-j)}^i)$ .

The polynomial  $h_i(x)f_i(x) = \sum_{p=0}^{2k} h_p^i x^p f_i(x)$  corresponds a vector  $b = (b_0^i, b_1^i, \dots, b_{n-1}^i) \in C_i$ , for  $i = 1, \dots, a$ .

The vector  $\xi_i(b)^r = ((\xi_i(b_0^i), \xi_i(b_1^i), \dots, \xi_i(b_{n-1}^i)))^r$  is equal to the vector  $\xi_i(z)$ , where the vector  $z$  corresponds the polynomial  $\sum_{p=0}^{2k} \theta_i(h_p^i) x^{2k-p} f_i(x)$ , for  $i = 1, \dots, a$ .

Since  $z = (z_1^i, \dots, z_n^i) \in C_i$ , then  $\xi_i(C_i)$  is a reversible DNA code, for  $i = 1, \dots, a$ .

#### 4. THE OTHER METHOD THAT IS USED TO OBTAIN DNA CODES

In [4], S. Das et al. derived a special generator matrix of a linear code over  $M_1$ . By using it, the DNA codes with some constraints are obtained. Moreover, they proposed a new construction of DNA codes using Reed Muller-type generator matrices.

In this part, we generalize it to codes over a family of the finite rings  $M_e$ .

The following definitions are in [4].

**Definition 5.** For any DNA sequence  $m = m_1 \dots m_n$ , the reverse DNA sequence is  $m^r = m_n \dots m_1$  and the reverse complement DNA sequence is  $m^{rc} = m_n^c \dots m_1^c$  where  $A^c = T, T^c = A, C^c = G, G^c = C$ .

**Definition 6.** A set  $C \subset S_{D_4}^n$  of size  $M$  is called a DNA code with parameter  $(n, M, d_H)$ , where the minimum distance  $d_H = \min\{d_H(\mathbf{x}, \mathbf{y}) \mid \mathbf{x} \neq \mathbf{y}, \mathbf{x}, \mathbf{y} \in C\}$  and  $d_H(\mathbf{x}, \mathbf{y})$  is the Hamming distance between DNA sequences  $\mathbf{x}$  and  $\mathbf{y}$ .

Moreover, there are some constraints on  $(n, M, d_H)$  DNA code  $C$ . The reverse constraint: For any two codewords  $\mathbf{c}_1, \mathbf{c}_2 \in C$  such that  $\mathbf{c}_1^r \neq \mathbf{c}_2$ , the DNA code holds reverse constraints, if  $d_H(\mathbf{c}_1^r, \mathbf{c}_2) \geq d_H$ . The reverse complement constraint: For any two codewords  $\mathbf{c}_1, \mathbf{c}_2 \in C$  such that  $\mathbf{c}_1^{rc} \neq \mathbf{c}_2$ , the DNA code holds reverse complement constraints, if  $d_H(\mathbf{c}_1^{rc}, \mathbf{c}_2) \geq d_H$ .

In [4], a mapping was defined and a table was given. We define the following mapping. The mapping is different from it in [4];

$$\begin{aligned} \psi_1 & : M_1 \longrightarrow S_{D_4}^3 \\ x_0 + u_1y_0 + u_1^2z_0 & \longmapsto (\xi_0(x_0), \xi_0(y_0), \xi_0(z_0)) = KLN \end{aligned}$$

where  $\xi_0(0) = A, \xi_0(1) = G, \xi_0(2) = T, \xi_0(3) = C$  and  $K, L, N \in S_{D_4} = \{A, T, C, G\}$ .

We give the following table according to the mapping;

elements $\alpha_1$	DNA 3-mers
0	AAA
$u_1$	AGA
$2u_1$	ATA
$3u_1$	ACA
$u_1^2$	AAG
$u_1 + u_1^2$	AGG
$2u_1 + u_1^2$	ATG
$3u_1 + u_1^2$	ACG
$2u_1^2$	AAT
$u_1 + 2u_1^2$	AGT
$2u_1 + 2u_1^2$	ATT
$3u_1 + 2u_1^2$	ACT
$3u_1^2$	AAC
$u_1 + 3u_1^2$	AGC
$2u_1 + 3u_1^2$	ATC
$3u_1 + 3u_1^2$	ACC
1	GAA
$1 + u_1$	GGA
$1 + 2u_1$	GTA
$1 + 3u_1$	GCA
$1 + u_1^2$	GAG
$1 + u_1 + u_1^2$	GGG
$1 + 2u_1 + u_1^2$	GTG
$1 + 3u_1 + u_1^2$	GCG
$1 + 2u_1^2$	GAT
$1 + u_1 + 2u_1^2$	GGT
$1 + 2u_1 + 2u_1^2$	GTT
$1 + 3u_1 + 2u_1^2$	GCT
$1 + 3u_1^2$	GAC

elements $\alpha_1$	DNA 3-mers
$1 + u_1 + 3u_1^2$	<i>GGC</i>
$1 + 2u_1 + 3u_1^2$	<i>GTC</i>
$1 + 3u_1 + 3u_1^2$	<i>GCC</i>
2	<i>TAA</i>
$2 + u_1$	<i>TGA</i>
$2 + 2u_1$	<i>TTA</i>
$2 + 3u_1$	<i>TCA</i>
$2 + u_1^2$	<i>TAG</i>
$2 + u_1 + u_1^2$	<i>TGG</i>
$2 + 2u_1 + u_1^2$	<i>TTG</i>
$2 + 3u_1 + u_1^2$	<i>TCG</i>
$2 + 2u_1^2$	<i>TAT</i>
$2 + u_1 + 2u_1^2$	<i>TGT</i>
$2 + 2u_1 + 2u_1^2$	<i>TTT</i>
$2 + 3u_1 + 2u_1^2$	<i>TCT</i>
$2 + 3u_1^2$	<i>TAC</i>
$2 + u_1 + 3u_1^2$	<i>TGC</i>
$2 + 2u_1 + 3u_1^2$	<i>TTC</i>
$2 + 3u_1 + 3u_1^2$	<i>TCC</i>
3	<i>CAA</i>
$3 + u_1$	<i>CGA</i>
$3 + 2u_1$	<i>CTA</i>
$3 + 3u_1$	<i>CCA</i>
$3 + u_1^2$	<i>CAG</i>
$3 + u_1 + u_1^2$	<i>CGG</i>
$3 + 2u_1 + u_1^2$	<i>CTG</i>
$3 + 3u_1 + u_1^2$	<i>CCG</i>
$3 + 2u_1^2$	<i>CAT</i>
$3 + u_1 + 2u_1^2$	<i>CGT</i>
$3 + 2u_1 + 2u_1^2$	<i>CTT</i>
$3 + 3u_1 + 2u_1^2$	<i>CCT</i>
$3 + 3u_1^2$	<i>CAC</i>
$3 + u_1 + 3u_1^2$	<i>CGC</i>
$3 + 2u_1 + 3u_1^2$	<i>CTC</i>
$3 + 3u_1 + 3u_1^2$	<i>CCC</i>

Similarly, we can define a one-to-one correspondence between the DNA  $3^i$ -mers and

the elements of  $M_i$ , where  $i = 2, \dots, e$  as follows.

$$\begin{aligned} \psi_i & : M_i \longrightarrow S_{D_4}^{3^i} \\ a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1} & \longmapsto (\psi_{i-1}(a_{i-1}), \psi_{i-1}(b_{i-1}), \psi_{i-1}(c_{i-1})). \end{aligned}$$

The map  $\psi_i$  satisfies the following two conditions:

1) For any  $a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1} \in M_i$ , where  $i = 1, 2, \dots, e$ , then  $[\psi_i(a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1})]^c = (\psi_{i-1}(a_{i-1}), \psi_{i-1}(b_{i-1}), \psi_{i-1}(c_{i-1}))^c = ((\psi_{i-1}(a_{i-1}))^c, (\psi_{i-1}(b_{i-1}))^c, (\psi_{i-1}(c_{i-1}))^c)^c = \psi_i(a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1} + \mathbf{2} + \mathbf{2u} + \mathbf{2u}^2)$ , where all coefficients of  $\alpha = \mathbf{2} + \mathbf{2u} + \mathbf{2u}^2 \in M_i$  are  $2 + 2u_1 + 2u_1^2$ .

2) For any  $a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1} \in M_i$  where  $i = 1, 2, \dots, e$ , then  $[\psi_i(a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1})]^r = (\psi_{i-1}(a_{i-1}), \psi_{i-1}(b_{i-1}), \psi_{i-1}(c_{i-1}))^r = \psi_i((a_{i-1} + u_i b_{i-1} + u_i^2 c_{i-1})^r) = \psi_i(c_{i-1}^r + b_{i-1}^r u_i + a_{i-1}^r u_i^2)$ , where  $(a_0 + u_1 b_0 + u_1^2 c_0)^r = c_0 + u_1 b_0 + u_1^2 a_0$  for any  $a_0 + u_1 b_0 + u_1^2 c_0 \in M_1$ .

**Example 5.** For  $i = 2$ , the element  $\mathbf{2} + \mathbf{2u} + \mathbf{2u}^2$  is equal to  $(2 + 2u_1 + 2u_1^2) + u_2(2 + 2u_1 + 2u_1^2) + u_2^2(2 + 2u_1 + 2u_1^2)$ . For  $i = 3$ , the element  $\mathbf{2} + \mathbf{2u} + \mathbf{2u}^2$  is equal to  $[(2 + 2u_1 + 2u_1^2) + u_2(2 + 2u_1 + 2u_1^2) + u_2^2(2 + 2u_1 + 2u_1^2)] + u_3[(2 + 2u_1 + 2u_1^2) + u_2(2 + 2u_1 + 2u_1^2) + u_2^2(2 + 2u_1 + 2u_1^2)] + u_3^2[(2 + 2u_1 + 2u_1^2) + u_2(2 + 2u_1 + 2u_1^2) + u_2^2(2 + 2u_1 + 2u_1^2)]$ .

**Example 6.** Let  $(1 + 2u_1 + 0u_1^2) + 3u_2 + 0u_2^2 + 2u_3 + 1u_3^2 \in M_3$ .  $[\psi_3((1 + 2u_1 + 0u_1^2) + 3u_2 + 0u_2^2 + 2u_3 + 1u_3^2)]^c = ((\psi_2((1 + 2u_1) + 3u_2))^c, (\psi_2(2))^c, (\psi_2(1))^c)^c = ((\psi_1(1 + 2u_1), \psi_1(3), \psi_1(0))^c, (\psi_1(2), \psi_1(0), \psi_1(0))^c, (\psi_1(1), \psi_1(0), \psi_1(0))^c)^c = ((\psi_1(1 + 2u_1))^c, (\psi_1(3))^c, (\psi_1(0))^c, (\psi_1(2))^c, (\psi_1(0))^c, (\psi_1(0))^c, (\psi_1(0))^c, (\psi_1(1))^c, (\psi_1(0))^c, (\psi_1(0))^c)^c = ((GTA)^c(CAA)^c(AAA)^c(TAA)^c(AAA)^c(AAA)^c(GAA)^c(AAA)^c(AAA)^c)^c = CATGTTTTATTTTTTTTCTTTTTTTT$ .

On the other hand,  $\psi_3((1 + 2u_1 + 0u_1^2) + u_2 3 + 0u_2^2 + 2u_3 + 1u_3^2) + [(2 + 2u_1 + 2u_1^2) + u_2(2 + 2u_1 + 2u_1^2) + u_2^2(2 + 2u_1 + 2u_1^2)] + u_3[(2 + 2u_1 + 2u_1^2) + u_2(2 + 2u_1 + 2u_1^2) + u_2^2(2 + 2u_1 + 2u_1^2)] + u_3^2[(2 + 2u_1 + 2u_1^2) + u_2(2 + 2u_1 + 2u_1^2) + u_2^2(2 + 2u_1 + 2u_1^2)] = (\psi_1(3 + 2u_1^2), \psi_1(1 + 2u_1 + 2u_1^2), \psi_1(2 + 2u_1 + 2u_1^2), \psi(2u_1 + 2u_1^2), \psi_1(2 + 2u_1 + 2u_1^2), \psi_1(2 + 2u_1 + 2u_1^2), \psi_1(3 + 2u_1 + 2u_1^2), \psi_1(2 + 2u_1 + 2u_1^2), \psi_1(2 + 2u_1 + 2u_1^2)) = CATGTTTTATTTTTTTTCTTTTTTTT$ .

**Example 7.**  $[\psi_3((1 + 2u_1 + 0u_1^2) + u_2 3 + 0u_2^2 + 2u_3 + 1u_3^2)]^r = [\psi_2(1 + 2u_1) + 3u_2, \psi_2(2), \psi_2(1)]^r = [(\psi_1(1 + 2u_1), \psi_1(3), \psi_1(0)), (\psi_1(2), \psi_1(0), \psi_1(0)), (\psi_1(1), \psi_1(0), \psi_1(0))]^r = [GTACAAAAATAAAAAAGAAAAAAA]^r = AAAAAAAGAAAAA AATAAAAACATC$ .

On the other hand,  $\psi_3(1^r + 2^r u_3 + u_3^2(1 + 2u_1 + 3u_2)^r) = (\psi_2(1^r), \psi_2(2^r), \psi_2((1 + 2u_1) + 3u_2)^r) = (\psi_1(0), \psi_1(0), \psi_1(u_1^2), \psi_1(0), \psi_1(0), \psi_1(2u_1^2), \psi_1(0), \psi_1(3u_1^2), \psi_1(2u_1 + u_1^2)) = AAAAAAAGAAAAA AATAAAAACATC$ .

In [4], S. Das et al. defined the Gau distance  $d_G$ . This mapping

$$d_G : M_1 \times M_1 \longrightarrow R$$

was defined by  $d_G(x, y) = \min\{1, (l+3l') \bmod 4\} + \min\{1, (j+3j') \bmod 4\} + \min\{1, (k+3k') \bmod 4\}$  where  $(l, j, k)$  and  $(l', j', k')$  are the positions of two elements  $x$  and  $y$ , the letter  $R$  represents real numbers. It is shown that this map is a metric. Moreover they defined the minimum Gau distance for any code  $C$ , as follows.

For any two elements  $x = (x_1, \dots, x_n)$  and  $y = (y_1, \dots, y_n)$  of length  $n$  over  $M_1$ , the Gau distance between  $x$  and  $y$  is defined by

$$d_G(x, y) = \sum_{v=1}^n d_G(x_v, y_v)$$

For any code  $C$ , the minimum Gau distance  $d_G$  is defined by  $d_G = \min\{d_G(x, y) \mid x, y \in C, x \neq y\}$ .

Similarly, we define the Gau distance on  $M_i$  as follows

$$d_G : M_i \times M_i \longrightarrow R$$

$$(x, y) \longmapsto d_G(x, y) = \sum_{s=1}^{3^i} \min\{1, (t_s + 3j_s) \bmod 4\}$$

where  $(t_1, \dots, t_{3^i})$  and  $(j_1, \dots, j_{3^i})$  are the positions of two elements  $x$  and  $y$ , where  $i = 1, \dots, e$ . The mapping is also a metric. The Gau distance of two elements and the Gau distance of any code  $C_i$  are defined similarly, where  $i = 1, \dots, e$ .

**Proposition 1.** *The map  $\psi_i$  is a distance conserving map from  $(M_i^n, d_G)$  to  $(S_{D_4}^{3^i n}, d_H)$  for  $i = 1, 2, \dots, e$ , where  $d_H = \min\{d_H(\mathbf{a}, \mathbf{b}) \mid \mathbf{a} \neq \mathbf{b}, \mathbf{a}, \mathbf{b} \in C_{DNA}\}$  and  $d_H(\mathbf{a}, \mathbf{b})$  is the Hamming distance between the DNA sequences  $\mathbf{a}$  and  $\mathbf{b}$ .*

*Proof.* If  $t_s$  and  $j_s$  are the same, then  $\min\{1, (t_s + 3j_s) \bmod 4\}$  is equal to 0, otherwise 1, where  $s = 1, \dots, 3^i$ . It is easily seen that  $d_G(\mathbf{a}, \mathbf{b}) = d_H(\psi_i(\mathbf{a}), \psi_i(\mathbf{b}))$  for every  $\mathbf{a}, \mathbf{b} \in M_i$ , where  $i = 2, \dots, e$ .

**Example 8.** *Let  $\mathbf{a} = (1 + 2u_1 + u_1^2, 3u_1)$ ,  $\mathbf{b} = (2u_1, 1 + 3u_1^2)$  be in  $M_1^2$ . Then  $d_G(\mathbf{a}, \mathbf{b}) = d_G(1 + 2u_1 + u_1^2, 2u_1) + d_G(3u_1, 1 + 3u_1^2) = 2 + 3 = 5$ . On the other hand,  $d_H(GTCACA, ATAGAC) = 5$ .*

**Proposition 2.** For two elements  $\mathbf{a}$  and  $\mathbf{b}$  in  $M_i^n$ , the map  $\psi_i$  satisfies

$$\psi_i^{-1}(\psi_i(\mathbf{sa} + \mathbf{pb})^r) = s\psi_i^{-1}(\psi_i(\mathbf{a})^r) + p\psi_i^{-1}(\psi_i(\mathbf{b})^r)$$

where  $\psi_i^{-1}(\psi_i(\mathbf{a})^r) = (\psi_i^{-1}(\psi_i(a_{i,n})^r), \dots, \psi_i^{-1}(\psi_i(a_{i,1})^r))$  for  $\mathbf{a} = (a_{i,1}, \dots, a_{i,n}) \in M_i$  for  $i = 1, 2, \dots, e$ .

**Theorem 4.** For any given generator matrix  $G_i$  over  $M_i$ , where  $i = 1, 2, \dots, e$ , the code  $\psi_i(\langle G_i \rangle)$  is closed under complement DNA sequences, if  $\mathbf{2} + \mathbf{2u} + \mathbf{2u}^2 \in \langle G_i \rangle$  where  $\mathbf{2} + \mathbf{2u} + \mathbf{2u}^2$  stands for the vector of length  $n$  with all  $2 + 2u_1 + 2u_1^2$ .

*Proof.* Since  $a^c = a + 2$ , for each  $a \in M_0$ , the proof is easily seen.

**Theorem 5.** The DNA code  $\psi_i(\langle G_i \rangle)$  is closed under reverse DNA sequence if  $\mathbf{g}^r = \psi_i^{-1}(\psi_i(\mathbf{g})^r) = (\psi_i^{-1}(\psi_i(g_{i,n})^r), \dots, \psi_i^{-1}(\psi_i(g_{i,1})^r)) \in \langle G_i \rangle$  for each row  $\mathbf{g}$  where  $i = 1, \dots, e$ .

*Proof.* For  $i = 1$ , it was proven in the Theorem 2 in [4]. Similarly, it is proven for  $i = 2, \dots, e$ .

**Corollary 6.** The code  $\psi_i(\langle G_i \rangle)$  satisfies the reversible complement constraints, for a given  $G_i$  over  $M_i$ , if  $\psi_i(\langle G_i \rangle)$  is closed under both reverse and complement DNA sequences, where  $i = 1, \dots, e$ .

For any code  $C_i$  of length  $n$  over  $M_i$ ,  $\psi_i(C_i) = \{\psi_i(\mathbf{x}) | \text{each } \mathbf{x} \in C_i\} \subset S_{D_4}^{3^i n}$  represents the DNA code of length  $3^i n$ , where  $i = 1, 2, \dots, e$ .

**Theorem 7.** If  $C_i$  is a linear  $(n, M, d_G)$  code over  $M_i$  where  $i = 1, \dots, e$  and the matrix  $G_i$  is associated generator matrix of  $C$  such that the rows of  $G_i$  hold the conditions described in Theorem 20 and Theorem 21, then  $\psi_i(C_i)$  is a DNA code with the parameters  $(3^i n, M, d_G = d_H)$  and the code  $\psi_i(C_i)$  holds reversible and reversible complement constraints.

For any  $\nu$  from  $T = \{2, 2u_1, 2u_1^2, 2u_2, 2u_2^2, \dots, 2u_i, 2u_i^2, \dots, 2u_1^2 2u_2^2 \dots 2u_i^2\}$ , where  $|T| = 3^i$ , we get that the number of elements of ideal generated by  $\nu$  is equal to  $2^{3^i}$ , where  $i = 1, \dots, e$ .

**Theorem 8.** Let  $C_i$  be a linear code over  $M_i$ , where  $i = 1, \dots, e$ . For any  $\nu \in T$ , if the generator matrix  $G_i$  over  $\langle \nu \rangle$  satisfies the conditions in Theorem 20 and 21, the DNA code  $\psi_i(\langle G_i \rangle)$  satisfies reversible, reversible complement constraint.

*Proof.* It follows from Theorem 4 and Theorem 5.

### 5. REED MULLER TYPE CODES OVER $M_i$

In [4], by using Reed-Muller types codes over  $M_1$ , new constructions of DNA codes were presented. The parameters of the DNA codes obtained by this method were given.

In this section, we construct DNA codes, by using Reed Muller types codes over  $M_i$ , where  $i = 2, \dots, e$ .

The generator matrix  $G_{1,m}^i$  of the Reed Muller type code over  $R(1, m)$  of length  $2^m$  is

$$G_{1,j+1}^i = \begin{pmatrix} G_{1,j}^i & G_{1,j}^i \\ \mathbf{0}_{2^j} & \nu_{2^j} \end{pmatrix}$$

$$G_{1,1}^i = \begin{pmatrix} \nu & \nu \\ 0 & \nu \end{pmatrix}$$

where  $\mathbf{0}_{2^j} = [000\dots 0]$ ,  $\nu_{2^j} = [\nu\nu\dots\nu]$  with  $\nu \in M_i$ ,  $i = 1, \dots, e$  and  $j = 1, 2, \dots, m - 1$ . The order of this matrix is  $(m + 1) \times 2^m$ .

**Theorem 9.** *Let  $R(1, m)$  be the code over  $M_i$ , where  $i = 1, \dots, e$ . Then there exists a DNA code  $\psi_i(R(1, m))$  and the code is with the parameter  $(3^i 2^m, (4^{3^i})^{m+1}, d_H = 2^{m-1})$ . Moreover, it satisfies both reversible and reversible complement constraints.*

**Theorem 10.** *Let  $R(1, m)$  be the code over  $M_i$  and  $\nu \in T$ , where  $i = 1, \dots, e$ . Then the code  $R(1, m)$  over  $M_i$  has the length  $2^m$ , size  $(2^{3^i})^{m+1}$  and the minimum Gau distance  $d_G = 2^{m-1}$ .*

**Example 9.** *For  $m = 4$  and  $i = 3$ , the  $(432, 2^{270}, 8)$ -DNA code  $\psi_3(R(1, 4))$  holds the reversible and reversible complement constraints.*

**Example 10.** *For  $m = 5, i = 5$  and  $\nu = 2u_5^2$ , the  $R(1, 5)$  is a  $(32, 2^{1458}, 16)$ -DNA code. Also, the DNA code  $\psi_3(R(1, 4))$  satisfies reversible and reversible complement constraints.*

### 6. CONCLUSION

It is shown that the skew cyclic codes over the ring  $M_i$  can be used to construct the reversible DNA codes and Reed-Muller types codes over  $M_i$  can be used to construct the reversible and reversible complement DNA codes, where  $i = 1, 2, \dots, e$ .

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