ANALYSIS OF NUCLEOTIDEREPEATS OF *Babesiabigemina*

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Abstract: Babesia genus is a group of apicomplexan protozoans which spend a part of their life cycle in host and other part in the vector. Genome of the Babesiabegiminaconsists of five chromosomes. When the genetic sequence of Babesiabegiminawas observed then different nucleotide repeats and inverted repeats were observed. Among the nucleotide repeats, dinucleotides, trinucleotides, tetranucleotide and multinucleotides of the four nitrogenous bases were observed. In the case of inverted repeats, palindromic sequences which are read same in the forward direction as that in the reverse direction were observed.

Keywords: Apicomplexan, Nucleotide repeats, Palindromic sequences

1. INTRODUCTION

Babesia is a large genus that contains round to pyriform protozoans of the family babesia. The genus belongs to the eukaryotic kingdom and apicomplexan phylum. This genus consists of different species including *Babesiabegimina, Babesiabovis* and some other ones that causs diseases in cattle in tropics and sub tropics with B.begimina having wider distribution world wide (OIE *et al.*, 2010). It is an etiological agent of African red water that is cause of the mortality in Zimbabwe. The organisms of Babesia genus are protozoan parasite (Norwal*et al.*, 1979). They are transmitted by tick (vector).

Microscopic examination of the parasites in the smears enables the differentiation between these parasites. B. begimina are large, intra erythrocytic organism while the B. bovis are small. This variation in size enables one to differentiate the two .However, it is difficult to differentiate the organisms microscopically (Vos*et al.*, 1994). Indirect fluorescent antibody test (IFAT) and enzyme-linked immunosorbent assay (ELISA) are widely used for detection of antibodies against *Babesia* infections in cattle. Further, for detection of *Babesia* organism in vector ticks, its parasitic forms like ookinetes and sporozoites have been observed under microscope using different staining methods (Bock *et al.*, 2004).

These prorozans pass part of their life cycle in erythrocytes. Their life cycle consists of two stages asexual and sexual reproduction. Their asexual reproduction occurs in vertebrate blood cells and sexual reproduction takes place in vector. In the vector sporozoites are produced and are transfered through the vector to the host and cause disease known as babesiosis.

The most commonly clinical signs are high grade fever, anemia, hemoglobunaria,ataxia and sometimes death occurs. A characteristic feature is that when an organism recovered from this then it bcomes the carrier and is susceptible to the other organism (Bock*et al.*, 2004).

When the genomic sequence of *Babesiabigemina*was observed then different nucleotide repeats and inverted repeats were found to be present (Chauvin *et al*., 2009)

2. METHODOLOGY

- **Collection of data**

In order to find out the nucleotide repeats, we need to find the genetic sequence of *Babesiabigemina.* For this purpose we used **NCBI**. We simply selected the search category named as genome in NCBI and entered the name of our microorganism in search bar. Then a page was appeared with the links of nucleotide sequence of different chromosomes. We clicked on the links one by one and collected the genetic sequence of chromosomes in **FASTA format**. We copied and pasted the genetic sequence in microsoft word and saved the file.

- **Finding the nucleotide repeats**

Nucleotide repeats in genome of *Babesiabigemina*were observed using different methods. **Simple sequence repeats** were found using **Gramene SSR Tool**. Genomic sequence was taken in FASTA format and it was added in query box and simple sequence repeats were observed.

Microsatellites (tendom repeats) were found in the genome of *Babesiabigemina* using **Microsatellite repeats finder.** Tandem Repeats are copies of DNA sequences which lie adjacent to each other. When these repeats are short, the term Microsatellite Repeats is used for them.Genomic sequence was taken in FASTA format and it was added in query box. Different parameters of tool were set according to requirementand microsatellites were observed.

Then pairs of nucleotides as dinucleotide, trinucleotide and tetranucleotide were prepared using a **combination generator tool**. We simply put our sequence in query box and found **dinucleotide**, **trinucleotide** and **tetranucleotide** combinations along with their total number in the each chromosome and entire genome. Actually these combinations show the nucleotide repeats and their total number in genome.

3. RESULTS

- **Simple sequence repeats in genetic sequence of *Babesiabigemina***

Using Gramene SSR Tool different simple sequence repeats were observed in the genome of *Babesiabigemina*as shown in the table below:

Table 1: Simple sequence repeats in genome of Babesiabigemina

Sequence	Motif	No.of Repeats	SSR start	SSR end	SeqLength

M85187.1-1	ca	2	6	9	1962
M85187.1-2	gc	2	13	16	1962
M85187.1-3	tg	2	39	42	1962
M85187.1-4	cg	2	45	48	1962
M85187.1-5	at	2	85	88	1962
M85187.1-6	ac	2	132	135	1962
M85187.1-7	gt	4	202	209	1962
M85187.1-8	ct	3	217	222	1962
M85187.1-9	ta	2	255	258	1962
M85187.1-10	gt	2	271	274	1962
M85187.1-11	ag	2	284	287	1962
M85187.1-12	ga	2	295	298	1962
M85187.1-13	tg	2	299	302	1962
M85187.1-14	at	2	370	373	1962
M85187.1-15	ga	2	399	402	1962
M85187.1-16	ag	2	454	457	1962
M85187.1-17	tg	2	480	483	1962
M85187.1-18	gc	2	614	617	1962
M85187.1-19	cg	2	693	696	1962
M85187.1-20	ga	2	717	720	1962
M85187.1-21	ca	2	818	821	1962
M85187.1-22	cg	2	918	921	1962
M85187.1-23	tc	2	991	994	1962
M85187.1-24	ct	2	1012	1015	1962
M85187.1-25	cg	2	1049	1052	1962
M85187.1-26	ag	2	1057	1060	1962
M85187.1-27	tg	2	1088	1091	1962
M85187.1-28	tc	3	1132	1137	1962
M85187.1-29	ac	2	1156	1159	1962
M85187.1-30	ag	2	1175	1178	1962
M85187.1-31	ca	2	1179	1182	1962
M85187.1-32	at	2	1222	1225	1962
M85187.1-33	gt	2	1234	1237	1962
M85187.1-34	ga	2	1287	1290	1962
M85187.1-35	tg	2	1358	1361	1962
M85187.1-36	ag	2	1403	1406	1962
M85187.1-37	cg	2	1430	1433	1962
M85187.1-38	ga	2	1500	1503	1962
M85187.1-39	gc	3	1568	1573	1962
M85187.1-40	gt	2	1655	1658	1962
M85187.1-41	at	2	1677	1680	1962
M85187.1-42	tc	2	1700	1703	1962
M85187.1-43	gt	2	1732	1735	1962
M85187.1-44	at	2	1738	1741	1962
M85187.1-45	ga	2	1760	1763	1962

M85187.1-46	gt	2	1782	1785	1962
M85187.1-47	at	2	1787	1790	1962
M85187.1-48	ta	2	1795	1798	1962
M85187.1-49	at	2	1799	1802	1962
M85187.1-50	gc	2	1816	1819	1962
M85187.1-51	gc	2	1835	1838	1962
M85187.1-52	gt	2	1861	1864	1962
M85187.1-53	gt	2	1892	1895	1962
M85187.1-54	cg	2	1913	1916	1962
M85187.1-55	ta	2	1926	1929	1962
M85187.1-56	ag	2	1944	1947	1962
M85187.1-57	aat	2	81	86	1962
M85187.1-58	ctg	2	113	118	1962
M85187.1-59	gag	2	188	193	1962
M85187.1-60	ctt	2	194	199	1962
M85187.1-61	cag	2	280	285	1962
M85187.1-62	ggt	2	287	292	1962
M85187.1-63	agc	2	350	355	1962
M85187.1-64	tga	2	410	415	1962
M85187.1-65	tga	2	482	487	1962
M85187.1-66	gaa	2	599	604	1962
M85187.1-67	gag	2	632	637	1962
M85187.1-68	agc	2	636	641	1962
M85187.1-69	ttg	2	661	666	1962
M85187.1-70	ttg	2	672	677	1962
M85187.1-71	gaa	3	677	685	1962
M85187.1-72	tgt	2	686	691	1962
M85187.1-73	atg	2	709	714	1962
M85187.1-74	tac	2	756	761	1962
M85187.1-75	cgg	2	787	792	1962
M85187.1-76	ttc	2	798	803	1962
M85187.1-77	caa	2	803	808	1962
M85187.1-78	cca	2	910	915	1962
M85187.1-79	atg	2	948	953	1962
M85187.1-80	cta	2	1003	1008	1962
M85187.1-81	ggt	2	1060	1065	1962
M85187.1-82	ctt	2	1094	1099	1962
M85187.1-83	gtc	2	1200	1205	1962
M85187.1-84	gat	2	1253	1258	1962
M85187.1-85	caa	2	1272	1277	1962
M85187.1-86	aat	2	1277	1282	1962
M85187.1-87	gtt	2	1335	1340	1962
M85187.1-88	aag	2	1341	1346	1962
M85187.1-89	agc	2	1394	1399	1962
M85187.1-90	gaa	2	1455	1460	1962

M85187.1-91	tac	2	1478	1483	1962
M85187.1-92	agg	2	1486	1491	1962
M85187.1-93	cga	2	1514	1519	1962
M85187.1-94	cag	2	1539	1544	1962
M85187.1-95	tga	2	1574	1579	1962
M85187.1-96	ttc	2	1595	1600	1962
M85187.1-97	ttc	2	1604	1609	1962
M85187.1-98	gat	2	1611	1616	1962
M85187.1-99	aat	2	1667	1672	1962
M85187.1-100	ata	2	1796	1801	1962
M85187.1-101	gct	2	1818	1823	1962
M85187.1-102	aat	2	1881	1886	1962
M85187.1-103	aga	2	1941	1946	1962
M85187.1-105	gctt	2	809	816	1962
M85187.1-106	accc	2	897	904	1962
M85187.1-107	tagc	2	925	932	1962
M85187.1-108	cagg	2	1181	1188	1962
M85187.1-109	acca	2	1381	1388	1962
M85187.1-110	acgc	2	1908	1915	1962
M85187.1-111	gccgt	2	60	69	1962
M85187.1-112	tcgca	2	724	733	1962
M85187.1-113	gctgc	2	1813	1822	1962
M85187.1-114	ttcggt	2	831	842	1962

In the above table the first column named “sequence” shows the specific tag for each sequence. Motif is the sequence that is repeated. SSR start and SSR shows the respective nucleotide number from which the sequence starts and the number of the nucleotide at which SSR ends.

- **Microsatellites in genetic sequence of *Babesiabigemina***

Using the microsatellite repeat finder different microsatellites were observed in the genome of *Babesiabigemina*as shown in the table below:

Table 2: Microsatellites in genome of *Babesiabigemina*

Position	Repeats	Sequence
228	4	GTGTGTGT
243	3	CTCTCT
703	3	GAAGAAGAA
1158	3	TCTCTC
1594	3	GCGCGC
1735	3	TTTTTT

- **Dinucleotide repeats in genetic sequence of *Babesiabigemina***

Using the combination generator tool, dinucleotide repeats were observed in all chromosomes of *Babesiabigemina*. About 16 different kinds of dinucleotide repeats were observed. The kinds and abundance of different dinucleotide repeats is enlisted in the table 3.1.

Table 3.1: Dinucleotide repeats in different chromosomes of *Babesiabigemina*

Sr. no	Dinucleotide Repeats	Chromosome 1	Chromosome 2	Chromosome 3	Chromosome 4	Chromosome 5	Genome sequence
1	AA	121791	133449	173236	45358	25110	498944
2	AT	150198	163506	213402	53703	32095	612904
3	AG	142905	157595	199467	51746	26595	578308
4	AC	156659	172802	216081	55571	29818	630931
5	TA	113858	123431	164161	41632	24630	467712
6	TT	121737	133786	175009	43278	26138	499948
7	TG	181339	201771	250701	62730	36692	733233
8	TC	153249	171088	212384	52529	29606	618856
9	GA	153213	169803	212632	54762	29096	619506
10	GT	156766	173789	215190	541367	31129	1118241
11	GG	122674	137359	169212	42423	22510	494178
12	GC	196678	222308	257748	67172	34720	778626
13	CA	182547	200558	252326	64678	34768	734877
14	CT	141464	159141	198716	48990	27705	576016
15	CG	182392	206445	235403	61593	31730	717563
16	CC	121816	138665	169397	42054	22301	494233

- **Trinucleotide repeats in genetic sequence of *Babesiabigemina***

Using the combination generator tool, trinucleotide repeats were observed in all chromosomes of *Babesiabigemina*. About 64 different kinds of trinucleotide repeats were observed. The kinds and abundance of different trinucleotide repeats is enlisted in the table 3.2.

Table 3.2: Trinucleotide repeats in different chromosomes of *Babesiabigemina*

Sr. no	Trinucleotide repeats	Chromosome 1	Chromosome 2	Chromosome 3	Chromosome 4	Chromosome 5	Genome Sequence
1.	AAA	28980	31655	41848	10990	6268	119741
2.	AAT	35127	38124	50503	12959	7779	144492
3.	AAG	35914	39760	52004	13832	7119	148629
4.	AAC	39667	43431	54689	14324	7843	159954
5.	ATA	29913	32087	42253	10893	6635	121781
6.	ATT	35130	37871	51030	13006	7878	144915
7.	ATG	44140	48047	61574	15529	9265	178555
8.	ATC	36748	40752	52411	12777	7341	150029
9.	AGA	30312	33420	43519	11593	5989	124833
10.	AGT	30337	33096	44030	10985	6063	124511
11.	AGG	34973	38901	49371	12682	6392	142319
12.	AGC	43893	48444	57660	15208	7479	172684
13.	ACA	40628	44056	56401	14836	8068	163989
14.	ACT	36122	33098	44214	10677	6074	130185
15.	ACG	44947	50201	58193	15498	7974	176813
16.	ACC	35923	40155	50603	12677	6699	146057
17.	TAA	25923	28404	39466	9871	5670	109334
18.	TAT	29699	32085	42241	10583	6821	121429
19.	TAG	22528	23846	32500	8221	4612	91707
20.	TAC	31970	35040	44566	11615	6663	129854
21.	TTA	26051	28168	39653	9733	5840	109445

22.	TTT	28758	32165	42824	10632	6575	120954
23.	TTG	43917	48189	63025	15385	9539	180055
24.	TTC	40801	45207	55826	14176	8230	164240
25.	TGA	40703	45091	58137	14719	8370	167020
26.	TGT	40269	44345	56396	13574	8529	163113
27.	TGG	41473	46256	58487	14450	8270	168936
28.	TGC	53517	60060	70567	18176	10376	212696
29.	TCA	41098	44633	58515	14241	8036	166523
30.	TCT	30308	33694	43312	10528	6392	124234
31.	TCG	42890	48248	55600	14437	7737	168912
32.	TCC	35359	40528	49884	12064	6739	144574
33.	GAA	41008	44539	55408	15012	8202	164169
34.	GAT	36473	40241	52520	13260	7511	150005
35.	GAG	35087	39334	48965	12275	6068	141729
36.	GAC	36904	41446	50464	12887	6579	148280
37.	GTA	32144	34719	44665	11402	6712	129642
38.	GTT	39646	43775	55313	13833	8334	160901
39.	GTG	42904	48312	58973	14629	8215	173033
40.	GTC	37305	41803	50118	12541	6930	148697
41.	GGA	35901	39627	49818	12583	6618	144547
42.	GGT	36334	40156	50469	12679	7027	146665
43.	GGG	21740	24219	30495	7603	4140	88197
44.	GGC	43686	49971	59182	14948	7628	175415
45.	GCA	53647	59533	71109	18849	9844	212982
46.	GCT	43335	48908	57344	14851	7915	172353
47.	GCG	49621	56464	62686	16535	8341	193647
48.	GCC	43846	50320	59085	14937	7616	175804

49.	CAA	43747	48286	62490	16256	8846	179625
50.	CAT	44597	48454	62017	15394	9022	179484
51.	CAG	45723	50669	60899	16175	8098	181564
52.	CAC	43348	47777	60162	15013	7822	174122
53.	CTA	22016	24337	32152	8267	4582	91354
54.	CTT	35984	39910	52180	12410	7433	147917
55.	CTG	45224	51667	60428	15343	8605	181267
56.	CTC	34757	39204	48669	11793	6372	140795
57.	CGA	42751	47711	56122	14582	7446	168612
58.	CGT	44798	50605	57656	15189	8420	176668
59.	CGG	39456	44641	51628	13068	6657	155450
60.	CGC	49414	56633	62858	16789	8278	193972
61.	CCA	41736	46552	58949	14760	7702	169699
62.	CCT	34439	39648	48915	11747	6625	141374
63.	CCG	38964	44710	51801	13166	6729	155370
64.	CCC	21198	24444	30665	7422	4020	87749

- **Tetranucleotide repeats in genetic sequence of *Babesiabigemina***

Using the combination generator tool, tetranucleotide repeats were observed in all chromosomes of *Babesiabigemina*. About 256 different kinds of tetranucleotide repeats were observed. The kinds and abundance of different tetranucleotide repeats is enlisted in the table 3.3.

Table 3.3: Tetranucleotide repeats in different chromosomes of *Babesiabigemina*

Sr. no	Tetranucleotide repeats	Chromosome 1	Chromosome 2	Chromosome 3	Chromosome 4	Chromosome 5	Genome sequence
1.	AAAA	8384	9146	12060	3205	1782	34577
2.	AAAT	10290	11258	14748	3772	2290	42358
3.	AAAG	7946	9035	12057	3157	1726	33921
4.	AAAC	9619	10106	13424	3635	2014	38798

5.	AATA	7940	8562	11407	2971	1741	32621
6.	AATT	8103	8774	12338	3055	1815	34085
7.	AATG	10204	11122	14219	3708	2324	41577
8.	AATC	8196	8949	11560	2989	1749	33443
9.	AAGA	8162	9149	12190	3504	1656	34661
10.	AAGT	8019	8677	11624	2899	1628	32847
11.	AAGG	8162	10337	13359	3486	1852	37196
12.	AAGC	9923	10761	13779	3644	1840	39947
13.	AACA	11220	12171	15787	4175	2307	45660
14.	AACT	8344	8951	11839	2940	1706	33780
15.	AACG	11039	12316	14232	3826	2059	43472
16.	AACC	8226	9029	11690	3081	1604	33630
17.	ATAA	7428	8060	11031	2870	1586	30975
18.	ATAT	9191	9925	13085	3179	2122	37502
19.	ATAG	5840	6088	8078	2032	1314	23352
20.	ATAC	2309	8985	11290	3098	1852	27534
21.	ATTA	6601	7208	10129	2478	1519	27935
22.	ATTT	10174	11170	15086	3840	2321	42591
23.	ATTG	9099	9676	13370	3287	2121	37553
24.	ATTC	8633	9136	11474	3180	1769	34192
25.	ATGA	10253	10970	14432	3873	2160	41688
26.	ATGT	11573	12397	16638	3782	2403	46793
27.	ATGG	9704	10912	13696	3408	2112	39832
28.	ATGC	11635	12820	15484	4136	2400	46475
29.	ATCA	10012	10816	14148	3434	1894	40304
30.	ATCT	7897	8589	11495	2864	1721	32566
31.	ATCG	9925	11254	13838	3452	1964	40433

32.	ATCC	8074	9124	11772	2763	1620	33353
33.	AGAA	8683	9717	12442	3314	1813	35969
34.	AGAT	7877	8820	11477	3257	1618	33049
35.	AGAG	6686	7295	9988	2445	1261	27675
36.	AGAC	7421	7989	10165	3733	1388	30696
37.	AGTA	6063	6438	8580	2300	1247	24628
38.	AGTT	8392	8883	12029	3017	1754	34075
39.	AGTG	8705	9814	13403	3175	1696	36793
40.	AGTC	6618	7385	9273	2292	1282	26850
41.	AGGA	8707	9648	12049	3117	1579	35100
42.	AGGT	9223	10218	13110	3349	1831	37731
43.	AGGG	6643	7300	9914	2434	1213	27504
44.	AGGC	9613	10868	13302	3521	1657	38961
45.	AGCA	12373	13626	16715	4367	2157	49238
46.	AGCT	10393	11390	13551	3650	1821	40805
47.	AGCG	11588	12879	14707	3961	1921	45056
48.	AGCC	8422	9326	11310	2873	1411	33342
49.	ACAA	10821	11694	15299	4043	2259	44116
50.	ACAT	10011	12406	16291	4062	2374	45144
51.	ACAG	9434	10420	12699	3550	1755	37858
52.	ACAC	9984	10792	13664	3638	1973	40051
53.	ACTA	5068	5674	7675	1959	1091	21467
54.	ACTT	7941	8658	11961	2729	1681	32970
55.	ACTG	9077	9893	12689	3128	1800	36587
56.	ACTC	7511	8303	11053	2688	1381	30936
57.	ACGA	10620	11632	13683	3710	1862	41507
58.	ACGT	11287	12896	14960	4013	2153	45309

59.	ACGG	9584	10805	12730	3238	1697	38054
60.	ACGC	12481	13821	15542	4187	2098	48129
61.	ACCA	10185	11424	14619	3680	1892	41800
62.	ACCT	9235	10400	12930	3222	1737	37524
63.	ACCG	9014	9897	12227	3135	1636	35909
64.	ACCC	6726	7575	9688	2411	1300	27700
65.	TAAA	7078	7923	10876	2720	1636	30233
66.	TAAT	6649	7265	10201	2388	1461	27964
67.	TAAG	5220	5536	8206	2246	1111	22319
68.	TAAC	6493	7158	9396	2323	1365	26735
69.	TATA	6876	7353	9640	2449	1613	27931
70.	TATT	7937	8505	11456	2841	1868	32607
71.	TATG	8497	9127	11679	2023	1961	33287
72.	TATC	7402	8138	10863	2617	1635	30655
73.	TAGA	6007	6211	8777	2144	1258	24397
74.	TAGT	5265	5686	7742	1823	1129	21645
75.	TAGG	4611	4950	7121	1816	1027	19525
76.	TAGC	6238	6554	8223	2284	1107	24406
77.	TACA	9666	10580	13481	3587	2014	39328
78.	TACT	5945	6481	8676	2197	1304	24603
79.	TACG	8770	9499	11430	3075	1732	34506
80.	TACC	7079	7911	10206	2558	1497	29251
81.	TTAA	6395	2010	10387	2446	1498	22736
82.	TTAT	7365	2235	10901	2647	1687	24835
83.	TTAG	4980	1441	7698	1890	1027	17036
84.	TTAC	6829	2038	9848	2552	1513	22780
85.	TTTA	7207	2324	11021	2862	1643	25057

86.	TTTT	8276	2382	12467	3001	1908	28034
87.	TTTG	10793	3657	16061	3866	2500	36877
88.	TTTC	9700	3048	14076	3501	622	30947
89.	TTGA	10041	11312	15227	3676	2242	42498
90.	TTGT	10890	11770	15241	3622	2347	43870
91.	TTGG	9371	10361	14018	3364	2064	39178
92.	TTGC	12722	13814	17239	4448	2682	50905
93.	TTCA	11368	12240	15701	4013	2305	45627
94.	TTCT	8878	9836	12580	2968	1899	36161
95.	TTCG	10463	11644	13558	3616	1976	41257
96.	TTCC	9284	10532	12896	3296	1884	37892
97.	TGAA	11297	12260	15852	4184	2420	46013
98.	TGAT	9733	10773	14090	3491	2106	40193
99.	TGAG	9229	10210	13173	3385	1741	37738
100	TGAC	9632	10915	13814	3345	1922	39628
101	TGTA	9486	10434	13848	3276	2037	39081
102	TGTT	11136	12354	15779	3739	2476	45484
103	TGTG	10770	11815	14483	3626	2316	43010
104	TGTC	10046	11087	13800	3326	2003	40262
105	TGGA	10966	12230	15833	3842	2167	45038
106	TGGT	10176	11314	14447	3417	2016	41370
107	TGGG	7494	8296	10635	2680	1574	30679
108	TGGC	12015	13468	16354	4237	2346	48420
109	TGCA	14098	15598	18561	4805	2829	55891
110	TGCT	12185	13662	16307	4139	2340	48633
111	TGCG	13983	15890	17559	4643	2561	54636
112	TGCC	12064	13566	16625	4186	2398	48839

113	TCAA	10332	11182	15164	3649	2037	42364
114	TCAT	10182	11141	14616	3460	2158	41557
115	TCAG	9115	10061	12469	3196	1734	36575
116	TCAC	10332	11273	14981	3643	1966	42195
117	TCTA	5786	6398	8754	2171	1255	24364
118	TCTT	8401	9294	12227	2827	1788	34537
119	TCTG	9201	10229	12468	3150	1947	36995
120	TCTC	7258	8118	10402	2543	1488	29809
121	TCGA	16530	11876	14009	3602	1882	47899
122	TCGT	10775	11827	13382	3542	2075	41601
123	TCGG	8975	10104	11610	2900	2075	35664
124	TCGC	11659	13428	15467	4077	2057	46688
125	TCCA	11145	12410	15874	3826	2089	45344
126	TCCT	8453	9934	11965	2791	1661	34804
127	TCCG	8789	10142	11471	3031	1609	35042
128	TCCC	6196	7151	9590	2212	1238	26387
129	GAAA	9871	10668	13701	3706	2123	40069
130	GAAT	8683	9085	11592	3239	1896	34495
131	GAAG	11971	13122	16330	4406	2204	48033
132	GAAC	9541	10689	12537	3312	1800	37879
133	GATA	7282	8131	10813	2743	1637	30606
134	GATT	8161	8744	11611	3047	1777	33340
135	GATG	13023	14367	18918	4690	2580	53578
136	GATC	7089	7999	9886	2445	1340	28759
137	GAGA	7318	8330	10436	2661	1423	30168
138	GAGT	7569	8402	11178	2797	1353	31299
139	GAGG	4528	11202	14012	3423	1649	34814

140	GAGC	7677	13368	13943	3577	1738	40303
141	GACA	9971	10863	14044	3560	1861	40299
142	GACT	6578	7255	9226	2283	1249	26591
143	GACG	11812	13368	15402	4095	1943	46620
144	GACC	7702	9044	10620	2624	1392	31382
145	GTAA	6777	7315	9873	2411	409	26785
146	GTAT	8287	8882	11378	2924	1915	33386
147	GTAG	7604	8131	10810	2824	1446	30815
148	GTAC	8868	9709	11793	3028	1712	35110
149	GTTA	6581	7129	9536	2322	1454	27022
150	GTTT	9488	10606	13581	3465	2147	39287
151	GTTG	13050	14313	18099	4464	2699	52625
152	GTTC	9597	10762	12860	3273	1827	38319
153	GTGA	13053	11522	14919	3530	1995	45019
154	GTGT	9743	11160	13201	3423	2073	39600
155	GTGG	11394	12484	15959	3881	2058	45776
156	GTGC	12234	13938	15899	4139	2251	48461
157	GTCA	9926	10684	14016	3317	1918	39861
158	GTCT	7386	8218	10134	2577	1488	29803
159	GTCG	11754	13379	14889	3890	2006	45918
160	GTCC	7355	8512	9999	2462	1367	29695
161	GGAA	9684	10318	12657	3449	1872	37980
162	GGAT	8020	8769	11705	2794	1714	33002
163	GGAG	10011	11359	14416	3482	1650	40918
164	GGAC	7425	8248	9929	2608	1258	29468
165	GGTA	7247	7788	10104	2528	1512	29179
166	GGTT	8383	9360	11898	3102	1719	34462

167	GGTG	11926	13401	16497	4129	2192	48145
168	GGTC	7932	8644	10763	2609	1439	31387
169	GGGA	6487	7086	9297	2290	1266	26426
170	GGGT	7058	7564	9723	2624	1370	28339
171	GGGG	4528	5044	6630	1459	810	18471
172	GGGC	7677	8960	10649	2487	1399	31172
173	GGCA	11919	13398	16631	4235	2227	48410
174	GGCT	8170	9388	11193	2833	1565	33149
175	GGCG	13935	15974	18281	4654	2276	55120
176	GGCC	8520	9897	11559	2890	1389	34255
177	GCAA	12423	13745	16980	4648	2501	50297
178	GCAT	11861	13025	15962	4181	2353	47382
179	GCAG	15677	17473	20232	5373	2661	61416
180	GCAC	12333	13782	16306	4194	2123	48738
181	GCTA	11861	6583	8254	2261	1227	30186
182	GCTT	9993	10801	13685	3468	1918	39865
183	GCTG	15564	18140	19908	5245	2759	61616
184	GCTC	10403	11867	13879	3496	1814	41459
185	GCGA	11923	13295	15647	3932	2030	46827
186	GCGT	12315	14075	15223	4112	2228	47953
187	GCGG	11918	13548	15242	3980	1886	46574
188	GCGC	14678	16959	17887	4865	2404	56793
189	GCCA	12256	13409	16506	4410	2124	48705
190	GCCT	9541	11055	13160	3256	1841	38853
191	GCCG	13333	15430	17390	4313	2102	52568
192	GCCC	7684	9134	10517	2599	1377	31311
193	CAAA	10871	11819	15650	4140	2246	44726

194	CAAT	8910	9849	13047	3317	1977	37100
195	CAAG	9948	11086	14272	3734	1925	40965
196	CAAC	13081	14455	18149	4712	2502	52899
197	CATA	8761	9132	11841	3056	1907	34697
198	CATT	10310	11165	14666	3851	2281	42273
199	CATG	11345	12344	15304	3733	2184	44910
200	CATC	13168	14673	18774	4414	2461	53490
201	CAGA	9187	10163	12636	3481	1760	37227
202	CAGT	8964	12344	12724	3276	1822	39130
203	CAGG	10540	11467	13735	3668	1736	41146
204	CAGC	15730	17730	20139	5306	2575	61480
205	CACA	10995	11628	14649	3965	2163	43400
206	CACT	8799	9856	13744	3079	1709	37187
207	CACG	12297	13919	15797	4126	2089	48228
208	CACC	12055	13243	16940	4138	2053	48429
209	CTAA	4826	5310	7347	1952	959	20394
210	CTAT	5767	6182	8102	2125	1334	23510
211	CTAG	3651	3893	5277	1295	729	14845
212	CTAC	7349	8467	10731	2716	1462	30725
213	CTTA	5163	5417	8174	1874	1108	21736
214	CTTT	8011	9143	12474	2908	1859	34395
215	CTTG	9984	11017	14141	3417	2009	40568
216	CTTC	11975	13410	16181	3897	2274	47737
217	CTGA	9140	10329	12316	3314	1790	36889
218	CTGT	9140	10368	12771	3127	1942	37348
219	CTGG	10162	11567	13608	3489	1882	40708
220	CTGC	15634	17946	20256	5015	2791	61642

221	CTCA	8897	9951	13450	3173	1759	37230
222	CTCT	6481	7457	9756	2280	1379	27353
223	CTCG	9827	10874	12176	3182	1613	37672
224	CTCC	9856	11454	14077	3309	1736	40432
225	CGAA	10524	11326	13322	3765	1958	40895
226	CGAT	10091	11032	14138	3445	1940	40646
227	CGAG	9644	10963	12045	3118	1502	37272
228	CGAC	11544	13331	15336	3911	1875	45997
229	CGTA	8785	9481	11369	3123	1800	34558
230	CGTT	10854	12262	14440	3686	2209	43451
231	CGTG	12301	14042	15509	4014	2175	48041
232	CGTC	11811	13666	15122	4002	2045	46646
233	CGGA	8993	9782	11638	3062	1486	34961
234	CGGT	9104	10186	12087	3025	1688	36090
235	CGGG	7048	8013	9130	2301	1246	27738
236	CGGC	13276	15451	17439	4349	2082	52597
237	CGCA	13985	15529	17594	5031	2434	54573
238	CGCT	11525	13290	14948	3871	1998	45632
239	CGCG	11468	13287	13544	3709	1811	43819
240	CGCC	13771	16205	18158	4629	2239	55002
241	CCAA	10871	10698	13789	3588	1886	40832
242	CCAT	10011	10841	13807	3384	1951	39994
243	CCAG	10268	11380	13984	3651	1770	41053
244	CCAC	11255	12778	16201	3838	1928	46000
245	CCTA	4652	5210	6855	1737	916	19370
246	CCTT	8959	10275	13199	3136	1887	37456
247	CCTG	10102	11859	13751	3413	1892	41017

248	CCTC	9966	11380	13974	3231	1798	40349
249	CCGA	8779	9910	11535	3028	1527	34779
250	CCGT	9449	10731	12900	3177	1783	38040
251	CCGG	7996	9080	10798	2622	1375	31871
252	CCGC	11784	13865	15305	4051	1882	46887
253	CCCA	7298	8356	10650	2585	1460	30349
254	CCCT	6500	7418	9800	2248	1246	27212
255	CCCG	6847	8084	9381	2374	1216	27902
256	CCCC	4416	5165	6574	1616	837	18608

- **Multinucleotide repeats in genetic sequence of *Babesiabigemina***

Table 3.4: Multinucleotide repeats consisting of nitrogeneous base A in different chromosomes of *Babesiabigemina*

Sr. no	Multinucleotide	Chromosome 1	Chromosome 2	Chromosome 3	Chromosome 4	Chromosome 5	Genome sequence
1	A	610989	670346	859025	221207	122025	2483592
2	AA	121791	133433	173236	45358	25110	498928
3	AAA	28980	31650	41848	10990	6268	119736
4	AAAA	8384	9144	12060	3205	1782	34575
5	AAAAA	2222	2436	3191	818	451	9118
6	AAAAAA	526	605	765	198	117	2211
7	AAAAAAA	143	163	207	66	24	603
8	AAAAAAAA	46	34	54	22	4	160
9	AAAAAAAAA	12	8	14	2	3	39
10	AAAAAAAAAA	5	2	2	1	1	11

Table 3.5: Multinucleotide repeats consisting of nitrogeneous base C in different chromosomes of *Babesiabigemina*

Sr. no	Multinucleotide	Chromosome 1	Chromosome 2	Chromosome 3	Chromosome 4	Chromosome 5	Genome sequence
1	C	659774	740710	900292	228268	122384	2651428
2	CC	121816	138649	169397	42054	22301	494217
3	CCC	21198	24444	30665	7422	4020	87749
4	CCCC	4416	5165	6574	1616	837	18608
5	CCCCC	870	1037	1264	315	166	3652
6	CCCCCC	164	142	242	56	20	624
7	CCCCCCC	41	24	55	15	3	138
8	CCCCCCCC	7	5	9	3	0	24
9	CCCCCCCCC	1	0	3	0	0	4
10	CCCCCCCCCC	1	0	1	0	0	2

Table 3.6: Multinucleotide repeats consisting of nitrogeneous base G in different chromosomes of *Babesiabigemina*

Sr. no	Multinucleotide	Chromosome 1	Chromosome 2	Chromosome 3	Chromosome 4	Chromosome 5	Genome sequence
1	G	661350	738790	899133	229622	123474	2652369
2	GG	122674	137348	169212	42423	22510	494167
3	GGG	21793	24217	30495	7603	4140	88248
4	GGGG	4528	5044	6630	1459	810	18471
5	GGGGG	847	915	1271	290	163	3486
6	GGGGGG	155	159	231	53	27	625
7	GGGGGGG	36	22	45	9	3	115

8	GGGGGGGG	10	6	3	1	0	20
9	GGGGGGGGG	2	0	0	0	0	2
10	GGGGGGGGGG	1	0	0	0	0	1
11	GGGGGGGGGGG	1	0	0	0	0	1
12	GGGGGGGGGGGG	1	0	0	0	0	1
13	GGGGGGGGGGGGG	1	0	0	0	0	1

Table 3.7: Multinucleotide repeats consisting of nitrogeneous base T in different chromosomes of *Babesiabigemina*

Sr. no	**Multinucleotide**	**Chromosome 1**	**Chromosome 2**	**Chromosome 3**	**Chromosome 4**	**Chromosome 5**	**Genome sequence**
1	T	609389	673842	860309	214505	125856	2483901
2	TT	121733	133771	175009	43277	26138	499928
3	TTT	28758	32161	42824	10632	6575	120950
4	TTTT	8276	9236	12467	3001	1908	34888
5	TTTTT	2118	2382	3403	785	483	9171
6	TTTTTT	524	558	830	193	112	2217
7	TTTTTTT	124	134	230	38	23	549
8	TTTTTTTT	26	42	54	8	3	133
9	TTTTTTTTT	7	15	11	2	0	35
10	TTTTTTTTTT	2	3	1	0	0	6
11	TTTTTTTTTTT	0	1	0	0	0	1

4. DISCUSSION

When the nucleotide repeats in *Babesiabigemina*were observed then it was found that these repeats occurs in different numbers. Some repeats are found in large numbers and some are found in low numbers. When dinucleotides were observed then it was found that GT pair is most abundant and TA pair is least abundant in genome. In the case of trinucleotides TGC pair was found to be most abundant and GGG pair was found to be least abundant. Among tetranucleotides AGCA, TGCA, GCTG, CAGC pairs were present in large number and ACTA, TTAG, GGGG, CTAG pairs were present in lowest number. Different multinucleotides were also observed in genome. It was observed that among the multinucleotides of A, T, G and C are least abundantly present in genome.

5. CONCLUSION

From the study of nucleotide repeats of *Babesiabigemina*, it is concluded that nucleotides are not found in single form in the genome, rather they are present in combinations. These combinations can be of two, three, four or multiple nucleotides and results in the formation of dinucleotides, trinucleotides, tetranucleotides and mutinucleotides. All these combinations occur in different numbers in genome.

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